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Genetic Control of Floral Transition in Cereals

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The transition from vegetative to reproductive phase is of great fundamental and applied interest but is still poorly understood. Recently genetic-molecular approaches have been used to dissect this process in *Arabidopsis*. As the genes controlling floral induction in *Arabidopsis* become better defined, there is a need to address how they correspond to genes that regulate flowering in other agronomically important species. A focused effort on comparative mapping will be required to establish the potential correspondence of different genes in different species. Isolation of putative orthologs in different species and mutant's expression patterns reveal evolutionary conserved elements in flower development pathway. Here, overviewed with respect to the recent progress is molecular and genetic approaches for the elucidation of the mechanisms controlling reproductive development of rice and other grass species.

Key Words: ABC model, MADS-box, Flower development, *Arabidopsis*, Rice

Introduction

After seed germination, morphogenesis in higher plants originates from shoot and root apical meristem. After a certain phase of vegetative growth, the transition to flowering is brought about by the concerted action of endogenous and environmental factors that synchronize plants of a given species to ensure their reproductive development under optimal conditions. The most important environmental factors that control flower induction are low temperatures (vernalization) and the length of the day light period (photoperiodism). Whereas the vernalization temperature is recognized by the shoot apical meristem, flower induction by a favourable day length takes place in the leaves. In photoperiodic plants growing under the appropriate day length, a flowering stimulus is released from the leaves and transported to the apical meristem (Bernier *et al.*, 1993). If the apical meristem is competent to respond to this signal, the vegetative meristem becomes either an inflorescence or a floral meristem, from which floral development continues.

Although different plant species exhibit a wide range of flowering responses to environmental and developmental signals, physiological and genetic studies indicate that some of the basic mechanisms controlling flowering time may be conserved. Genetic analyses have revealed that single gene differences can alter the flowering response type; for example mutations that introduce or eliminate an effect of photoperiod on flowering have been described in tobacco (Allard, 1919), maize (Galinat and Naylor, 1951), pea (Murfet, 1989),

sorghum (Quinby and Karper, 1945) and *Arabidopsis* (Zagotta *et al.*, 1992). A mutation in gibberellin biosynthesis has recently been shown to inhibit the ability of *Arabidopsis* to flower in noninductive photoperiods (Wilson *et al.*, 1992).

Unlike many developmental transitions in animals, the shoot apical meristem (SAM) of plants is not irreversibly "committed" to reproductive development once flowering commences. In some species and genotypes under certain environmental conditions, leafy shoots are formed after flowers in a phenomenon known as "inflorescence reversion" (Battey and Lyndon, 1990). This observation implies that the genes and processes involved in the transition to flowering are required to both initiate and maintain reproductive development.

Studies beginning in the early 1980s of mutations in *Arabidopsis* that alter either floral induction or floral meristem fate or floral organ fate were starting points for analysis of molecular genetics of flowering (Raghavan, 2001). In *Arabidopsis*, upon seed germination the shoot apical meristem (SAM) produces on its flanks primordia/meristems for leaves. The leaves are generated in spiral fashion and are separated by short lengths of stem (internode). Upon floral induction, SAM reorganizes to form an inflorescence meristem that first produces a few spirally placed leaf primordia with axillary second order inflorescence meristems. These leaves are called cauline leaves and will be separated by long internodes. After this, the inflorescence meristem produces meristems for individual flowers, again in spiral fashion. The floral

meristem is determinate in its development. Each floral meristem specifies formation of concentric rings of floral organ primordia in an invariant order: sepals, petals, stamens and carpels from periphery to the centre of the flower. The result is a plant with a basal rosette of leaves and racemose inflorescence, where individual flowers bear organs in the pattern (sepals) 4, (petals) 4, (stamens) 6 and (carpels) 2.

From a genetic perspective, two phenotypic changes that control vegetative and floral growth are programmed in the plant. The first genetic change involves the switch from the vegetative to the floral state. If this genetic change is not functioning properly, then flowering will not occur. The second genetic event follows the commitment of the plant to form flowers. The observation that the organs of the plant develop in a sequential manner suggests that a genetic mechanism exists in which a series of genes are sequentially turned on and off. This switching is necessary for each whorl to obtain its final unique identity.

A series of *Arabidopsis* mutants have been identified in which normal flowers are replaced with structures that resemble inflorescence meristems and the shoots that normally develop from them. One such mutant is *LEAFY*. *LEAFY* mutants often do not develop floral meristems and late flowers lack petals and stamens. This gene must be involved in the development of these flower organs (Weigel *et al.*, 1992). The analogous gene in snapdragon to *LEAFY* is *floricaula (flo)*. *flo* mutants also fail to undergo transition from inflorescence to floral meristem, and the flowers have the appearance of an inflorescence shoot. *flo* does differ from *LEAFY* with regards to organ development in that it does not appear to affect petal and stamen development (Coen *et al.*, 1990). This clearly shows a functional deviation during the evolution of the two species.

Flowers of *APETALA1* mutants express a partial inflorescence meristem phenotype where secondary floral meristems appear in the axis region of the sepal. But when the *APETALA1* and *LEAFY* mutants are combined, the flowers appear as an inflorescence shoot. *APETALA1* also affects the normal development of sepals and petals (Greg *et al.*, 2001). The snapdragon analog to the *APETALA1* gene, *SQUAMOSA* (Mandel *et al.*, 1992) is much more severe, and the flowers appear as inflorescence shoots. Another gene, *CAULIFLOWER*, does not express its effects unless coupled with another mutant. *CAULIFLOWER* and *APETALA1* double mutants have inflorescence meristems developing in place of floral

meristems. Phenotypic functions maintained by the *CAULIFLOWER* gene are duplicated by *APETALA1*. The *ap2* mutations also enhance flower meristem defects of *ap1* and *lfy* mutants, indicating that *ap2* also contributes floral meristem identity.

In *Arabidopsis*, *TERMINAL FLOWER1 (TFL1)* and its *Antirrhinum* ortholog *CENTRORADIALIS (CEN)*, respectively, are required for the inflorescence meristem to maintain its indeterminate growth fate. Mutations in *TFL1* and *CEN* result in the inflorescence meristem becoming a terminal flower. In *Arabidopsis*, *TFL1* inhibits the expression of *LFY* and *AP1* at the centre of the shoot apex to prevent the inflorescence meristem from becoming a floral meristem (Liljegren *et al.*, 1999); in turn *LFY* and *AP1* inhibit *TFL1* expression in the lateral meristems committed to a floral fate.

The ABC Model of Flower Development

The flowers of well studied dicot species like *Arabidopsis* and *Antirrhinum* consist of four whorls with, from outside to inside, the sepals, petals, stamens and carpels. The determination of the identity of these floral organs has been extensively studied. In these two species using homeotic flower mutants and these studies resulted in the formation of so called ABC model (Weigel and Meyerowitz, 1994). This model proposes that floral organ identity is regulated by three classes of master genes, A, B and C. These genes act in over lapping domains, each of which extends over two adjacent whorls. The model suggests that the A and C functions specify sepals and carpels, respectively, whereas the combined activities of A and B, and B and C specify petals and stamens, respectively. The model further suggests that the A and C activities are mutually antagonistic, such that in class A loss of function mutants, the C domain expands to include all whorls, the converse occurring in class C loss of function mutants. The proposed domains of A, B and C gene actions were supported by the observed expression patterns for the several of the cloned homeotic genes in wild type flowers as well as flowers mutant for one A, B or C function; this being the case for the *Arabidopsis* *AP1*, *AG*, *PI*, *AP3*, and as well the *Antirrhinum* *SQUA*, *DEFA*, *GLO* and *PLE* genes. Therefore, organ identity is controlled to great extent at the level of transcription of these regulators in specific domains of the floral meristem (Raghavan, 2001). The model was later extended to *Arabidopsis* and *Petunia* with the class D genes, necessary for ovule development (ABCD model) (Colombo *et al.*, 1995) and with class E

genes (*SEP* genes) indispensable for the determination of petal, stamen, carpel and ovule identity.

Examples of A, B, and C group genes involved in flowering, these have been identified in *Arabidopsis thaliana*.

A group	<i>APETALA1 (AP1)</i> and <i>APETALA2 (AP2)</i>
B group	<i>APETALA3 (AP3)</i> and <i>PISTILLATA (PI)</i>
C group	<i>AGAMOUS (AG)</i>

Floral Organ Identity genes

The two A function genes are *APETALA2* and *APETALA1*. Alleles of these two genes have been isolated that show varying degrees of effect, but in general if an A function gene is mutated, the first whorl develops as a carpel and the second whorl develops as a stamen. *ovulata* is an A function gene of snapdragon similar to *APETALA2*. The B gene functions are defined by the genes *APETALA3* and *PISTILLATA*. The net effect of B gene mutations is that whorl 2 develops as a sepal rather than a petal, and whorl 3 develops as a carpel not a stamen. *deficiency* and *globosa* are snapdragon genes that have homologous functions to the *Arabidopsis* B function genes (Sommer *et al.*, 1990)

Finally, C gene functions are defined by the gene *AGAMOUS*. Mutants of this gene have the third whorl stamen replaced by a petal, and the fourth whorl develops into a new flower with the sepal-petal-petal pattern. Furthermore, flower development in *AGAMOUS* mutants is indeterminate, not determinate. A snapdragon gene similar to *AGAMOUS* is *pleniflora*.

Phenotype				
Mutation	Whorl 1	Whorl 2	Whorl 3	Whorl 4
Wild Type	Sepal	Petal	Stamen	Carpel
A Function	Carpel	Stamen	Stamen	Carpel
B Function	Sepal	Sepal	Carpel	Carpel
C Function	Sepal	Petal	Petal	New Flower

The genetic model predicts that the A organ identity genes will be expressed in the tissues from which sepals and petals are derived. Although *APETALA2* is classified as an A function gene (Jofuku *et al.*, 1994), mutants of this genes also affect stamen and carpel development. This gene is shown to be expressed in all four whorls. The

expression of the other A gene, *APETALA1* appears to be restricted to whorls 1 and 2, which is consistent with mutant patterns. The genetic model has also suggested that C organ identity genes are negatively regulated by the expression of A genes. This would lead to a hypothesis stating that the expression of C genes such as *AGAMOUS* would not appear in cells giving rise A function organs. *In situ* hybridizations with the *AGAMOUS* genes demonstrated that early expression of this gene is restricted to whorls 3 and 4.

B gene function genes have been suggested to control petal and stamen function (whorl 2 and 3, respectively) (Goto and Meyerowitz, 1994). Both *APETALA3* and *PISTILLATA* are found to be expressed in the appropriate whorls. *PISTILLATA* though is also found to be expressed in whorl 4 that gives rise to carpels.

Later in development, the expression of *AGAMOUS* is restricted to specific cell types. In stamens, the gene is not found in any cells that give rise to the pollen, nor it is expressed in the pollen grain itself. And in the carpel cells, *AGAMOUS* is only expressed in the outer cells of the ovule.

<i>Arabidopsis</i>	Snapdragon (<i>Antirrhinum majus</i>)
LEAFY	FLORICAULA
<i>APETALA1</i>	<i>SQUAMOSA</i>
<i>APETALA 3</i>	<i>DEFICIENS</i>
<i>PISTILLATA</i>	<i>GLOBOSA</i>
<i>AGAMOUS</i>	<i>PLENIFLORA/FARINELLI</i>

Several conclusions can be drawn regarding the functions of these genes by studying single and double mutants. Because a mutation of an A function gene results in the expression of organ phenotypes controlled by C function genes, it appears that A gene functions repress the expression of the C gene functions in the whorls giving rise to sepals and petals. Likewise, the appearance of the petal in the third whorl of C gene mutants, suggest that C genes repress the activities of A genes in the organs that they control. These conclusions are based on single mutants. For example, *APETALA2* A function mutants develop C function organs, carpels and stamens, in the first two whorls, respectively. A and C double mutant would not be expected to have any functions exclusively controlled by the A and C function genes. And indeed this is what was seen when the *APETALA2/AGAMOUS* double mutant was developed. The first whorl develops as a leaf and the second whorl has stamen-like petals. This second whorl phenotype of this mutant is the result of the activities of the B gene functions. A, B and C

function triple mutant would have no genes functioning that determine normal floral organ development. As expected, the triple mutants lack any floral organs, and the flower essentially consists of leaves developing from each of the whorls.

In *Arabidopsis*, A-function (specification of sepal and petal identity) is attributed to two unrelated genes, *APETALA1* (*AP1*) and *APETALA2* (*AP2*). An examination of the available information regarding orthologues and paralogues of these genes in other species shows that although some are required for sepal identity, none is required for both sepal and petal identity. Combined with phylogenetic analyses that show gene duplication and loss specific to Brassicaceae, this suggests that the two-whorl phenotype attributed to loss of A-function in *Arabidopsis* may be unique to Brassicaceae. Furthermore, all genes that are required for proper sepal identity, including *AP1* and *AP2*, are also implicated in floral meristem identity, suggesting that these two functions may not be separable. Available data are all consistent with a previous *Antirrhinum*-based model for floral organ identity that required only two gene functions. The loss of sepal identity seen in some *AP1*- and *AP2*-lineage mutants can be explained as loss of floral meristem identity; the available evidence suggests that a discrete perianth identity gene function is not required (Amy Litt, 2007).

The ABCDE Model

The ABC model (Coen and Meyerowitz, 1991) proposes that class A genes specify sepals and, together with class B genes, specify petals. Class B and C genes specify stamens, and C alone determines the identity of carpels. The model was later extended, both in *Arabidopsis* and *Petunia*, with the class D genes, necessary for ovule development and with class E genes (*SEP* genes), indispensable for the determination of petal, stamen, carpel, and ovule identity.

In *Arabidopsis* the class D gene is *SEEDSTICK* (*STK*), which is like *FBP7* and *FBP11* specifically expressed in ovules (Pinyopich *et al.*, 2003; Favaro *et al.*, 2003). In *Arabidopsis* class E genes or *SEPALLATA* (*SEP*) genes consist of four members, *SEP1*, *SEP2*, *SEP3*, and *SEP4*, encoding MADS-box factors that show partial redundant functions in floral organ identity determination. The triple knock-out *SEP1*, *SEP2* and *SEP3* has indeterminate flowers with petals, stamens, and carpels homeotically transformed into sepals. Class B and C expression was not altered in the sep triple mutant which shows that *SEP* genes do not act down-stream of B and C

genes and that they are not required for the activation of these genes (Pelaz *et al.*, 2000). Recently, a *SEP1 SEP2 SEP3 SEP4* quadruple mutant was described in which all floral organs were transformed into organs similar to leaves (Ditta *et al.*, 2004). These results show that the *SEP* genes are necessary for the function of class A, B, and C genes since the quadruple *SEP1 SEP2, SEP3, SEP4* mutant phenocopies the *abc* triple mutant. The majority of the class A, B, C, D, and E homeotic genes belong to the MADS box transcription factor family and they are characterized by a typical modular structure

The MADS box (M), a highly conserved DNA-binding domain, is located at the N terminus. This domain is followed by a less conserved I region (I) and by the moderately conserved K box (K; keratin-like coiled-coil structure), both important for dimerization. The C terminus (C) is the most variable part and is involved in ternary complex formation and transcriptional activation (Egea-Cortines *et al.*, 1999). The ABC model has been shown to be widely applicable in dicot species (Pnueli *et al.*, 1994; Kater *et al.*, 1998; Berbel *et al.*, 2001; Kater *et al.*, 2001; Immink *et al.*, 2003).

Furthermore, MADS box genes that are homologous to the dicot (*Arabidopsis thaliana* and *Antirrhinum majus*) ABC genes have also been identified in monocot species including rice, maize, barley and orchids (Mena *et al.*, 1995; Ambrose *et al.*, 2000; Jeon *et al.*, 2000a; Lim *et al.*, 2000; Schmitz *et al.*, 2000; Fornara *et al.*, 2003; Xiao *et al.*, 2003).

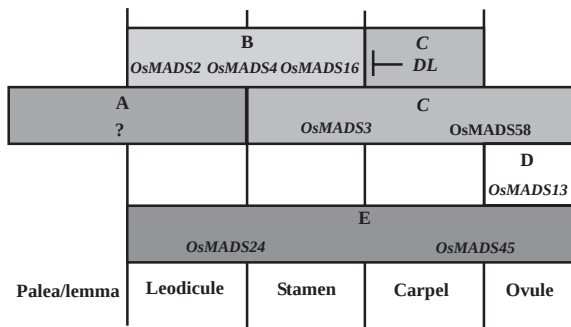
MADS-Box genes

The coding regions of most of the floral regulatory genes share nucleotide and amino acid sequence similarities with the DNA binding and dimerization domains of two previously identified transcription factors: *Mini Chromosome Maintenance* gene product of yeast (*MCM1*) and mammalian *Serum Response Factor* (*SRF*). This region of homology has been termed MADS box that stands for *MCM1*, *AG*, *DEFA*, *SRF* genes that are important developmental regulators found first in animals and yeast, and subsequently in plants. Each of these genes contains a 56 amino acid that is necessary for the protein to bind to DNA. This sequence is located near amino terminal end of the protein. The plant MADS domain containing proteins have additional with moderate sequence similarity. One such is the K domain, with predicted structural similarity to the intermediate filament protein Keratin. The predicted role for the K domain is to mediate protein-protein interactions. In addition, plant

MADS domain proteins have two divergent regions, the I region (for Inter domain) that lies between the MADS and K domain, and the C region that contributes the most C-terminal portion of the protein.

ABCDE Model for Rice

In recent years the ABC model has been extended with two classes of genes, named class D and E genes. Class D genes control ovule identity and were first identified in *Petunia* where they have been termed *FLORAL BINDING PROTEIN 7 (FBP7)* and *FBP11* (Angenent and Colombo, 1996). These two genes are both necessary and sufficient to determine ovule identity in *Petunia* flowers, since co suppression of both genes caused loss of ovule identity whereas ectopic expression resulted in ectopic ovule formation on sepals and petals.



ABCDE model for rice (Martin *et al.*, 2006)

Class A genes

In the rice genome there are four genes that encode such *FUL*-like proteins, *OsMADS14*, *OsMADS15*, *OsMADS18*, and *OsMADS20*. *OsMADS14* (Moon *et al.*, 1999) represents most likely the genes named *FDRMADS6* (Jia *et al.*, 2000) and *RAP1B* (Kyojuka *et al.*, 2000). Its expression is restricted to inflorescences and developing kernels.

Class B genes

GLO- (*Os-MADS2* and *OsMADS4*) and *DEF*-like (*OsMADS16*) genes have been identified in rice (Chung *et al.*, 1995; Moon *et al.*, 1999). *OsMADS16* is also named *SUPERWOMAN1 (SPW1)* and is specifically expressed in lodicules and stamens (Moon *et al.*, 1999; Nagasawa *et al.*, 2003). Recessive mutations in *SPW1* transform stamens into carpels and lodicules into palea- or outer bract like organs.

Class C genes

In *Arabidopsis* there is one typical class C gene which is *AGAMOUS (AG)*. An *AG* flower develops petals instead

of stamens and in the centre of the flower a new *AG* flower develops instead of the pistil which shows that the *AG* gene, as proposed by the ABC model, is necessary for specifying stamen and carpel identity and for floral determinacy.

In the rice genome four *AG*-like genes have been found, termed *OsMADS3* (Kang *et al.*, 1995), *OsMADS58* (Yamaguchi *et al.*, 2006), *OsMADS13* (Lopez-Dee *et al.*, 1999), and *OsMADS21* (Lee *et al.*, 2003). The expression of *OsMADS3* and *OsMADS58* is restricted to stamens and carpels which suggest that they might have functions similar to class C genes (Kang *et al.*, 1995; Kyojuka *et al.*, 2000; Yamaguchi *et al.*, 2006). However, the temporal expression of these two genes is quite different. *OsMADS3* is mainly expressed in stamen, carpel, and ovule primordia, but its expression is excluded when these organs differentiate. In rice plants in which *OsMADS3* was silenced by an antisense approach, partial transformations of stamens into lodicules were observed, while carpels were replaced by abnormal flowers with undifferentiated stamens and carpels (Kang *et al.*, 1998).

Class D genes

In rice, based on phylogenetic reconstruction, two *AG* like genes belonging to the class D gene lineage have been identified, namely *OsMADS13* (Lopez-Dee *et al.*, 1999) and *OsMADS21* (Lee *et al.*, 2003). *OsMADS13* is specifically expressed in the ovule with an expression pattern very similar to *STK (Arabidopsis)*. RT-PCR analysis showed that *OsMADS21* is only expressed in developing seeds (Lee *et al.*, 2003). However, *in situ* analysis suggests that *OsMADS21* is also weakly expressed in the carpel wall and ovules.

Class E genes

In line with the ABC nomenclature this new class of floral-organ-identity genes were termed E-function genes (Theissen, 2001). Phylogenetic analysis clusters these class E genes together in the so-called *SEP* clade (previously called *AGL2* clade). In rice five *SEP*-like genes have been identified, which are *OsMADS1*, *OsMADS5*, *OsMADS24* (allelic to *OsMADS8*), *OsMADS34* (allelic to *OsMADS19*), and *OsMADS45* (allelic to *OsMADS7*) (Kang and An, 1997; Kang *et al.*, 1997; Pelucchi *et al.*, 2002; Malcomber and Kellogg, 2004).

Of these five *SEP*-like genes *OsMADS1* is the one that has been studied in most detail (Jeon *et al.*, 2000; Lim *et al.*, 2000; Prasad *et al.*, 2005; Malcomber and

Kellogg, 2004; Agrawal *et al.*, 2005; Chen *et al.*, 2006). Mutations at amino acid positions 24 and 27 in the MADS domain of *OsMADS1* were found to cause the leafy hull sterile 1 (*lhs1*) mutant phenotype in rice (Jeon *et al.*, 2000).

Rice, a model cereal

Rice (*Oryza sativa* L.) is the cereal that has been selected to be sequenced as a priority. It has the smallest genome of all the cereals: 430 million nucleotides. The corn genome is five times larger, and that of wheat, 40 times larger. However, preliminary comparisons between different cereal genomes revealed large blocks of homologous genes whose order is relatively conserved. This phenomenon, which is known as synteny, makes rice a good entry point for characterizing the genes of other cereals, and associating them with various agronomic traits. Furthermore, rice can serve as a model genome for one of the two main groups of flowering plants, the monocotyledons, in the same way as *Arabidopsis thaliana* is the model for the other group, the dicotyledons.

Rice reproductive development

Rice reproductive development exhibits several features that are not observed in *Arabidopsis*. One big difference between rice and *Arabidopsis* is found in their photoperiodic responses. Transition to the reproductive phase is induced under short day (SD) conditions in rice, whereas it is enhanced under long day (LD) in *Arabidopsis*. Differences in their inflorescence morphologies are also of great interest.

Rice inflorescence development

The grass inflorescence, called either spike or panicle, according to its branching pattern, is formed from the original apical meristem at the top of the plant. Rice inflorescence is a panicle because it is highly branched. In grass species, flowers, called florets, are produced into a group that is enclosed by a pair of small leaf like structures called glumes. Only a single floret is formed in rice or a barley spikelet.

The genetics of inflorescence and flower development in maize and other grasses has been recently reviewed by other authors (McSteen *et al.*, 2000; Bommert *et al.*, 2005). The basic unit of grass inflorescence architecture is the spikelet, a compact axillary branch that consists of two bracts subtending one to several reduced flowers (Clifford, 1987). Maize is a monoecious plant that produces male flowers on a terminal tassel and female flowers on lateral ears, which arise in the axils of vegetative leaves. The tassel initiates several long, indeterminate branches at the base while the ear consists

of a single spike with no long branches. The tassel's main spike and branches, and the entire ear, produce short branches (spikelet pairs) that bear two spikelets. The branches and spikelet pairs arise in the axils of small, undeveloped leaves referred to as bracts. In maize, spikelet and spikelet pair meristems are considered determinate because they produce a defined number of organs (Vollbrecht *et al.*, 2005).

Maize and rice appear to have conserved mechanisms of meristem maintenance and organ identity. Other pathways, such as sex determination, are likely to be found only in maize with its separate male and female flowers. A rich genetic history has resulted in a large collection of maize mutants. The advent of genomic tools and synteny across the grasses now permits the isolation of the genes behind inflorescence architecture and the ability to compare function across the Angiosperms (Esteban Bortiri and Sarah Hake, 2007).

Genes involved in floral transition in rice

Recently, several genes involved in the determination of flowering time have been isolated from rice. *Hd1* and *Hd6* correspond to quantitative trait loci (QTLs) controlling the heading date of rice (Yano *et al.*, 2000). *Hd1* encodes a homolog of *CONSTANS* (*CO*), which functions on the photoperiodic control of flowering in *Arabidopsis*. *Hd1* might function in the promotion of flowering under SD conditions and inhibition under LD conditions. *Hd6* is a weaker QTL than *Hd1*. It encodes a sub unit of casein kinase 2 (*CK2*) which is important for photoperiodism. In the *photoperiodic sensitivity5* (*se5*) mutant of rice, photoperiod sensitivity is completely lost, which results in very early flowering under both SD and LD (Yokoo and Okuno, 1993). Photoperiod response is not greatly altered in the loss of function mutants of *HY1*, a putative *se5* ortholog in *Arabidopsis*.

Meristem identity genes in rice

Putative orthologs of dicot floral meristem identity genes have been isolated from several grass species. Two MADS box genes *RAP1A* and *RAP2B* were isolated (Kyoizuka *et al.*, 2000). They are having extensive sequence similarities to *AP1*. The *RAP1A* was specifically expressed in very young floral meristems and outer whorls of the young rice floret, as *AP1* in *Arabidopsis*. On the other hand, the expression pattern of *RFL*, rice *LFY* was distinct from that of *LFY*. *RFL* expression started in the inflorescence meristem from a very early stage of rice panicle development, whereas *LFY* is expressed in floral meristems. Ectopic expression of *LFY* in *Arabidopsis* confers a striking change in the inflorescence form from

indeterminate to determinate with production of a terminal flower in addition to an extreme early flowering phenotype (Weigel and Nilsson, 1995). In contrast, ectopic expression of a same gene in rice did not cause a dramatic change in panicle morphology but only conferred weak early flowering phenotypes. *LFY* homology was isolated from rice and rye grass. *RFL* of rice is divergent from *Arabidopsis LFY* gene.

In rice *FZP2* (Himi *et al.*, 2001) mutant plants, spikelets are led to the indeterminate generation of meristems to inflorescence shoots, as shown in the *lfy* mutants as well as mutants of *LFY* orthologs in other dicot species.

Determinacy of meristems in rice

The determinacy of the meristem is an important feature for the establishment of the inflorescence structure. When the growth of the main axis ends in a flower, the inflorescence is classified as determinate, whereas in an indeterminate inflorescence, the main axis continues to produce lateral structures without turning into a terminal flower. The primary and secondary inflorescences of *Arabidopsis* do not produce a terminal flower. Thus, *Arabidopsis* inflorescences are indeterminate. This is also the case in maize inflorescence. Rice has determinate inflorescence.

There are several possibilities to explain the mechanism that controls the production of the terminal flower in the rice panicle.

1. *TFL1* functions may be lacking
2. *TFL1* functions are present in rice; however owing to the divergence in their expression pattern, they do not prevent the expression of floral meristem identity genes at the centre of the shoot apex, allowing the formation of a terminal flower.
3. Over expression of rice *TFL1* homologs in transgenic rice plants causes delay in the transition from the vegetative to the reproductive phase and from branch shoot to floral meristems (Ratcliffe *et al.*, 1998).

LFY homologs in various genera

<i>LFY</i>	-	<i>Arabidopsis</i>
<i>RFL</i>	-	Rice
<i>LOLIUM LFY</i>	-	Lolium
<i>PRFLL</i>	-	Pinus
<i>NEEDY</i>	-	Pinus
<i>UNI</i>	-	Pisum
<i>NFL1, NFL2</i>	-	Nicotiana
<i>ALF</i>	-	Petunia
<i>FLO</i>	-	<i>Antirrhinum</i>

The determinacy of spikelet meristem is controlled

by *IDS* gene in maize. In the *indeterminate spikelet (IDS)* mutant, the spikelet meristem acquires a partial indeterminacy, leading to the production of additional florets in a single spikelet instead of the two florets observed in normal maize spikelets. The *IDS1* gene was cloned and shown to have a strong homology to *APETALA2* although it is still unclear whether it is the closest homology of *APETALA2* in maize (Jofuku *et al.*, 1994).

The determinacy of floral meristem of *Arabidopsis* is controlled by *AGAMOUS (AG)*. Rice and maize orthologs have been isolated and their loss of function phenotypes reported. Reduction of floral meristem determinacy was observed in maize and rice plants, in which *AG* orthologs, *ZAG1* and *OsMADS3*, respectively was decreased (Mena *et al.*, 1996).

Genes Involved in Floral Organ Development

Grass species have flowers with highly derived structures. Basic mechanisms of flower development are probably conserved between grasses and dicots; therefore ABC Model can be extended to grass species.

The expression pattern of putative rice and maize class B and class C genes strongly suggest the applicability of the ABC model to grass species. In the mutant of maize *AP3* ortholog, *Silky1 (sil1)*, stamens and lodicules are homeotically transformed into carpels and palea/lemma like structures respectively (Ambrose *et al.*, 2000). Reduction of rice *PI* ortholog (*OsMADS4*) function by antisense methods also resulted in similar phenotype. These findings imply that there is a homologous relationship between lodicules and petals and that the B function is conserved in grass flowers.

In rice, homeotic conversion from lodicules to stamens is caused by the ectopic expression of *OsMADS3*, a rice *AG* ortholog, by a strong *Actin1* promoter. This added further strong evidence for the interpretation of the lodicule's identity. However, in contrast to the progress made toward understanding the identity of lodicules, the nature of lemma and palea is still unclear. The expression pattern of *RAP1A* and the phenotype of *sil1* mutant suggest that the palea/lemma are probably the equivalent of the sepals. To confirm this assumption, analysis of loss of function mutants of the grass class A genes is necessary.

MADS Box genes in rice

MADS box genes	Family
Os MADS1, Os MADS5	AGL2
Os MADS7 and Os MADS8	
Os MADS2 and Os MADS4	GLO
Os MADS3	AGAMOUS

OsMADS1

OsMADS1 is also involved in the determinacy of a floret. It is most similar to *AGL2*, *AGL4*, *AP1* and *SQUA*. The *OsMADS1* gene is actively expressed at the young inflorescence stage, and the expression continues into the early and vacuolated pollen stage (Chung *et al.*, 1994) and it is initially expressed in young flower primordia but becomes more localized in the palea, lemma and ovary at later developmental stages. Vegetative tissues do not show any expression of the gene. Ectopic expression of the *OsMADS1* in homologous and heterologous plants results in early flowering. Therefore it is likely that the rice *OsMADS1* product regulates expression of genes involved in the induction of flowers.

Its expression pattern is most similar to *AP1* and *SQUA*. Southern blot analysis revealed that there are at least ten genes which share a significant homology with *OsMADS1*. Over expression of *OsMADS1* results in an extremely early flowering phenotype. Although *RAP1A* and *RAP1B* are closer to *AP1* than *OsMADS1* on the basis of their sequence, *OsMADS1* seems to have a closer function than *AP1* with respect to its function. The *OsMADS1* amino acid sequences shows 56.2% identity to *AGL2* and 44.4% identity to *AP1* (Chung *et al.*, 1994).

OsMADS3

OsMADS3 is an AG homologue in both AG gene from *Arabidopsis* and PL gene from *Antirrhinum* share similarities in amino acid sequences, expression patterns and effects of ectopic expression. The transgenic plants expressing the antisense *OsMADS3* transcript produced abnormal flowers and sterile seeds. Flowers of these plants showed homeotic alterations in their carpels and stamens. In the fourth whorl carpel is replaced by several abnormal flowers with undifferentiated stamens and carpels. The third whorl stamen was changed into lodicule like structure. Such alterations in the inner two whorls of the flower are similar to the phenotypes of *Arabidopsis* AG mutants and *Antirrhinum* PLE mutants (Kang *et al.*, 1998).

OsMADS4

Antisense expression of the *OsMADS4* gene caused the lodicules to change so that they resembled the palea/lemma like organs and stamens changed to carpel like organs. In dicots, an alteration of petals towards sepal is a typical phenotype in the mutants that have lost the class B organ identity genes. Therefore, the observations are consistent with the hypothesis that the palea/lemma and sepals have a common ancestry (Krizek and Meyerowitz,

1996).

The *OsMADS4* protein is most homologous to *GLO* (54%) and *PI* (51%) and the homology was much lower with *AP3* (35%) and *DEF* (32%). However, the expression pattern of *OsMADS4* was more similar to *DEF*, since the *OsMADS4* transcript is present in the fourth whorl.

OsMADS14 and -15

Two MADS box *OsMADS14* and -15 were highly homologous to the maize MADS box gene *ZAP1* which is an orthologue of the floral homeotic gene *APETALA1* (*AP1*). These were identified by their identification with *OsMADS1* in the yeast two hybrid system. It was supposed that these two proteins were major *OsMADS1*-binding proteins expressed at the early stage of rice flower development, since only these genes were repeatedly found during the two hybrid screening process using a cDNA library generated from mRNAs of young rice flowers (Lim *et al.*, 2000). The *OsMADS15* protein shows high similarity to *OsMADS14* and *ZAP1* (Mena *et al.*, 1995). The amino acid sequence comparison of *OsMADS15* revealed 66% sequence identity and 67% sequence homology to *ZAP1*.

OsMADS16

OsMADS16 gene was isolated by yeast two-hybrid screening using *OsMADS4* as bait. The protein is most homologous to various MADS genes of *AP3* family. In mature floral organs, *OsMADS16* was expressed in lodicules and stamens, whereas *OsMADS4* was in lodicules, stamens, and carpels. These organ specific expression patterns of *OsMADS4* and *OsMADS16* are identical to those *PI* and *AP3*, respectively, indicating functional similarity between these MADS genes (Goto and Meyerowitz, 1994).

Heading date is an important agronomic trait of cereal crops such as rice and early heading varieties are required for certain regions in which rice is cultivated. Constitutive expression of *LEAFY* from the cauliflower mosaic virus 35S promoter caused early flowering in transgenic rice, with a heading date that was 26-34 days earlier than that of wild type plants. Early flowering was accompanied by a small yield penalty and some panicle abnormality (He *et al.*, 2000).

OsMADS18

OsMADS18 from rice (*Oryza sativa*) belongs to the phylogenetically defined *AP1/SQUA* group. The MADS box genes of this group have functions in plant

development, like controlling the transition from vegetative to reproductive growth, determination of floral organ identity, and regulation of fruit maturation. Fabio Fornara *et al.*, 2004 reported the functional analysis of *OsMADS18*. This rice MADS box gene is widely expressed with its transcripts accumulated to higher levels in meristems. Overexpression of *OsMADS18* in rice induced early flowering, and detailed histological analysis revealed that the formation of axillary shoot meristems was accelerated. Silencing of *OsMADS18* using an RNA interference approach did not result in any visible phenotypic alteration, indicating that *OsMADS18* is probably redundant with other MADS box transcription factors. Surprisingly, overexpression of *OsMADS18* in *Arabidopsis* caused a phenotype closely resembling the *ap1* mutant. Yeast two-hybrid experiments showed that some of the natural partners of AP1 interact with *OsMADS18*, suggesting that the *OsMADS18* overexpression phenotype in *Arabidopsis* is likely to be due to the subtraction of AP1 partners from active transcription complexes. Thus, when compared to *AP1*, *OsMADS18* during evolution seems to have conserved the mechanistic properties of protein-protein interactions, although it cannot complement the *AP1* function.

Wheat

The genetic control of floral transition or heading time in wheat (*Triticum aestivum*), is determined by three characters, vernalization requirement, photoperiodic sensitivity and narrow-sense earliness (earliness per se), that is the autonomous promoting pathway (reviewed in Worland and Snape, 2001). Vernalization requirement refers to the sensitivity of the plant to cold treatment for accelerating spike primordium formation, and vernalization insensitivity is controlled mainly by three major genes, *Vrn-A1*, *Vrn-B1* and *Vrn-D1*, earlier designated *Vrn1*, *Vrn2* and *Vrn3* (McIntosh *et al.* 1998), each having two or more allelic forms (Puggsley 1971; Snape *et al.* 1976) located on chromosomes 5A, 5B and 5D, respectively (reviewed in Flood and Halloran, 1986). The photoperiodic (long-day) response is determined by the dominant genes, *Ppd-A1*, *Ppd-B1* and *Ppd-D1* (formerly *Ppd3*, *Ppd2* and *Ppd1*) that control sensitivity to photoperiod. These genes are located on chromosomes 2A, 2B and 2D, respectively (reviewed in Laurie, 1997).

Wheat *APETALA1* homolog *WAP1* identified on the group 5 homoeologous chromosomes is a promising candidate of the *Vrn* genes. The *vrn* and *ppd* genes controlling flowering response provide an example of

genes that can be manipulated to improve adaptation (Halloran, 1975; Pirasteh & Welsh, 1980;). Narrow-sense earliness or earliness per se is the earliness of fully vernalized plants grown under long-day conditions, and involves polygenes with minor effects (G. Ortiz Ferrara, 1998; Koji Murai *et al.*, 2005).

Wheat *APETALA1* (*WAP1*) is a key gene in the regulatory pathway that controls phase transition from vegetative to reproductive growth in common wheat. *WAP1* is an ortholog of the *VRN1* gene that is responsible for vernalization insensitivity in einkorn wheat (*Triticum monococcum*) mutant, *maintained vegetative phase (mvp)*. The *mvp* mutant resulted from deletion of the *VRN1* coding promoter regions, demonstrated that *WAP1/VRN1* is an indispensable gene for phase transition in wheat. Expression analysis of flowering related genes in *mvp* plants indicated that wheat *GIGANTIA (GI)*, *CONSTANS (CO)* and *SUPPRESSOR OF OVER EXPRESSION OF CONSTANS 1 (SOC1)* genes act in a different pathway to *WAP1/VRN1* (Naoki Shitsukawa *et al.*, 2007)

The molecular and genetic bases of the interaction between environmental factors and the floral transition in winter cereals are still unknown. However, the recent identification of the wheat, TaVRT-1 gene provides an opportunity to decipher the molecular basis of the flowering-time regulation in cereals. Kane *et al.*, 2005 described the characterization of another gene, named TaVRT-2, possibly involved in the flowering pathway in wheat. Molecular and phylogenetic analyses indicated that the gene encodes a member of the MADS-box transcription factor family that belongs to a clade responsible for flowering.

Maize

During maize ear and tassel development, male and female organs are initiated, but stamen in ear spikelets and the gynoecium in tassel spikelet do not reach maturity. Some maize MADS box genes have been isolated and exclusive expression in developing ears has been shown for *ZAG2*, where the expression is largely restricted to developing carpels (Schmidt *et al.*, 1993). Other maize MADS box genes are expressed in developing male and female inflorescences.

Two novel maize MADS box cDNAs, *ZmMADS1* and *ZmMADS3*, were isolated after screening cDNA libraries of maize egg cells (EC) and mature pollen. Comparisons of *ZmMADS1* and *ZmMADS3* protein sequences with the other MADS box proteins revealed that *ZmMADS1* can

be classified as a member of the *TM3* subfamily of the MADS box proteins, whereas *ZmMADS3* belongs to the *SQUMOSA* subfamily. *ZmMADS3* exhibits 95% overall AA identity to the maize MADS box protein *ZAP1* (Mena *et al.*, 1995). Transcripts of both the genes *ZmMADS1* and *ZmMADS3* are detectable in egg cells and in *in vivo* zygotes of maize. *ZmMADS1* is additionally expressed in synergids and in central antipodal cells. During early somatic embryogenesis, *ZmMADS1* expression is restricted to cells with the capacity to form somatic embryos and to globular embryos at later stages. During flower development *ZmMADS1* and *ZmMADS3* are co-expressed in all ear spikelet organ primordia at intermediate stages. Among vegetative tissues, *ZmMADS3* is expressed in stem nodes and displays a gradient with highest expression in the uppermost node (Heuer *et al.*, 2001).

The *ZAP1* gene, an *AP1* homologue in maize, was isolated but its function has not been well characterized (Mena *et al.*, 1995). A transposon induced mutation *ZAG1*, the maize *AG* homologue, did not greatly affect the identity of reproductive organs. However, a loss of function experiment showed that the *ZAG1* mutation generated indeterminate floral meristems instead of a carpel in the center of the ear. Northern blot experiments from male and female inflorescences of maize revealed *ZAP1* expression only in non reproductive parts of the florets (Mena *et al.*, 1995).

To elucidate the molecular determinants involved in the process of floral transition, Olga N. Danilevskaya *et al.*, 2008 performed genome-wide RNA expression profiling on maize shoot apices at vegetative and early reproductive stages using massively parallel signature sequencing technology. Profiling revealed two closely related MADS-box genes, *ZMM4* and *ZMM15*, which were significantly up regulated in post transitional apices. *ZMM4* and *ZMM15* are linked to other MADS-box genes and form duplicate gene pairs *ZMM4-ZMM24* and *ZMM15-ZMM31* that are syntenic to the wheat *vernalization1* (*vrn1*) locus that controls the floral transition in winter wheat (*Triticum monococcum*) varieties and similar loci in other cereals in response to a cold treatment (Yan *et al.*, 2005, Messing and Dooner, 2006 and Petersen *et al.*, 2006).

Analyses of temporal and spatial expression patterns indicated that the duplicated pairs *ZMM4-ZMM24* and *ZMM15-ZMM31* are coordinately activated after the floral transition in early developing inflorescences. More

detailed analyses revealed *ZMM4* expression initiates in leaf primordial of vegetative shoot apices and later increases within elongating meristems acquiring inflorescence identity. Expression analysis in late flowering mutants positioned all four genes downstream of the floral activators *indeterminate1* (*id1*) and *delayed flowering1* (*dlf1*). Over expression of *ZMM4* leads to early flowering in transgenic maize and suppresses the late flowering phenotype of both the *id1* and *dlf1* mutations. The results suggest that, *ZMM4* may play roles in both floral induction and inflorescence development.

Barley

Six barley MADS box cDNA clones, *BM1*, *BM3*, *BM5*, *BM7*, *BM8* and *BM9* were isolated and characterized. The derived protein sequences reflect the typical modular structure common to most plant MADS box proteins. Phylogenetic analysis on the basis of conserved MADS domains classified the barley MADS box genes into three subfamilies (Schmitz *et al.*, 2000). *BM3*, *BM5* and *BM8* are members of the *SQUA* subgroup. Highest sequence homologies within this group were found with *BpMADS5* from *Betula pendula* which shares 70% homology to *BM3*. *TaMADS11* from *Triticum aestivum* (Murai *et al.*, 1998) is 96% homologous to *BM5*, and *ZAP1* from *Zea mays* shows 92% homology to *BM8*. The MADS box gene *LtMADS2* from *Lolium temulentum* shows 95% homology to *BM8*.

BM7 and *BM9* are members of *AGL2* subfamily. Database comparison of the predicted *BM7* protein showed 84% homology to *OsMADS1* from *Oryza sativa*, while *BM9* shares 91% homology to the rice gene *OsMADS5*. *BM1* is homologous to genes that form the orphan gene group. Database comparison revealed that the deduced *BM1* protein is most similar to *StMADS16* from *Solanum tuberosum* (Carmona *et al.*, 1998) with 65% overall homology at the protein level.

Expression analysis of the barley MADS box genes revealed expression patterns that are not characteristic of the barley MADS box genes of the *SQUA* subgroup, while expression of *BM7* and *BM9* was largely as expected for *AGL2* subgroup. *BM1* is mainly expressed in vegetative tissues and its primary transcript undergoes alternative splicing such that the corresponding mRNAs differ by two codons. The genes *BM1*, *BM3* and *BM8* were mapped by analysis of single nucleotide polymorphism onto barley chromosomes 4, 2 and 7, respectively. Previously, *BM7* was mapped on chromosome 1 in the vicinity of *nudum*,

a locus 3 cM distant from the *multiovary* mutant (Tazhin, 1980)

BM1 expression resembles that of *StMADS11* with the exception that *BM1* is not exclusively expressed in vegetative tissues, but also in young inflorescences. *BM1* was detected in a single layer present in the first node, which could suggest a role in the regulation of vegetative stem growth. The barley genes *BM3*, *BM5* and *BM8* of the *SQUA* subgroup are abundantly expressed in all organ primordial and the vascular tissue of the barley floret throughout inflorescence development. In contrast to the *BM8*, the transcripts of *BM3* and *BM5* were additionally detected in vegetative tissues (nodes, leaves). In this respect, *BM3* and *BM5* resemble that of *TaMADS11* from wheat (Murai *et al.*, 1998). The observed expression pattern of the barley *AGL2* like genes *BM7* and *BM9* is identical to the homologous rice genes *OsMADS1* and *OsMADS45*, respectively, with the expression that *BM7* transcripts were found additionally in lodicules of barley florets (Greco *et al.*, 1997).

Short Vegetative Phase (SVP)-Like MADS-Box Genes Inhibit Floral Meristem Identity

In *Arabidopsis* (*Arabidopsis thaliana*), the Short Vegetative Phase (SVP) gene encodes a MADS-box transcription factor that delays the floral transition (Hartmann *et al.*, 2000). Mutations that disrupt SVP cause early flowering (Hartmann *et al.*, 2000), whereas ectopic expression of SVP results in late flowering. Ectopic expression of SVP also inhibits floral meristem identity, causing floral abnormalities such as the conversion of sepals and petals to leaf-like structures (Brill and Watson, 2004; Masiero *et al.*, 2004) and causing inflorescence-like structures to develop within flowers (Brill and Watson, 2004). The development of inflorescences within flowers indicates that meristematic cells within the flower have lost floral identity and have formed an inflorescence instead of floral organs, a phenomenon known as floral reversion (Tooke *et al.*, 2005). Presumably, ectopic expression of SVP causes floral reversion by interfering with a mechanism that maintains floral meristem identity.

The *Arabidopsis* gene, *AGAMOUS-LIKE 24* (*AGL24*), is closely related to *SVP* (Yu *et al.*, 2002; Michaels *et al.*, 2003). Unlike *SVP*, *AGL24* promotes the floral transition. Mutations that disrupt *AGL24* cause late flowering, whereas over expression of *AGL24* accelerates flowering (Yu *et al.*, 2002; Michaels *et al.*, 2003). *AGL24* is expressed during vegetative development and is induced by treatments that accelerate floral transition, such as

vernalization (prolonged exposure to low temperatures), long days, or the application of gibberellins (Yu *et al.*, 2002; Michaels *et al.*, 2003). These data suggest that *AGL24* acts to promote floral transition in response to vernalization and long-day conditions (Yu *et al.*, 2002; Michaels *et al.*, 2003). Although *AGL24* has the opposite effect on flowering time compared to *SVP*, plants that ectopically express *AGL24* exhibit floral abnormalities similar to those caused by ectopic expression of *SVP*, and ectopic expression of *AGL24* also causes floral reversion. Thus, *AGL24* promotes the floral transition but inhibits floral meristem identity. It has been suggested that *AGL24* promotes inflorescence meristem identity (Yu *et al.*, 2004).

Analysis of the functions of *Short Vegetative Phase* (*SVP*)-like MADS-box genes in barley (*Hordeum vulgare*) indicated a role in determining meristem identity. Three *SVP*-like genes are expressed in vegetative tissues of barley: Barley *MADS1* (*BM1*), *BM10*, and Vegetative to Reproductive Transition gene 2. These genes are induced by cold but are repressed during floral development. Ectopic expression of *BM1* inhibited spike development and caused floral reversion in barley, with florets at the base of the spike replaced by tillers. Head emergence was delayed in plants that ectopically express *BM1*, primarily by delayed development after the floral transition, but expression levels of the barley *VRN1* gene (*HvVRN1*) were not affected. Ectopic expression of *BM10* inhibited spike development and caused partial floral reversion, where florets at the base of the spike were replaced by inflorescence-like structures, but did not affect heading date. Floral reversion occurred more frequently when *BM1* and *BM10* ectopic expression lines were grown in short-day conditions. *BM1* and *BM10* also inhibited floral development and caused floral reversion when expressed in *Arabidopsis* (*Arabidopsis thaliana*). *SVP*-like genes function to suppress floral meristem identity in winter cereals (Ben Trevaskis *et al.*, 2007)

MADS box genes control vernalization-induced flowering in cereals

Many plants from temperate regions are induced to flower by an extended exposure to low temperature: vernalization. In winter cereal crops, such as wheat and barley, plant breeders have selected for variation in vernalization responsiveness to produce cultivars suited to plantings in different climatic zones. Winter cultivars are sown in autumn, vernalized by the low temperatures of winter, and subsequently flower and develop grain in

spring. Spring cultivars do not require vernalization and usually are planted in the late winter period. The genetics of the vernalization response have been studied in a number of cereals.

In hexaploid bread wheat, where the effects of recessive traits are masked by the redundancy resulting from the three genomes, the dominant *Vrn-1* gene has been found to be the major determinant of vernalization responsiveness. *Vrn-1* is located on chromosome 5 in each of the A, B, and D genomes of wheat. Winter wheats carry only winter *Vrn-1* alleles (*vrn-A1_vrn-B1_vrn-D1*), and without vernalization are late flowering. Spring alleles of *Vrn-1* are dominant and reduce the requirement for vernalization. Spring alleles of the *Vrn-1* gene on the A genome, *Vrn-A1*, have the strongest effect on flowering time, and plants with the *Vrn-A1* spring allele do not require any vernalization (Pugsley, 1971). The effects of spring alleles of the *Vrn-1* genes from the B and D genomes are weaker. Plants that carry *Vrn-B1* or *Vrn-D1* spring alleles (in the absence of a *Vrn-A1* spring allele) flower earlier than winter wheats but still show some acceleration in flowering time when vernalized. Such plants are classed as semispring wheats.

By comparing expression levels of MADS box transcription factor genes between near-isogenic winter and spring lines of bread wheat, *Triticum aestivum*, (Ben Trevaskis *et al.*, 2003) have identified 10 wheat MADS box genes that are expressed in vegetative tissues before the floral transition, including two vernalization-responsive MADS box genes. One of these is the hexaploid wheat orthologue of *TmAP1*, *WAP1*, suggest that this gene corresponds to the *Vrn-1* locus of hexaploid wheat and *WAP1* was identified as the probable candidate for the *Vrn-1* gene, the major locus controlling the vernalization flowering response in wheat. *WAP1* is strongly expressed in spring wheats and moderately expressed in semispring wheats, but is not expressed in winter wheat plants that have not been exposed to vernalization treatment.

Vernalization promotes flowering in winter wheats and strongly induces expression of *WAP1*. *WAP1* is located on chromosome 5 in wheat and, by synteny with other cereal genomes, is likely to be collocated with *Vrn-1*. These results in hexaploid bread wheat cultivars extend the conclusion made by Yan *et al.*, 2003 in the diploid wheat progenitor *Triticum monococcum* that *WAP1* (*TmAP1*) corresponds to the *Vrn-1* gene.

The role of *WAP1*-like genes in controlling the

vernalization response of cereals was further examined in the important (diploid) cereal crop barley. The barley MADS box gene *BM5* shares a high degree of predicted amino acid similarity (95%) with *WAP1* (Schmitz *et al.*, 2000). The barley homologue of *WAP1*, *BM5*, shows a similar pattern of expression to *WAP1* and *TmAP1*. *BM5* is not expressed in winter barleys that have not been vernalized, but as with *WAP1*, expression of *BM5* is strongly induced by vernalization treatment (Murai, K *et al.*, 2002 and Schmitz *et al.*, 2000). In spring barleys, the level of *BM5* expression is determined by interactions between the *Vrn-H1* locus and a second locus for spring habit, *Vrn-H2*.

In cereals, two MADS box proteins with opposite effects appear to be involved in the regulation of the vernalization response. This pathway resembles the vernalization response pathway of *Arabidopsis*, where *SOC1*, a MADS box gene that promotes flowering, is repressed by *FLC*, also a MADS box gene, in plants that have not been vernalized (Lee *et al.*, 2000; Sheldon *et al.*, 1999 and Michaels *et al.*, 1999). No *FLC*-like genes have been identified in cereals, making it unlikely that *Vrn-2* is closely related to *FLC*. There is no evidence that *AP1*-like genes mediate the vernalization response in *Arabidopsis*, but over expression of *AP1* does result in early flowering (Mandel and Yanofsky, 1995). The vernalization response may have evolved separately in the ancestors of the cereals (monocots) and the *Brassicaceae* (dicots) through the recruitment of different MADS box transcription factor genes into a cold regulated switch that promotes flowering in vernalized plants. There is now evidence that *AP1*-like genes determine the time of flowering in a range of cereal and grass species.

Floral Genome Project

Recently a floral genome project was established to extend knowledge of developmental genes known from model species more broadly across a selection of angiosperms (Soltis *et al.*, 2002). This project will generate large EST datasets, capturing thousands of sequences of genes expressed during early flower development in each species families. This will help test the generality of function of already known genes, although genes not yet identified, or those that do not function in the model species, are unapproachable by this strategy (Baum *et al.*, 2002). Baum *et al.*, (2002) argue that a more informative approach would be to develop a wider range of model species in which function is examined in depth. The floral genome project will examine the site and timing of gene

expression for the unique genes detected in each species using a combination of microarray analysis and new methods of high throughput *in situ* hybridization. Expression patterns will be evaluated for hundreds of genes in each species. Already, functional and genomic information is accumulating in other model species, with rice (Shimamoto and Kyoizuka, 2002) and maize (Lawrence *et al.*, 2004) providing divergent monocot information that is intrinsically important as well as allowing comparisons with data from established core eudicots. This data base will provide annotated links to genomic and functional information in *Arabidopsis*, rice and maize, and to expressed gene studies in tomato, maize, and many other important crop species. The floral genome project will provide a key resource for generating hypotheses about common gene functions in plants and potential sources of variation among diverse species.

Advantages

- Harnessing the regulatory genes controlling timing and differentiation of floral organs has opened the potential for increased yield through the manipulation of plant growth and development (Gynheungan, 1994).
- *FPF* gene can be manipulated to alter flowering time; suppression of *FPF* delays flowering, over expression of *FPF* causes earlier floral induction
- Helpful in managing flowering time for optimal flower, fruit and seed production
- Creation of transgenics – time of flowering can be altered (*FLC* genes)
- Suppression of flowering – increase timber, forage, sugarcane production
- Off-season flowering can be induced
- Induction of early flowering – escapes stresses due to biotic and abiotic factors
- Synchronization of flowering – helps in hybrid seed production
- Induce male sterility for the production of hybrids
- Mono sexual plants can be made to bisexual which avoids the need for maintenance of either sex
- Genes determining rice floral morphology have been identified allowing rice spikelet development to be manipulated.
- In wheat, vernalization is controlled by the MADS-box gene *WAP1*. Unlocking vernalization should

allow quality wheat to be produced in warm climates.

- Bolting is another aspect of cold temperature-induced flowering. An anti-bolting MADS-box gene has been identified in Chinese cabbage.
- The main commercial transgenic crops now available are modified for herbicide resistance or insect resistance, the MADS-box constructions are modified with flowering controls or flowering timing, even alterations in yield are contemplated
- The anther-specific transcription regulator can be manipulated to produce male-sterile varieties used to produce high value hybrid seeds.
- A root nodule-specific MADS-box gene was identified in alfalfa root nodules. Transferring nitrogen-fixing ability to non-legumes has been discussed for decades, and this discovery may spur developments in that area
- In rice, for example, MADS-box genes have been identified which control the timing of flowering. As flowering time determines regional adaptability of rice varieties, manipulating that timing will allow greater use of regional varieties.
- Recently a floral transcription factor was found to control the agronomic trait - seed yield.

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Morphological Characterization of Notified Varieties of Cabbage for Conducting DUS Tests

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Six notified varieties of cabbage, viz., Golden Acre, Pusa Mukta, Pusa Drum Head, Pusa Ageti, Pride of India and Kinner Red were characterized morphologically using 21 qualitative and 12 quantitative characters. Except 5 qualitative characters, all exhibited polymorphism between varieties, thus explaining their immense potential for varietal characterization. However, varietal distinctness reference to cumulative characters has an edge over single character. The slight variation, might be due to environment, was apparent in the expression of characters for three consecutive seasons confirming uniformity and stability of the varieties.

Key Words: Cabbage, *Brassica oleracea* L. var. *capitata*, Characterization, Notified varieties

Introduction

Being signatory member of World Trade Organization (WTO), India made provisions for protecting plant varieties. Thus, Indian Government passed an Act “Protection of Plant Varieties and Farmers’ Rights (PPV & FR)” in 2001, which provides the registration of a variety of a crop if it conforms to the criteria of distinctness, uniformity and stability (DUS). The main objective of this is to protect unlawful commercial exploitation of varieties, the rights of farmers and plant breeders, and to strengthen the research activities in this field. Although, different varieties/hybrids of the crop are available but providing genetically pure seed of these varieties is a great challenge. For attaining high genetic purity and avoiding exploitation of varieties, it is imperative to define each variety with suitable descriptors. Moreover, characterization is also desired for their protection under PPV & FR Act.

Cabbage (*Brassica oleracea* L. var. *capitata*) is an important member of family, *Brassicaceae*, which ranks first in production and second in area among cole crops in India (FAO, 2005). Cabbage has been classified into three distinct groups based upon their leaf characters, viz., white cabbage (with almost smooth leaves), red cabbage (with red-purple leaves) and savoy cabbage (blistered and puckered leaves). White cabbage is commonly grown in India but savoy and red cabbages which are less important are mainly grown in Europe. In general, cabbages are distinguished by the formation of a thickened main bud called ‘head’. The shape of heads varies from flat-topped to conical in outline. There are many morphological characters, which help in making distinction between different varieties of cabbage. Thus, the present study was

conducted with the aim to distinguish cabbage varieties using morphological characters for the assessment of distinctness.

Materials and Methods

Genetically pure seeds of six notified varieties of white cabbage, viz., Pusa Ageti, Pusa Drum Head, Pusa Mukta, Golden Acre, Pride of India and one red cabbage variety, namely, Kinner Red were characterized for qualitative and quantitative characters at IARI, Regional Station, Katrain. Pusa Ageti represented sub-tropical origin and rest of the five varieties belongs to the temperate group. The varieties and their sources of availability are given in Table 1.

Available notified varieties of cabbage were grown during Rabi 2004-05, 2005-06 and 2006-07 cropping season with two replications and assessed for 33 different morphological characters on randomly selected five plants as per UPOV guidelines (2004), proposed Indian DUS test guidelines (2004) and Gangopadhyay (2001). Details of parameters and criterion for their assessment are presented in Table 2.

Results and Discussion

The data pertaining to qualitative/ quantitative traits are presented in Table 3. All the varieties included in the present study were of temperate type except Pusa Ageti which represented sub-tropical origin. In the present study, the varieties have shown differences for morphological attributes, hence grouped into different categories, and have been discussed separately to facilitate, distinction among varieties.

Qualitative Characters

The character which distinguished Pusa Drum Head from

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Table 1. Cabbage varieties available for characterization

S.No.	Varieties	Source
1.	Pusa Drum Head, Pusa Mukta, Golden Acre, Pusa Ageti	IARI
2.	Pride of India and Kinner Red	UHF, Solan

Table 2. Detail of parameters and criterion for their assessment

S.No.	Parameters	Type of observation/ optimum stage
1.	Time of initiation of head formation	VS/1
2.	Time of harvest maturity	VS/2
3.	Plant height (cm) (soil surface to tip of the head)	MS/2
4.	Plant: max. diameter (frame size, cm)	MS/2
5.	Outer leaf shape	VS/2
6.	Outer leaf profile of upper side of blade	VS/2
7.	Plant attitude of outer leaves	VS/2
8.	Leaf margin	VS/2
9.	Outer leaf blistering	VS/2
10.	Outer leaf crimping	VS/2
11.	Outer leaf colour (with wax)	VS/2
12.	Outer leaf waxiness	VS/2
13.	Outer leaf incision of margin	VS/2
14.	Outer leaf reflection of margin	VS/2
15.	Outer leaf undulation of margins	VS/2
16.	Head anthocyanin colouration of cover leaf	VS/2
17.	Head colour of cover leaf (external colour)	VS/2
18.	Head cover	VS/2
19.	Head blistering of cover leaf	VS/2
20.	Head compactness	VS/2
21.	Number of non-wrapping leaves	MS/2
22.	Length of outer stem (stalk length) (cm)	MS/2
23.	Outer leaf size (cm)	
	a) Leaf length	
	b) Leaf breadth	MS/2
24.	Head length (cm)	MS/2
25.	Head diameter (cm)	MS/2
26.	Length of interior core stem axis (core length) (cm)	MS/2
27.	Head shape of longitudinal section	VS/2
28.	Head internal colour	VS/2
29.	Head shape of base in longitudinal section	VS/2
30.	Head internal structure	VS/2
31.	Etching type	VS/-
32.	Time of bursting after head maturity	VS/3
33.	Head shape (head index, length/width ratio)	MS/2

VS= Visual assessment of plants or parts of plant, MS= Measurement of plants or parts of plant, 1= Initiation of head formation (50%), 2= Appearance of compact heads (50%), 3= Bolting

rest of the varieties was shape of outer leaf, where as Pusa Drum Head expressed transverse broad elliptic shape in contrast to broad obovate shape in remaining varieties under study. Similarly, Pusa Ageti differed from other varieties by its erect plant attitude, while others had semi-erect attitude. Non-serrated margins were observed only in Pusa Ageti, whereas rest of the varieties had serrated leaf margins. The outer leaves of Golden Acre and Pusa Drum Head were strongly crimped in comparison to Pusa Ageti, Pride of India, Pusa Mukta and Kinner Red. The

colour of outer leaves in Pusa Ageti and Pusa Drum Head was light green in contrast to Pusa Mukta, Pride of India and Golden Acre, whereas characteristically purple coloured leaves were present in Kinner Red. The waxiness of outer leaves was absent/ very weak in Pusa Mukta and strong in Kinner Red. The character was weak in Golden Acre and Pusa Drum Head, followed by medium in Pusa Ageti and Pride of India. The margins of Pusa Mukta were strongly undulated clearly distinguishing it with medium undulation in Pusa Ageti, Pride of India, Kinner Red and Pusa Drum Head; Golden Acre, however, had weak undulation.

The typically circular heads were apparent in Golden Acre, Pusa Mukta and Pride of India. The respective shape, however, was broad ovate, transverse narrow elliptic and broad elliptic in Pusa Ageti, Pusa Drum Head and Kinner Red. The head was fully covered in Pusa Ageti, Golden Acre, Pusa Mukta, Pride of India and Kinner Red and partially covered in Pusa Drum Head. Only Kinner Red exhibited strong anthocyanin colouration of the outer leaf. Apparently, colour of the head of Pride of India, Pusa Mukta, Golden Acre and Pusa Drum Head was light green, followed by green in Pusa Ageti and purple in Kinner Red. The qualitative purple colour of interior of the head is the characteristic of Kinner Red, which was typically yellowish in rest of the varieties. The base of head in longitudinal section was raised in Kinner Red and level in rest of the varieties. The compact heads were observed in Golden Acre, Pride of India and Kinner Red, however, these were medium compact in Pusa Drum Head, Pusa Mukta and Pusa Ageti. Evidently, the internal head structure was fine in Golden Acre, Pusa Mukta and Kinner Red. The medium and coarse textures were apparent in Pusa Drum Head and Pride of India; and Pusa Ageti, respectively.

Quantitative Characters

The plants of Pride of India, Pusa Ageti and Kinner Red registered a height of more than 20 cm whereas it ranged between 15-20 cm in Golden Acre, Pusa Mukta and Pusa Drum Head. The minimum plant spread (<50 cm) was apparent in Golden Acre, Pride of India and Kinner Red, however, it was maximum (>60 cm) in Pusa Drum Head and remaining two had a medium spread. Except Pusa Ageti and Pusa Drum Head, the leaf length in rest of the varieties varied from 20-30 cm. In terms of leaf breadth, Pusa Mukta and Pusa Drum Head exhibited large leaves (>25 cm). Stalks were long (>1cm) in Kinner Red, while rest of the varieties had medium (0.5-1.0 cm) long stalks.

Table 3. Morphological characterization of cabbage varieties

S.No.	Characteristics	States	Note	Example varieties
A. Qualitative Characters				
1.	Outer leaf shape	Broad elliptic		-
		Broad ovate		-
		Circular		-
		Transverse broad elliptic	4	PDH
		Broad obovate	5	GA, PM, PoI, PA, KR
2.	Outer leaf profile of upper side of blade	Concave		-
		Flat		-
		Convex	3	PDH, GA, PM, PoI, PA, KR
3.	Plant attitude of outer leaves	Erect	3	PA
		Semi-erect	5	PDH, GA, PM, PoI, KR
		Horizontal		-
4.	Leaf margin	Serrate	1	PDH, GA, PM, PoI, KR
		Non-serrate	2	PA
5.	Outer leaf blistering	Absent/very weak	1	PDH, GA, PM, PoI, PA, KR
		Weak		-
		Medium		-
		Strong		-
6.	Outer leaf crimping	Weak	3	PA, PoI, PM, KR
		Medium		-
		Strong	7	GA, PDH
7.	Outer leaf colour (with wax)	Light green	1	PA, PDH
		Green	2	PoI, GA, PM
		Grey green		-
		Bluish green		-
		Purple	5	KR
8.	Outer leaf waxiness	Absent/ very weak	1	PM
		Weak	3	GA, PDH
		Medium	5	PA, PoI
		Strong	7	KR
9.	Outer leaf incision of margin	Absent		-
		Present	9	PDH, GA, PM, PoI, PA, KR
10.	Outer leaf reflection of margin	Absent	1	PDH, GA, PM, PoI, PA, KR
		Present	-	-
11.	Outer leaf undulation of margins	Absent/very weak		-
		Weak	3	GA
		Medium	5	PA, PoI, PDH, KR
		Strong	7	PM
		Very strong		-
12.	Head anthocyanin colouration of cover leaf	Absent/very weak	1	PDH, GA, PM, PoI, PA
		Weak		-
		Medium		-
		Strong	7	KR
13.	Head colour of cover leaf (external colour)	Light green	1	PoI, PM, GA, PDH
		Green	2	PA
		Grey green		-
		Blue green		-
		Purple	5	KR
14.	Head compactness	Very loose		-
		Loose		-
		Medium	5	PA, PDH, PM
		Compact	7	PoI, GA, KR
15.	Head shape of longitudinal section	Transverse narrow elliptic	1	PDH
		Transverse elliptic		-
		Circular	3	GA, PM
		Broad elliptic	4	PoI, KR
		Broad obovate		-
		Broad ovate	6	PA
		Angular ovate		-
16.	Head internal colour	Whitish		-
		Yellowish	2	PDH, GA, PM, PoI, PA
		Green		-
		Purple	4	KR

Contd.

Table 1. contd.

S.No.	Characteristics	States	Note	Example varieties
17.	Head shape of base in longitudinal section	Raised	1	PA
		Level	2	PDH, GA, PM, PoI, KR
		Arched		-
18.	Head cover	Uncovered		-
		Partially covered	2	PDH
		Covered	3	PA, GA, PM, PoI, KR
19.	Head blistering of cover leaf	Absent / very weak	1	PDH, GA, PM, PoI, PA, KR
		Weak		-
		Medium		-
		Strong		-
		Very strong		-
20.	Head internal structure	Fine	3	PM, GA, KR
		Medium	5	PDH, PoI
		Coarse	7	PA
21.	Etching type	Tropical		-
		Sub-tropical	2	PA
		Temperate	3	PDH, GA, PM, PoI, KR
B. Quantitative characters				
1.	Time of initiation of head formation	Early (<50 days)	1	GA, PoI, PM
		Medium (51-60 days)	3	PA, PDH
		Late (>60 days)	5	KR
2.	Time of harvest maturity	Early (<70days)	1	GA, PM, PoI, PA
		Medium (71-85 days)	3	PDH
		Late (>85 days)	5	KR
3.	Plant height (cm)	Short (< 15)		-
		Medium (15-20)	5	PDH, GA, PM
		Tall (> 20)	7	PoI, PA, KR
4.	Plant max. diameter (cm)	Small (< 50)	3	GA, PoI, KR
		Medium (50-60)	5	PA, PM
		Large (> 60)	7	PDH
5.	Number of non-wrapping leaves	Few (<10)		-
		Medium (10-15)	3	PDH, GA, PM
		Many (>15)	5	PoI, PA, KR
6.	Outer leaf size (cm)	Small (<20)		-
	a) Leaf length	Medium (20-30)	5	PoI, GA, PM, KR
		Long (>30)	7	PA, PDH
	b) Leaf breadth	Small (<20)		-
		Medium (20-25)	5	PoI, GA, PA, KR
		Large (>25)	7	PM, PDH
7.	Length of outer stem (cm)	Short (< 0.50)		-
		Medium (0.50-1.0)	5	PDH, GA, PM, PoI, PA
		Long (>1.0)	7	KR
8.	Head length (cm)	Short (<10)		-
		Medium (10-15)	5	PDH, GA, PM, PoI, KR
		Long (>15)	7	PA
9.	Head diameter (cm)	Small (<10)	3	KR
		Medium (10-15)	5	PA, PoI, GA
		Large (>15)	7	PDH, PM
10.	Length of interior core stem axis (cm)	Short (<5)		-
		Medium (5-8)	5	PoI, GA, PDH, PM, KR
		Long (>8)	7	PA
11.	Time of bursting after head maturity	Early (<10 days)	3	PM, PA, GA
		Medium (10-20 days)	5	PoI, PDH
		Late (>20 days)	7	KR
12.	Head shape (length/width ratio)	Flat (<0.85)	1	PDH,
		Round (0.85-1.10)	3	GA, PM
		Oval (1.11-1.25)	5	PoI, KR
		Conical (>1.25)	7	PA

PDH=Pusa Drum Head, GA = Golden Acre, PM= Pusa Mukta, PoI= Pride of India, PA= Pusa Ageti and KR= Kinner Red

Table 4. Distinction among the varieties expressed as descriptor note

S.No.	Descriptors/Varieties	Note						No. of varieties distinguished
		GA	PM	PoI	PDH	PA	KR	
1.	Time of initiation of head formation	1	1	1	3	3	5	3
2.	Time of harvest maturity	1	1	1	3	1	5	3
3.	Plant height (soil surface to tip of the head)	5	5	7	5	7	7	2
4.	Plant: max diameter (frame size)	3	5	3	7	5	3	3
5.	Outer leaf shape	5	5	5	4	5	5	2
6.	Outer leaf profile of upper side of blade*	3	3	3	3	3	3	0
7.	Plant attitude of outer leaves	5	5	5	5	3	5	2
8.	Leaf margin	1	1	1	1	2	1	2
9.	Outer leaf blistering*	1	1	1	1	1	1	0
10.	Outer leaf crimping	7	3	3	7	3	3	2
11.	Outer leaf colour (with wax)	2	2	2	1	1	2	2
12.	Outer leaf waxiness	3	1	5	3	5	7	3
13.	Outer leaf incision of margin*	9	9	9	9	9	9	0
14.	Outer leaf reflection of margin*	1	1	1	1	1	1	0
15.	Outer leaf undulation of margins	3	7	5	5	5	5	3
16.	Head anthocyanin colouration of cover leaf	1	1	1	1	1	7	2
17.	Head colour of cover leaf (external colour)	1	1	1	1	2	5	3
18.	Head cover	3	3	3	2	3	3	2
19.	Head blistering of cover leaf*	1	1	1	1	1	1	0
20.	Head compactness	7	5	7	5	5	7	2
21.	Number of non-wrapping leaves	3	3	5	3	5	5	2
22.	Length of outer stem (stalk length)	5	5	5	5	5	7	2
23.	Outer leaf size							
	a) Leaf length	5	5	5	7	7	5	2
	b) Leaf breadth	5	7	5	7	5	5	2
24.	Head length	5	5	5	5	7	5	2
25.	Head diameter	5	7	5	7	5	3	3
26.	Length of interior core stem axis (core length)	5	5	5	5	5	7	2
27.	Head shape of longitudinal section	3	3	4	1	6	4	4
28.	Head internal colour	2	2	2	2	2	4	2
29.	Head shape of base in longitudinal section	2	2	2	2	1	2	2
30.	Head internal structure	3	3	5	5	7	3	3
31.	Etching type	3	3	3	3	2	3	2
32.	Time of bursting after head maturity	3	3	5	5	3	7	3
33.	Head shape (length/ width ratio)	3	3	5	1	7	5	4

*Descriptor exhibiting no polymorphism among the varieties

PDH=Pusa Drum Head, GA = Golden Acre, PM= Pusa Mukta, PoI= Pride of India, PA= Pusa Ageti, and KR= Kinner Red

Pride of India, Pusa Ageti and Kinner Red had more than 15 non-wrapping leaves; however, these were within the range of 10-15 in Golden Acre, Pusa Drum Head and Pusa Mukta. The varieties, Pride of India, Golden Acre and Pusa Mukta took less than 50 days for head formation; whereas Pusa Drum Head and Pusa Ageti started head formation between 51-60 days; and Kinner Red took more than 60 days. The marketable maturity was achieved in less than 70 days in Golden Acre, Pusa Mukta, Pride of India and Pusa Ageti. Pusa Drum Head fell under medium maturity group (71-85 days), while Kinner Red under late maturity group (>85 days). Golden Acre, Pusa Mukta and Pusa Ageti must be harvested within 10 days of head maturity to avoid bursting. Pride of India and Pusa Drum Head may withstand for 10-20 days followed by more than 20 days in Kinner Red. Core length was longer in

Pusa Ageti and medium in Pride of India, Golden Acre, Pusa Drum Head, Pusa Mukta and Kinner Red. Based on their head index, Golden Acre and Pusa Mukta were categorized as round, Pride of India and Kinner Red as oval, Pusa Ageti as conical and Pusa Drum Head as flat headed.

Conclusions

Five qualitative characters, viz., outer leaf profile of upper side of blade, outer leaf blistering, outer leaf incision of margin, outer leaf reflection of margin and head blistering of cover leaf (Table 4) did not show polymorphism among the six varieties. Hence, while going for DUS testing, any one of the six varieties may be used as an example variety for the above 5 characters. Further, blistering of leaf is a characteristic of savoy type of cabbages and the

reference collection represented only white cabbages, therefore such descriptors may be excluded when testing is not to be done for savoy cabbage types. Similarly, none of the white cabbage varieties exhibited the characteristics as anthocyanin colouration of cover leaf and head internal colour as purple (as in case of variety Kinner Red) which is a characteristic of red cabbage types. From Table 4 it may also be deduced that a maximum of 4, varieties could be distinguished by each of the 2 descriptors, viz., head shape of the longitudinal section and head shape (head length/width ratio). Nine descriptors could distinguish 3 varieties each and the remaining 17 descriptors were able to distinguish 2 varieties each out of the 6 varieties under investigation.

This maiden attempt to characterize the notified varieties as per DUS test guidelines will serve as a ready reckoner for plant variety protection and their utilization in breeding programmes.

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Analysis of Genetic Variability for Nutritional Quality Traits in Hot Pepper (*Capsicum annuum* L.)

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Variability and association analysis were studied among 42 genotypes of hot pepper (*Capsicum annuum* L.) comprising exotic (Taiwan), landrace and open-pollinated varieties for some important nutritional quality traits. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits under study and difference between GCV and PCV was not high, indicating that these quality traits were not much influenced by the environmental factors. Heritability ranged from 38.8% (manganese $\mu\text{g g}^{-1}$) to 99.9% (capsaicin %). High heritability and high genetic advance were observed for ascorbic acid, total phenols, iron (Fe) and beta carotene content in fruits indicating involvement of additive gene action. Association analysis exhibited both positive and negative correlations among the traits under study.

Key Words: Hot pepper, Variability, Correlation, Nutritional quality

Introduction

Hot pepper (*Capsicum annuum* L.) is an important vegetable as well as spice crop, not only because of its economic importance, but also for the nutritional value of its fruits, mainly due to the fact that they are an excellent source of natural red pigment capsanthin and antioxidant compounds (Howard *et al.*, 2000). It is an excellent source of vital micronutrients such as vitamin C and vitamin E (Minguez-Mosquera & Hornero-Mendez, 1994, Daood *et al.*, 1996; Gnayfeed *et al.*, 2001). The important states growing hot pepper are Andhra Pradesh, Orissa, Maharastra, West Bengal, Karnataka, Rajasthan and Tamil Nadu. Total world production of hot pepper has been estimated to be 14–15 million t per year (Weiss, 2002). Capsaicinoids (heat principle), have aroused great interest lately owing to their biological and therapeutic importance (Surh and Lee, 1996; Szolcsanyi, 2004). Capsaicinoids are alkaloids specific for *Capsicum* sp. A wide spectrum of antioxidant compounds are present in pepper fruits. It includes antioxidant vitamins (Vitamin E, C and β -carotene), phenolic compounds, carotenoides and xanthophylls. One of the important antioxidant is phenolic compounds, which occurs in peppers in connection with sugars (Materska *et al.*, 2003 a, b). The level of antioxidants differs between accessions, generally hot peppers are a better source of them than the sweet ones (Daood *et al.*, 1996; Gnayfeed *et al.*, 2001). Phenolic compounds retard or inhibit lipid autoxidation by acting as radical scavengers (Namiki, 1990) and consequently, are essential antioxidants that protect against propagation of the oxidative chain. Another important antioxidant-

vitamin C, an important compound of pepper fruits, chelates heavy metal ions (Namiki, 1990), reacts with singlet oxygen and other free radicals, and suppresses per oxidation, reducing the risk of arteriosclerosis, cardiovascular diseases, and some forms of cancer (Harris, 1996). Carotenoid pigment, vitamin E, vitamin C are located in the pericarp of pepper fruit, whereas, capsaicinoids are distributed in different parts. Genetic variability, especially for quality in given sets of germplasm has not been studied much. Study related to pepper as functional food or as a source of micronutrient are not meager, but, systematic screening study for the quality evaluation of hot pepper and use of the information for the development of better varieties is lacking. Hence, the present was undertaken to analyze the extent of variability in respect of nutritional quality present in available germplasm of hot pepper to breed better quality hot pepper varieties.

Materials and Methods

The present experiment was conducted in VPKAS, Almora at experimental farm, Hawalbagh (29°36' N, 79°40' E and 1250 m asl). Forty two lines of hot pepper (exotic, local and open pollinated popular varieties) were grown in the field under completely randomized block design with three replications in *kharif* season (June-September), 2007. The crop was raised as per the recommended package of practices. Peppers were harvested at green mature stage. Three replicates of 42 genotypes were analyzed for different functional (β -carotene, ascorbic acid, total phenolics and capsaicin) and nutritional attributes (phosphorous, potassium, zinc,

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Copper, iron and manganese). The detailed information regarding source of chilli lines is mentioned in Table 1.

Chemical Analysis

Determination of ascorbic acid content

L-ascorbic acid (LAA) was estimated extracted and quantified by HPLC as described by Abdulnabi *et al.* (1997) with minor modifications. The sample (10 g) was homogenized with solution (10 ml) containing metaphosphoric acid (0.3 M) and acetic acid (1.4 M) for 15 minutes at room temperature. The mixture was filtered through Whatman No. 4 to obtain clear extract. All samples were extracted in triplicate. Mobile phase was Acetonitrile: Methanol: Tetrahydrofuran (45:50:5; v/v/v) at a flow rate of 1.0 ml min⁻¹ and detected at 254 nm.

Determination of β -carotene content

β -Carotene in the pepper samples was according to Ismail and Fun, 2003 with minor modifications. The β -carotene standard ($E_{1\text{cm}}^{1\%} = 2560$ in hexane) was obtained from Sigma Chemical Co. (St. Louis, MO). Pepper samples (10g) were extracted with 40 ml ethanol (99.8%) and 10 ml 100 % (w/v) potassium hydroxide and homogenized for three minutes. The mixture was saponified by heating for 30 minutes. Then, the mixture was partitioned thrice in n-hexane, followed by washing with distilled water and then passed through sodium sulfate. Hexane was

removed under reduced pressure at 45°C using rotary evaporator. The standards and pepper isolates were dissolved in 10 mL of hexane prior to HPLC analysis. A mobile phase ran at 0.8 ml min⁻¹ and consisted of water containing 0.01% formic acid: Acetonitrile (95:5 v/v). β -Carotene was detected at 450 nm using a UV-Vis detector. The column was equilibrated to the original mobile phase concentration prior to the next sample injection.

Determination of total phenolics content

Total phenolics content of the MeOH extracts was determined by the Folin-Ciocalteu assay and catechol was used as standard (Singleton and Rossi, 1965). Sample (500 mg) was weighed into 50 ml plastic extraction tubes and vortexed with 25 ml extraction solvent (80% ethanol). The sample with the extraction solvent was then heated at 60°C (water bath) for 1h, allowed to cool to room temperature, and homogenized for 30s with a sonicator. Two hundred fifty microlitres (three replicates) were introduced into screw cap test tubes; 1.0 ml of Folin-Ciocalteu's reagent and 1.0 ml of sodium carbonate (7.5%) were added. The tubes were vortexed and heated for 15 minutes at 45°C. The absorption at 765 nm was measured (Model U 2001, Hitachi UV/Vis spectrophotometer) and the total phenolic content was expressed as catechol equivalents in mg per 100 g dry material.

Determination of capsaicin content

Capsaicin content was determined using

Table 1. List of chilli lines analyzed for genetic variability

Accession No.	Code of lines	No. of lines	Source
ICPN 10 # 1	VLC-16-I-1, VLC-16-I-2, VLC-16-II-1,VLC-16-II-3	4	AVRDC through NBPGR
ICPN 10 # 3	VLC-18-I-1, VLC-18-I-2	2	AVRDC through NBPGR
ICPN 10 # 5	VLC-20-I-2, VLC-20-II-1	2	AVRDC through NBPGR
ICPN 10 # 6	VLC-21-II-3-1, VLC-21-II-3-2	2	AVRDC through NBPGR
ICPN 10 # 7	VLC-22-I, VLC-22-I-2-1, VLC-22-I-2-2, VLC-22-IV-1, VLC-22-V-1-1, VLC-22-V-1-2, VLC-22-VII-1,	7	AVRDC through NBPGR
ICPN 10 # 8	VLC-23-I-1-1, VLC-23-II-2-1, VLC-23-II-2-2	3	AVRDC through NBPGR
ICPN 10 # 9	VLC-24-I-1	1	AVRDC through NBPGR
ICPN 10 # 10	VLC-25-1	1	AVRDC through NBPGR
ICPN 10 # 13	VLC-28-II-1, VLC-28-II-2, VLC-28-III-1	3	AVRDC through NBPGR
ICPN 10 # 14	VLC-29-1, VLC-29-II-1-1, VLC-29-II-1-2	3	AVRDC through NBPGR
ICPN 10 # 15	VLC-30-I-1, VLC-30-II-1,VLC-II-2	3	AVRDC through NBPGR
ICPN 10 # 16	VLC-31-I-1	1	AVRDC through NBPGR
ICPN 10 # 17	VLC-32-1, VLC-32-3, VLC-32-4	3	AVRDC through NBPGR
ICPN 10 # 19	VLC-34-2	1	AVRDC through NBPGR
Lakhori Mirch	-	1	Salt, Dist. Almora, Uttarakhand
Janjeera Mirch	-	1	Salt, Dist. Almora, Uttarakhand
Berry Mirch	-	1	Salt, Dist. Almora, Uttarakhand
Lal Mirch	-	1	Salt, Dist. Almora, Uttarakhand
Pusa Sadabahar	-	1	Released variety from IARI
Pusa Jwala	-	1	Released variety from IARI

spectrophotometer. Sample (500 mg) was weighed into 50 ml plastic extraction tubes and extracted with 10 ml extraction solvent (acetone) for 3 h. Then, the sample with the extraction solvent was centrifuged and 1.0 ml extract was taken in a beaker and evaporated. The residue was dissolved in 0.4% sodium hydroxide solution (5 ml) and 3 ml 3% phosphomolibdic acid was added. The mixture was kept for 1.0 h and absorbance was taken at 650 nm after centrifugation. The capsaicin content was expressed as per cent dry material.

Determination of nutritional attributes

Peppers were analyzed for nutrient parameters after di-acid digestion (HNO_3 : HClO_4 ; 10:4 v/v). The K content was determined by flame photometry, while Fe, Zn, Cu and Mn contents were analyzed by using an atomic absorption spectrophotometer. Phosphorus (P) was estimated photometrically via development of phosphomolybdate complex (Taussky and Shorr, 1953).

Statistical analysis

The genotypic and phenotypic coefficient of variation, heritability (broad sense) were calculated by standard statistical procedure given by Burton and De Vane 1953; Johnson *et al.* (1955). The genotypic and phenotypic correlation coefficient was calculated by a method described by Singh and Choudhary (1979).

Results and Discussion

Variation among 42 genotypes of hot pepper was found highly significant for the characters under study (Table 2). The estimates depicting the genetic variability including genotype range, mean genotypic and phenotypic variation, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance are presented in Table 3.

Wide variation (0.20-0.36 mg 100g⁻¹) was observed in β -carotene content in evaluated pepper lines, suggesting considerable levels of genetic diversity. The result was not consistent with the report by Gnaifed *et al.* (2001), where it was reported that paprika red pepper contained 171-250 mg g⁻¹ β -carotene, but similar to the report by Howard *et al.* (2000). The latter reported 337-800 mg 100g⁻¹ β -carotene in *Capsicum annuum* fresh fruit. Ascorbic acid content in pepper accessions ranged from 25-217 mg 100g⁻¹, consistent with the report by Howard *et al.*, 2000 and Gnaifed *et al.*, 2001. Total phenolics ranged between 38.4-188.1 mg 100g⁻¹ catechol equivalent. Capsaicin content ranged between 0.08-0.67%, which is far below than the report by Contreras-Padilla and Yahla, 1998. It was reported that paprika accession contained 383-1075 mg g⁻¹ (Gnaifed *et al.*, 2001) and 997-1240 mg g⁻¹ (Ayuso *et al.*, 2008) dry matter capsaicinoid. Phosphorous and potassium content in pepper ranged between 0.33-0.59 and 2.9-6.7% (dry matter basis). It was reported that physiologically mature peppers were rich in mineral content than green one (Jadczak and Grzeszczuk, 2004). Iron and zinc content ranged from 146-317 mg g⁻¹ and 11.4-32.6 mg g⁻¹, respectively (Table 3). The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits under study and difference between GCV and PCV is not much except manganese contents (mg g⁻¹) in fruits indicating that these quality traits were not much influenced by the environmental factors. Similar findings were reported by Shirshat *et al.* (2007), that difference between PCV and GCV was less in case of ascorbic acid content in fruits (Table 3). The high heritability coupled with high genetic advance was recorded for ascorbic acid, total phenols, iron (Fe) and β -carotene contents in fruits indicating the

Table 2. Analysis of variance for quality nutritional attributes in forty-two genotypes of hot pepper

Traits	Mean Sum of Squares (d.f.)			CD (5%)
	Replication (02)	Genotypes (41)	Error (82)	
K	0.00055	1.7815**	0.0071	0.137
P	0.000003	0.011456**	0.000047	0.011
Zn	0.2729	51.937**	0.549	1.198
Cu	0.0213**	6.954**	0.0037	0.100
Fe	8.822	4429.450**	46.51	11.078
Mn	0.492	14.312**	4.925	3.604
α -carotene	0.0007	0.347**	0.0034	0.096
Ascorbic acid	52.66	6643.68**	33.88	9.455
Total Phenolics	279.50*	4532.57**	68.67	13.460
Capsaicin	0.0244**	0.045**	0.000019	0.007

** Significant at 1 per cent level

* Significant at 5 per cent level

Table 3. Range, mean, variance, coefficient of variation, heritability and genetic advance for different quality nutritional attributes of hot pepper

Traits	Units	Range	Mean	Variance		Coefficient of Variation (%)		Heritability in broad sense (%)	Genetic advance 5%
				Genotypic	Phenotypic	Genotypic	Phenotypic		
K	%	2.88-6.69	4.596	0.591	0.599	16.732	16.833	98.8	1.58
P		0.326-0.585	0.463	0.004	0.004	13.327	13.409	98.8	0.13
Zn	mg g ⁻¹	11.4-32.60	19.827	17.131	17.675	20.875	21.204	96.9	8.39
Cu		3.93-9.067	7.214	2.317	2.321	21.101	21.118	99.8	3.13
Fe		146.10-316.8	193.94	1460.98	1507.49	19.709	20.020	96.9	77.52
Mn		11.80-22.90	17.63	3.129	8.054	10.033	16.098	38.8	2.27
β-carotene	mg 100g ⁻¹	0.20-0.36	0.275	0.115	0.118	12.316	12.501	97.0	0.69
Ascorbic acid		25.00-217.00	67.79	2203.27	2237.15	69.246	69.777	98.5	95.96
Total phenolics		38.41-188.10	94.63	1487.97	1556.64	40.761	41.691	95.6	77.69
Capsaicin	%	0.08-0.670	0.267	0.015	0.015	46.240	46.268	99.9	0.25

Table 4. Genotypic (r_g) phenotypic (r_p) correlation coefficient among different quality nutritional attributes of hot pepper

Traits		K	P	Zn	Cu	Fe	Mn	â-carotene	Ascorbic acid	Tot. Phenolics	Capsaicin
K	r _g	1.0	0.6573	0.2048	-0.1852	-0.0163	0.6126	-0.1165	0.0449	0.0208	-0.0591
	r _p	1.0	0.6506	0.1965	-0.1849	-0.0116	0.3834	-0.1132	0.0438	0.0209	-0.0583
P	r _g		1.0	0.0585	-0.0953	0.0748	0.5806	-0.0982	0.0920	0.0480	0.0248
	r _p		1.0	0.0635	-0.0944	0.0839	0.3199	-0.0890	0.0913	0.0442	0.0246
Zn	r _g			1.0	0.2141	0.2547	0.4551	0.0237	-0.0213	-0.0430	0.0053
	r _p			1.0	0.2092	0.2611	0.2999	0.0210	-0.0210	-0.0389	0.0050
Cu	r _g				1.0	0.2402	0.0767	0.2277	-0.3681	0.0793	0.2286
	r _p				1.0	0.2353	0.0377	0.2256	-0.3646	0.0788	0.2280
Fe	r _g					1.0	0.4285	0.1754	-0.1198	0.3304	0.1169
	r _p					1.0	0.2364	0.1799	-0.1163	0.3170	0.1155
Mn	r _g						1.0	-0.1355	-0.1374	-0.0415	0.1884
	r _p						1.0	-0.1320	-0.0830	-0.0011	0.1164
â-carotene	r _g							1.0	-0.3311	-0.1105	0.0541
	r _p							1.0	-0.3230	-0.1052	0.0531
Ascorbic acid	r _g								1.0	0.2316	-0.0685
	r _p								1.0	0.2243	-0.0679
Total phenolics	r _g									1.0	0.1365
	r _p									1.0	0.1323
Capsaicin	r _g										1.0
	r _p										1.0

involvement of additive gene action for expression of these traits. Johnson *et al.* (1955) suggested that traits with high heritability coupled with high genetic advance would respond to select better than those with high heritability and low genetic advance. Heritability is not an exact parameter because it could be high even when genetic advance is very low (Table 3). However, expected genetic gain can be high only if the genetic variance is high (Allard, 1960). Burton and Devane (1953) suggested that GCV along with heritable estimates would give a better picture of the amount of progress expressed by phenotypic selection.

The assessment of genetic potentiality of important quality traits and their association is of paramount importance to carryout the effective selection of genotype with desired quality traits. Correlation coefficient of important quality traits were estimated at genotypic and phenotypic levels. In present study, the genotypic correlation coefficients were higher in magnitude than their respective phenotypic ones and positive correlation was observed (β carotene with P, Zn, Fe, Mn, β carotene and total phenols; total phenols with P, Fe, and ascorbic acid; ascorbic acid with K and P; β carotene with Zn and Cu, ascorbic acid and lycopene) indicating that there is an inherent association among these traits (Table 4).

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Genetic Diversity among Indigenous Landraces of Rice for Certain Quality Traits

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One hundred twenty indigenous rice genotypes collected from Jharkhand were evaluated for twelve quality characters to study genetic divergence by employing D^2 analysis. The genotypes were grouped into nine diverse clusters. The highest genetic divergence was observed between cluster I and cluster III, whereas cluster IV and VIII were the closest one. Hence, genotypes belonging to cluster I and III can be used as parents for hybridization programme for the development of high yielding rice genotypes.

Key Words: Rice, L/B ratio, Landraces, Quality traits, Genetic diversity

Introduction

The success of any crop breeding programme depends on the nature and amount of genetic variability available in the germplasm collections. Germplasm collected from different states/countries serves as the most valuable natural resource in providing needed attributes for developing successful varieties (Hawkes, 1981). The classification or grouping of germplasm collection is a pre-requisite for distinguishing genetically close and divergent types for various plant breeding programmes. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. By using advance biometrical techniques such as multivariate analysis based on Mahalanobis's D^2 statistics (Mahalanobis, 1936), it has now become possible to quantify the degree of genetic divergence amongst biological populations. Therefore, the present investigation is aimed at ascertaining the nature and magnitude of genetic diversity among one hundred twenty landraces of rice from Jharkhand State for quality characters.

Materials and Methods

The experimental material comprised of one hundred twenty traditional germplasm lines obtained from Jharkhand State through the NGO Gene Campaign, Ranchi, and were evaluated in a randomized block design experiment with three replications at Research Farm of Kisan P.G. College, Simbhaoli (Ghaziabad) during *kharif* 2005. Each genotype was assigned to two row plots of 3 m length with inter and intra-row spacing of 40 cm and 15 cm, respectively. Recommended agronomic practices were followed to raise a good crop. Data were recorded on five randomly selected competitive plants from each plot on twelve characters, namely, hulling (%), milling

(%), head rice recovery (%), kernel length (mm), kernel breadth (mm), length/breadth ratio, kernel length after cooking (KLAC), kernel breadth after cooking (KBAC), kernel elongation ratio (ER), alkali spreading value (ASV), aroma and 1000 grain weight (g). The data recorded on above characters were subjected to D^2 analysis (Mahalanobis, 1936; Rao, 1952).

Result and Discussion

Analysis of variance (Table 1) revealed the significant differences among the genotypes for all the characters studied indicating thereby the existence of genetic variability among the genotypes to identify desirable genotypes. Based on D^2 statistics, 120 genotypes were grouped into nine clusters of which cluster VII had maximum 25 genotypes, followed by cluster IV, V and VIII having 24, 22 and 18 genotypes, respectively (Table 2). The genotypes falling in the same cluster are more closely related and hence the clusters having the maximum number of genotypes, reflected narrow genetic diversity.

Results of cluster analysis indicated that the highest intra-cluster distance was observed for cluster VI followed by cluster III, cluster V, cluster II, cluster VIII, cluster IX, cluster IV, cluster VII and cluster I (Table 3). This suggested that the genotypes in cluster VI were relatively more diverse among themselves, however, in all cases, the inter-cluster distances were greater than the intra-cluster distances implying presence of greater degree of genetic diversity between the genotypes of two clusters than the genotypes present within the cluster.

From the inter-cluster distances for nine clusters (Table 3), it can be seen that the highest divergence occurred between cluster I and III (8.611) followed by cluster II and III (7.923) and cluster I and VI (7.507)

Table 1. Analysis of variance (ANOVA) for quality characters

Sources of variation	df	Hulling	Milling	HRR	KL	Mean squares		KLAC	KBAC	ER	Aroma	ASV	1000 GW
		% 1	% 2	% 3	mm 4	KB mm 5	L/B ratio 6	mm 7	mm 8	9	10	11	g 12
Replication	2	27.62	15.43	13.12	0.014	3.65	0.111	0.036	0.0008	0.0006	0.019	3.80	0.03
Genotypes	199	38.74**	66.33**	77.25*	0.782**	15.34*	0.033*	4.655**	0.1735**	0.0277**	1.077**	12.77**	100.43**
Error	238	0.52	0.30	1.80	0.003	1.78	0.075	0.003	0.0017	0.0003	0.027	0.20	0.07

** Significant at P=0.05; * P=0.01 levels, respectively

df = Degree of freedom

KLAC= Kernel length after cooking, KBAC= Kernel breadth after cooking, L/B ratio= Length/Breadth ratio, ER= Elongation ratio, ASV= Alkali spreading values, HRR+ head rice recovery, KL= Kernel length, KB= Kernel breadth, GW= Grain weight

Table 2 . Distribution of 120 genotypes of rice in different clusters

No. of cluster	No. of genotypes	Name of genotypes
I	3	Badya(B), U.L-4, Barka-Tilarar
II	8	Garib-Saal, Kanke-Saal, Anjani, Mehra-Dhan, Boka-Dhan, Ejaan, Asamia, U.L-2
III	7	Ujla Basmati1, Basmati 370, Pusa Basmati 1, Banphool(A), Choota-Dahia, Kalam-Dani, U.L-3
IV	24	Mehra-Dhan, Khir-Bhojni, Suga-Thor, Sonagoti, Bhadwa-Kalamdani, Tulsi-Ketki, Karhaini, Maina-Thori, KalamDani, Sitwa, Has-Kalma, Sir Hatti, Doodh-Kandhar(A), Lahri, Bara-Sitwa, Burah-Dhan, Sarna, Karijiri(A), Khutuwa, Karhaim-Chhota, Barah-Saal, Kherka, Rani-Kesar
V	22	Bagh-Panjar, Mehsuri-Nata, Amma-Dhoka, Ramdilal, Kanaschapar, U.L-1, Sanam-Dhan, Mirmitti, Kala-Zira, Makar Kalma, Khir-Bhat(B), Yes-Kalma, Badya(A), Thubka, Konhra-Phool, Naniya, Barka-Swarna, Raz-Bhokta, Daani-Gora, Sihul, Kherka-kuchi, Karhaini (B)
VI	4	Barkhadhan, Mirmitti, Panchsala, Kalam-Kathi (B)
VII	25	Katika, Sirhanthi, Chaaina-Gora, Dahiya-2, Barka-Kalma, Rani-Kajjar, Charka-Khairkakuchi, Charka-Nardha, TilaSaar, RupSari, Kalam-Katni(A), Chhotka-Suman, Dehati-Gora, Guda, Maiya-Dulari, Hans-Kalma, BanPhool(B), Budhnu-Nanhi, Karijiri(A), Makar Kalma, Khir-Bhat(B), Miri-Mitti, Ghuthia, Kala-Basmati, Sugandha
VIII	18	Sugandha, Ujla Basmati2, Ketki, Dehati-Gora, Nambri-Dhan, Barka-Dhusri, Lal-Mugdi, Type-III , Chhotka-Sitwa, Kodowa, Budhnu-Nanhi, Barka-Dhan, Kohra-Phool, Charka-Raes, Bihar-Dhan, Barka-Mansuri, Jhilli, Raz-Bhokta
IX	9	Raz-Bhokta, Sitwa-Dhan, Tulsi-Ketki, Kala-Zira, Yes-Kalma, Kalam-Kathi(B), Son-Piya, Dudh-Kandhar, Hardi Muri Lal

Table 3. Average inter and intra-cluster (bold values) distances involving 120 genotypes of rice

	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
I	1.750								
II	6.978	2.427							
III	8.611	7.923	2.900						
IV	7.005	4.188	6.981	2.003					
V	7.196	4.258	6.650	2.618	2.477				
VI	7.507	6.052	6.361	4.876	2.203	3.274			
VII	6.441	3.548	5.755	2.280	2.738	4.363	1.956		
VIII	6.915	4.371	5.346	2.061	2.279	4.338	2.131	2.211	
IX	6.962	4.818	5.104	3.994	3.093	4.623	2.574	3.291	2.138

Table 4. Cluster mean value for quality character

Characters	Cluster								
	I	II	III	IV	V	VI	VII	VIII	IX
Hulling (%)	75.93	74.35	80.49	78.37	75.00	79.15	75.71	80.41	77.14
Milling (%)	63.18	54.12	70.93	67.73	64.62	66.50	65.53	68.71	65.23
Head rice recovery (%)	53.29	45.32	62.44	59.78	58.36	61.84	58.31	57.00	58.51
Kernel length (mm)	5.02	4.88	6.49	4.62	4.79	4.17	5.07	5.03	5.18
Kernel breadth (mm)	16.00	2.06	1.61	2.13	1.88	1.93	1.98	1.96	1.72
L/B ratio	2.53	2.37	3.98	2.21	2.56	2.16	2.58	2.68	3.24
Kernel length after cooking	8.69	8.27	11.66	7.40	7.45	9.30	8.65	8.54	9.16
Kernel breadth after cooking	2.80	2.78	2.35	2.70	2.27	2.52	2.71	2.44	2.56
Elongation ratio	1.73	1.69	1.79	1.60	1.56	2.25	1.71	1.69	1.78
Aroma	0.67	0.00	1.76	0.04	0.14	1.33	0.04	0.31	0.11
Alkali spreads value	7.00	3.25	5.86	2.35	3.71	5.83	5.17	3.15	6.81
1000 grain weight	19.97	21.11	19.80	18.30	8.68	16.77	19.86	20.41	5.17

indicating the presence of greater diversity between genotypes of these groups. Hence, crossing between genotypes belonging to these clusters may result in high heterosis, which could be exploited in crop improvement. The least inter-cluster distance was noticed between cluster IV and VIII (2.061) followed by cluster VII and VIII (2.131) and cluster V and VI (2.203) indicating the close relationship and similarity for most of the characters of the genotypes in these clusters.

The cluster III showed the highest cluster means for hulling and milling (%), head rice recovery (%), kernel length, L/B ratio, kernel breadth after cooking (KBAC) and alkali spreading value (ASV). 1000 grain weight exhibited highest mean in cluster II whereas kernel breadth and elongation ratio exhibited highest mean values in cluster IV and cluster VI, respectively (Table 4). The percent contribution of the characters studied towards genetic divergence showed that 1000 grain weight contributed maximum (20.25%) followed by KLAC (17.56%), ASV (13.15) and HRR (6.83%). The results of the present study are in agreement with the findings of several earlier workers (Ratho, 1984; Pradhan and Roy, 1990; Singh, 2005 and Chand *et al.*, 2005).

The data on inter-cluster distance and performance of the genotypes was used to select genetically diverse and agronomically superior genotypes among 120

genotypes. As cluster I showed the maximum inter-cluster distances with other cluster hence, the three genotypes (UL-4, Badya and Barka-Jilasar) belonging to cluster I could be utilized as parents in future breeding programme with the desirable genotypes belonging to cluster II, III and VI. Inter-crossing between genotypes belonging to cluster I, II, III and VI may generate large variability and can be expected to produce desired genotypic combinations and transgressive segregants and form a good source material in further crop improvement programme.

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Observations on Diversity in Temperate Fruits in North Eastern Region, India

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This paper deals with temperate fruits germplasm collected from two states in the region i.e. Meghalaya and Arunachal Pradesh along with field notes. Standard methods pertaining to collection of genetic resources were followed. A total of 79 accessions involving 44 taxa were collected from both the states. Unlike western Himalaya, in both the states, commercial cultivation of temperate fruits has not been seen. Good variability in *Pyrus pashia*, *Docynia indica*, *Actinidia callosa*, *Malus baccata* and *Rubus moluccanus* are noticed. In Meghalaya, *Myrica esculenta*, *Prunus nepaulensis*, *Baccaurea ramiflora*, *Vangueria spinosa*, *Elaeagnus latifolia*, *Docynia indica*, etc. are noticed in transition process from wild to cultivated status while. *Pyrus pashia* and *Cornus capitata* in Arunachal Pradesh. More than one third of taxa collected are endemic to the region. Twenty one taxa not collected in previous explorations were collected including the wild form of *Diospyros kaki* in Khasi and Jaintia Hills and *Chaenomeles cathayensis* in Tawang. Exploration strategies to be followed in future in those areas are discussed.

Key Words: North eastern India, Temperate fruits, Wild relatives, Plant genetic resources

Introduction

North Eastern Region, due to high rainfall, moist and cold climate coupled with altitude, longitude and latitude provides a variety of microclimates and ecological niches. It is a region of active speciation and has been designed as cradle of flowering plants (Takhtajan, 1969). This region is the storehouse of many wild relatives of temperate fruits and few minor fruits of potential importance; many are endemic in nature. This paper deals with those collected material from two states in the region i.e. Meghalaya and Arunachal Pradesh offering some comments on variability, use and geographical distribution. Wild species were collected with the aim of genetic diversity study, conservation and also for phylogenetic and biosystematic studies.

Materials and Methods

Apart from personal communications with the experts in these regions, thorough literature survey was made (Kanjilal *et al.*, 1934-1940; Haridasan and Rao, 1985; Hajra *et al.*, 1996) on taxa falling in the temperate fruit genera, their distribution, flowering and fruiting time. Above survey revealed the presence of intended species belonging to genera *Malus*, *Pyrus*, *Prunus*, *Sorbus*, *Rubus*, *Actinidia*, *Juglans*, *Diospyros*, etc. in above 1000m msl. Based on above particulars, germplasm survey and collection was made in four districts of Meghalaya and two of Arunachal Pradesh. The explored areas and their physical features are depicted in Table 1. Collection routes and sites are shown in Fig. 1, which is not to the scale.

Global Positioning System was used to locate the site. Random sampling from wild population in case of live plants while in other cases selective sampling was being made. Field notes included salient feature of germplasm, characteristic habitats, frequency and density of populations, etc. All the collections were conserved at the field gene bank nursery of National Bureau of Plant Genetic Resources (NBPGR) Regional Station, Shimla. Most of the germplasm collections were accompanied by herbarium specimens deposited at National Herbarium of Cultivated Plants, NBPGR, New Delhi.

Results and Discussion

A total of 79 accessions involving 44 taxa were collected from both the states. Information on collection site, form of material collected, number of accessions, cultivation status, etc. are depicted in Table 2. Some salient observations are mentioned hereunder:

Meghalaya

Temperate fruits cultivation is limited to homestead only i.e. no systematic orchard for any of these crops was seen. Asiatic pear is semi-naturalized in the entire state. Peach and plum are other common kitchen garden plants. Apricot, cherry and almond were not seen anywhere. Apple was seen cultivated in Shillong, that too in few houses. Kiwifruit is becoming popular with few farmers. In Ummulong (Jaintia Hills), people did not know the use of walnut though stray trees are found to occur there. Some minor fruits seen in local markets are that of *Prunus nepaulensis* Ser. (Soh-iong in Khasi Language),

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Table 1. Physical features of the explored areas

S.No.	Particulars	Meghalaya	Arunachal Pradesh
1.	Districts and areas	Ri Bhoi (Summer, Umran, Nangpoh, Kyrdem, Umiam) East Khasi Hills (Sohra, Cherra, Laitkor Peak, Elephant Falls, Mawphlong, Mawngap, Laitlyngkot, Pynursla) West Khasi Hills (Nongstoin, Jakrem) Jaintia Hills (Jowai, Amladem, Rothiang, Saphai, Ummulong, Narthiang, Kandulli)	West Kameng (Dirang, Mandala, Munna, Bomdilla, Rupa, Shergaon, Nykmadung) Tawang (Jang, Jaswant Garh, Tawang, Bomdir, Lumla, PTSO)
2.	Boundary and location	West: East Garo Hills; North & East: Assam; South: Bangladesh Altitude varied from 530 m (Pahamrioh in Ri Bhoi Dt.) to 2007m (Laitkor Peak in East Khasi Hills Dt.). Latitude ranged from 25° 17' 819" N (Tiewkla in East Khasi Hills Dt.) and 25° 59' 180" N (Pahamrioh in Ri Bhoi Dt.) whereas longitude from 91° 17' 097" E (Nongstoin in West Khasi Hills Dt.) and 92° 37' 435" E (Saphai in Jaintia Hills Dt.)	Tibet region of China in the North, Bhutan in the West, East Kameng districts of Arunachal Pradesh in the East and Assam in the South. Altitude of the explored regions ranged from 1600 to 3176m MSL.
3.	Physiographical region & vegetation	Middle hill (600-1200 m MSL) and Upper hill region (>1200 m). In most of the explored, coalmines, iron ores and limestone are rich. Large waterfalls, swampy bog soils, heavy rainfall (600-1200 cm), frequent flood followed by landslides and force winds are common features. More than one third of the area is under forest cover. Above 1500 m, temperate elements are represented.	Above 1600 m, elevation the vegetation/feature is almost resembling that of other Himalayan regions i.e. dryness in atmosphere, landslide in rainy season, less plant density, etc. Average rainfall varies from 820 mm in the higher ranges to 3000 mm in the down areas, spread over 8 months. Unlike Meghalaya, here river valleys are considerably depressed with magnificent mountainous chain coupled with narrow cliffs clothed with coniferous forests. <i>Jhum</i> cultivation is noticed in few areas near habitations. Maize and finger millet are found grown in large scale in the most of the explored area.
4.	Agriculture	Main agricultural crops include rice and maize. Temperate fruits such as peach, plum and pear are cultivated.	



Fig. 1: Areas of botanical collection in Meghalaya (right down) and Arunachal Pradesh (right up)

Table 2. List of germplasm collected during the exploration trip

S. No.	Crop group	Local name(s) ^a	Type of Material	Collection site (s)	State(s)	Cultivated /wild ^b	Acc.	Remarks
A. Fruit and nut crops (28)								
1	<i>Chaenomeles cathayensis</i> (Hemsl.) Schneid.*	—	Scion	Garden	AR	C	1	Native of China
2	<i>Elaeagnus latifolia</i> L.	—	Live plant	Backyard	ML, AR	C,W	2	Recently domesticated
3	<i>Juglans regia</i> L.	—	Scion	Backyard	ML	C	1	—
4	<i>Malus pumila</i> Mill.	—	Scion	Garden	AR	C	4	—
5	<i>Passiflora edulis</i> Sims*	Soh-brap	Fruit	Market	ML	C	1	—
6	<i>Prunus armeniaca</i> L.	—	Scion	Backyard	AR	C	1	—
7	<i>Prunus cerasifera</i> Ehrh.*	—	Scion	Garden	AR	C	1	—
8	<i>Prunus jenkinsii</i> Hook. f.	Soh-iong-hlaw	Scion	Backyard	ML	C,W	1	Flowering during Aug.
9	<i>Prunus nepaulensis</i> Ser.	Soh-iong	Scion, seed	Backyard	ML	C,W	1	Preferred plant of cultivation
10	<i>Prunus persica</i> (L.) Batsch	Soh-phareng	Scion	Garden	ML, AR	C	5	—
11	<i>Prunus salicina</i> Lindl.	—	Scion	Garden	ML, AR	C	5	—
12	<i>Pyrus pyrifolia</i> (N.Burm.) Nakai var. <i>culta</i> (Makino) Nakai	—	Scion	Backyard	ML	C (semi-wild)	5	Very commonly seen
B Wild Relatives (51)								
1	<i>Actinidia callosa</i> Lindl.	Mei-soh-khan	Live plant	Natural and disturbed areas;	ML, AR	W	3	Very common in AR
2	<i>Corylus ferox</i> Wall.	—	Scion	>1200m >2500m; along roadsides	AR	W	1	Occasionally seen
3	<i>Diospyros kaki</i> L.f.*	—	Scion	Rare in Jaintia Hills; 1300-1600m	ML	W	2	It is purely wild form
4	<i>Diospyros lotus</i> L.*	—	Scion	Along roadsides; 1600 m	AR	C	1	Escape in Dirang
5	<i>Docynia indica</i> Decne	Soh-phokhasi	Scion	Natural and disturbed Areas; < 1800 m	ML, AR	C,W	4	Very common in ML; gigantic trees noticed
6	<i>Elaeagnus umbellata</i> Thunb.*	—	Live plant	Plenty; > 2500 m	AR	W	1	forms very big bush
7	<i>Fragaria daltoniana</i> J. Gay*	—	Live plant	Temperate broad-leaved forests; >2700 m	AR	W	1	—
8	<i>Malus baccata</i> (L.) Borkh. var. <i>baccata</i>	Soh-shur	Scion	Along riversides; 1900-2200 m	ML, AR	W	3	Variability seen
9	<i>Prunus carmesina</i> Hara*	—	Scion	Hilltops; >1900 m	ML	W	1	Rarely noticed
10	<i>Prunus cerasoides</i> D. Don*	Diengkadi-tusso	Scion	Subtropical forests up to 1700 m	ML, AR	C,W	2	Very common in AR
11	<i>Prunus cornuta</i> (Wall.exRoyle) Steud. forma <i>cornuta</i> *	—	Scion	Natural areas; >2400 m	AR	W	1	Common in AR
12	<i>Prunus cornuta</i> (Wall. ex Royle) Steud. forma <i>villosa</i> (Hara) Hara*	—	Scion	Rare; >2600 m in oak forests	AR	W	1	Endemic to the region
13	<i>Prunus phaeosticta</i> (Hance) Maxim.*	Dieng-ning-iong	Scion	Along riversides; 1500 m	ML	W	1	Rarely noticed
14	<i>Prunus rufa</i> Steud.	—	Scion	Natural areas; >2700 m	AR	W	2	—
15	<i>Prunus venosa</i> Koehne	Dieng-tyrkhum	Scion	Along riversides; 1500 m	ML	W	1	Common in ML
16	<i>Pyrus pashia</i> Buch.-Ham.	Soh-jhur	Scion	Natural and disturbed areas; >1400 m	ML, AR	C,W	5	Very common in both the areas; variability
17	<i>Rubus acuminatus</i> Sm.	—	Live plant	Natural areas; 1400 m	ML	W	1	Rarely noticed
18	<i>Rubus pentagonus</i> Wall.*	—	Live plant	Natural areas; >2400 m	AR	W	1	Occasional
19	<i>Rubus assamensis</i> Focke	—	Live plant	Natural areas; 1800m	ML	W	1	—
20	<i>Rubus calycinus</i> Wall. ex D.Don	—	Live plant	Natural areas; 1800-2400 m	ML, AR	W	2	Frequent
21	<i>Rubus foliolosus</i> D. Don*	—	Live plant	Natural areas; >2400 m	AR	W	1	Rarely noticed
22	<i>Rubus hexagynus</i> Roxb.	—	Live plant	Natural areas; 1400 m	ML, AR	W	2	Endemic to the region
23	<i>Rubus macilentus</i> Camb.*	—	Live plant	Natural areas; >2400 m	AR	W	1	—
24	<i>Rubus moluccanus</i> L.	—	Live plant	Natural areas; 1400-1800 m	ML	W	3	Very common
25	<i>Rubus niveus</i> Thunb.	—	Live plant	Natural areas; 1700-2800 m	ML, AR	W	2	Common; highly variable

Contd.

Table 2 Contd.

S. No.	Crop group	Local name(s) ^a	Type of Material	Collection site (s)	State(s)	Cultivated /wild ^b	Acc.	Remarks
26	<i>Rubus opulifolius</i> Bertol.	—	Live plant	Natural areas; 1700 m	ML	W	1	Endemic to the region
27	<i>Rubus rosifolius</i> Sm.*	—	Live plant	Natural areas; 1700 m	ML	W	1	—
28	<i>Rubus rosifolius</i> Sm. forma <i>coronarius</i> Sm.*	—	Live plant	Garden	ML	C (as ornament)	1	Double-flowered
29	<i>Rubus splendidissimus</i> Hara*	—	Live plant	Natural areas; 2800 m	AR	W	1	Most ornamental plant
30	<i>Rubus thomsonii</i> Focke*	—	Live plant	Natural areas; 2500 m	AR	W	1	Rarely noticed
31	<i>Sorbus cuspidata</i> (Spach) Hedl.*	—	Scion	Natural areas; 2930 m	AR	W	1	Rarely noticed
32	<i>Sorbus foliolosa</i> Spach*	—	Live plant	Natural areas; 2600 m	AR	W	1	Frequent

*Not collected in earlier explorations from these states; ML: Meghalaya; AR: Arunachal Pradesh

^aLocal names are pertaining to Khasi language only (i.e. for Meghalaya)

^bMentioned based on observation: W—wild; C—cultivated

Baccaurea ramiflora Lour. and *Docynia indica* Decne (Soh-phokhasi) indicating the scope for their cultivation in a big way. There are few plants such as *Myrica esculenta* Buch.-Ham. ex D. Don, *Prunus nepaulensis*, *Vangueria spinosa* Roxb., *Elaeagnus latifolia* L., *Docynia indica*, etc. in transition process from wild to cultivated status. They are either protected in the wild or often selected for big sized fruits and planted in village backyards and homesteads. In Shillong, *Castanea sativa* Mill. and double-flowered peach were employed as ornamentals whereas *Ficus carica* L. and *Cyphomandra betacea* (Cav.) Sendt. as homestead fruits. In Jowai (Jaintia Hills), *Eugenia jambos* L. was found in backyards of some houses. Other observations are as follows:

1. *Diospyros kaki* L.f. was noticed in purely wild condition in both Khasi and Jaintia Hills (1300-1600 m). Also it is reported to be wild in Naga Hills in India while in rest of the country, its introduced cultivars are under cultivation. The plant is small tree with leaves oblong-acuminate whereas the cultivated types are broadly elliptic. Its fruits mature during September- October; size 2 x 1.5 cm, oblate with four prominent ridges.
2. *Prunus jenkinsii* Hook. f. was noticed only under cultivation. It is a medium sized tree flowering during August-September. Leaves are linear-oblong, undulate without serrations. Fruit size is bigger than that of *Prunus nepaulensis* and ripen during March-April. It was identified as one of the rare species (Arora and Nayar, 1983).
3. *Prunus nepaulensis* is distributed from 1200 to 2600 m; flowers during lean season (Oct.-Nov.) and fruits take more time to mature i.e. mature only in July-August. Fruits are pulpier than other wild species. It is often cultivated for fruits in home gardens. It is

related to *P. cornuta* (Wall. ex Royle) Steud. and *P. undulata* Buch.-Ham. (Arora and Nayar, 1984).

4. Tremendous variability in *Pyrus pashia* Buch.-Ham. with respect to habit (branching pattern), leaf shape, fruit size, pedicel length, fruit colour and shape was noticed in Laitlyngkot area of East Khasi Hills.

Arunachal Pradesh

Barring apple, all temperate fruits are localized to homestead only. Young apple orchards are now coming up in few places above 1600 m. Plum (cv. Santa Rosa), Asiatic pear and peach are common backyard plants whereas apricot is rare. Cherry and raspberry plants were not seen in cultivation although many wild species related to them were found. Walnut occurs wild in between 1200 m and 3000m; apart from this, it was found planted for afforestation and along roadside etc. Like Meghalaya, Kiwifruit is becoming popular with few farmers of the state. Protected types of *Pyrus pashia* and *Cornus capitata* Wall. for fruit purposes are often observed. Here owing to the limited presence of crop germplasm, our attention in those areas was directed towards looking for useful wild biodiversity. Some interesting observations are as follows.

1. The area from Dirang to Mandala (~25 km) is a paradise for collection of *Rubus* species i.e. *Rubus ellipticus* Sm., *R. macilentus* Camb., *R. moluccanus* L., *R. hexagynus* Roxb., *R. niveus* Thunb., *R. calycinus* Wall. ex D. Don, *R. splendidissimus* Hara, *R. pentagonus* Wall. and *R. foliolosus* D. Don. All appearing in sympatric distribution. Of them, species worthy for immediate utilization includes *R. macilentus* (2000-3000 m; sweet fruit), *R. niveus* (2000-3300m; sweet fruit) and *R. moluccanus* (up to 2300m; large-sized fruit). All are related to raspberry (*R. idaeus* L.).

2. *Diospyros lotus* L. was found escaped between 1700 and 2000 m. It is adjudged as the best rootstock for cultivated persimmon (*D. kaki*) in subtropical and temperate areas though we have not seen persimmon cultivation in areas explored. It is the only cold adaptable species of *Diospyros* existing in India apart from the cultivated one. The fruits are slightly oval in contrast to western Himalayan forms which are more or less round.
3. *Fragaria daltoniana* is distributed at an altitude from 2000 to 3600 m. Darrow (1966) suggested its potential for increasing the fruit size and inducing cold hardiness in strawberry. It may be used in rock-gardens or for carpeting.
4. Two possible introgression between *Malus baccata* (L.) Borkh. and *M. pumila* Mill. were seen in home garden in the outskirts of Tawang town. The fruit diameter was about 1.8-3.0 cm with 5-8 fruits in single cluster. The pedicel attachment with fruit is highly depressed. In another introgression, the fruit base is grooved with many angles. The leaf shape and size are of intermediate nature.
5. *Chaenomeles cathayensis* (Hemsl.) Schneid., a native of China, not reported in the flora of Arunachal Pradesh (Hajra *et al.*, 1996), but we found it commonly cultivated in home garden in Tawang area. It might have been brought via Tibet Region (China) where it was reported (eFloras, 2008) to occur in wild condition. Apart from its ornamental value, this plant has been used as rootstock for apple but needs validation (pers. comm.). Fruit is used for making pickles.
6. *Corylus ferox* Wall., a relative of hazelnut was spotted out by us in the outskirts of Tawang town (2700-3000 m) growing in semi-wild condition in partly disturbed areas. Local people rarely know its nut value. Sucker production unlike hazelnut, was found very less which a desired trait. Leaves resemble that of elm. Fruits are in cluster of 6-8, which mature during October.
7. Comparing to other states, pressure on agro-biodiversity is less except in the periphery of human dwelling because of low population density. People do have awareness on biodiversity conservation for instance Mr. Nasang Monpa, farmer of Lemberdung (Tawang) maintains five different wild primitive types of *Pyrus* (involving *P. pashia* and *P. pyrifolia*

(N.Burm.) Nakai) in his farm for the sake of inquisitiveness.

General Features

Apart from *Pyrus pashia*, variability was also observed in *Docynia indica* [fruit size, shape (oblong & round)], Asiatic pear (fruit size, intensity of brown coating over fruit), peach and plum (fruit size, season of harvest, flesh colour, stone attachment with flesh), *Actinidia callosa* (plant habit, degree of hairiness in stem), *Malus baccata* (fruit size, petiole length, leaf size and shape, degree of thorniness) and *Rubus moluccanus* [plant stature, flower colour (yellow & white)]. As against western Himalaya, the practice of *in situ* grafting of cultivated pears over *Pyrus pashia* was not seen in both the states. In this regard, *Sorbus* spp. also forms potential rootstock for pear. *In situ* budding of superior quality walnut can offer scope for extending walnut cultivation in Arunachal Pradesh.

Different collections in both states indicated that typical temperate and alpine Himalayan taxa were absent in Meghalaya e.g. *Sorbus foliolosa* Spach, *S. cuspidata* (Spach) Hedl., *Juglans regia* L., *Prunus rufo* Steud., *P. cornuta*, *Corylus ferox*, etc. Plenty of populations of *Pyrus pyrifolia* var. *culta* and *Docynia indica* were noticed in Meghalaya while a few plants in Arunachal Pradesh; converse is true with the case of *Actinidia callosa*. *Diospyros kaki* (wild form) and *P. jenkinsii* were seen only in Meghalaya.

During 1994 and 1997, staff of NBPGR Regional Station, Shimla surveyed and collected 81 and 58 temperate fruit germplasm from North Eastern India respectively (Annual Report, 1994, 1997). In this exploration, 21 taxa not previously collected were collected [see asterisk (*) marked taxa in Table 2]. More than one third of taxa collected are endemic to the region. Apart from it, novel variants in *Malus baccata*, *Pyrus pyrifolia* and *Malus pumila* were also collected. Notably few species which were expected to be collected such as *Fragaria nilgerrensis* Schlecht., *Prunus bracteopadus* Koehne, *Prunus punctata* Hook.f., *Sorbus granulosa* Rehd., *S. verrucosa* Rehd. in Meghalaya and *Malus dirangensis* Joshi & Singh, *M. sikkimensis* (Wenz) Koehne, *Sorbus ursina* (Wenzig) Hedl., *Pyrus expansa* (Koehne) Bennet, *Actinidia strigosa* Hook.f. & Thoms. in Arunachal Pradesh were not located indicating the need for more attention in future exploration programmes particularly their identification in the field and searching in more probable areas. Apart from above, areas not

surveyed in this exploration due to technical constraints such as Kalaktang, Talung Dzung in West Kameng district and entire East Kameng district of Arunachal Pradesh will also be worthy for future programmes. Serious collection of variability in *Docynia indica* can be undertaken in Meghalaya owing to its graft compatibility with apple. There is an urgent need to initiate researches on enhancing the life of scion/cuttings during transit because of poor transportation facilities in remote places of Arunachal Pradesh.

Overall out of 79 accessions collected, 33 taxa are potential wild relatives of crop plants. Typical temperate and alpine Himalayan taxa are absent in Meghalaya with respect to the intended wild species. This exploration filled the gap in the past collections from these areas as it yielded in the collection of 23 new taxa apart from some good variants in fruit crops. Future collection programmes should be made for uncollected variability in crops and related taxa and unexplored potential areas. Studies should be made on *in situ* conservation of *Rubus* spp. in West Kameng district of Arunachal Pradesh. Ways to speed up the domestication processes in protected forms, semi-domesticates such as selection of ecotypes of these fruits followed by standardization of agro-technologies (instant domestication) and as a long term strategy, by polyploidy breeding (*Rubus*), interspecific hybridization with their cultivated counter partners (*Rubus*, *Prunus*), and selection involving generations of sexual recombination (Pradheep *et al.*, 2006) will surely benefit the native people.

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Genetic Diversity Analysis in Aromatic Rice Germplasm using Agro-Morphological Traits

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During the present investigation, an attempt was made to analyze the relatedness and distances among different aromatic rices using 20 agro-morphological traits. The genetic divergence among 45 indigenous aromatic rice germplasm was estimated for 20 agro-morphological characteristics. Based on this analysis using agro-morphological characteristics, all the genotypes were grouped into 10 different clusters. Cluster I, II, III, IV, V, VI, VII, VIII, IX & X, comprised of 20, 8, 5, 2, 2, 2, 2, 2, 1, 1 genotypes, respectively. Among different traits, weight of panicle, plant height, 1000-grain weight and flag leaf length played major role in making of clusters. The maximum intra-cluster divergence was observed for cluster VI and least for clusters IX & X. As far as the inter cluster divergence is concerned cluster IX & X were highly divergent, and least inter cluster divergence was recorded between cluster VIII & II. This analysis was also followed by Dendrogram study which grouped all genotypes in 3 major clusters. The genotypes from these clusters may be used as potential donors for future hybridization programme to develop varieties with more grain as well as kernel length.

Key Words: Basmati rice, Genetic divergence, Agro-Morphological traits

Introduction

Rice (*Oryza sativa*) is the world's single most important food crop and a primary food source for more than a third of world's population. It is no longer a luxury food but has become the only cereal that constitutes a major source of calories for the urban and the rural (Sasaki and Burr, 2000). The intra-specific variation in rice is extensive and sub-specific classification has always been important for rice breeders and geneticists. India is one of the original centers of rice cultivation. The harvesting area of the rice in India is the largest in the world. India stands next only to China in terms of production and occupies second position in rice exports, next only to Thailand among the rice trading countries of world (The Hindu Survey of Agriculture, 2005). Aromatic rices forms a separate group and, is nature's gift exclusive to Indian sub continent (Glaszman 1987). The aroma associated with some domesticated rice varieties may have arisen from a gene mutation during evolution or be the outcome of a separate domestication event (Bradbury *et al.* 2005a). Among aromatic rices, *basmati* is accepted as best scented longest and slenderest rice in world. India is leading country in the export of scented rice and due to its importance, the basmati rice is considered as *Scented pearl* (Siddiq, 1996). An ever increasing global demand for aromatic rice has been noted in the recent times. Chaudhary *et al.* (2003) have discussed the economic aspects of aromatic rice detailing current trends, consumption pattern and global market demands. Presently, only traditional basmati rices

are accepted as Basmati. There is a strong need that the germplasm of this cash crop be collected preserved and characterized in detail. Indian rice varieties have been developed traditionally by selection, hybridization and back crossing with locally adapted high yielding lines. An important source for the introduction of new traits is the existence of genetically diverse pool of rice germplasm available in country, but lying unexplored. Many farmers in India still grow local germplasm under different names and they also bring some varieties from distant places and start cultivating them with local names. Present study was undertaken to evaluate variability and relatedness in forty five genotypes based on twenty agro-morphological traits.

Materials and Methods

Field performance of all the forty five germplasm was evaluated at Seed Production Centre (S.P.C) at G.B. Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India, during *kharif* 2004 in two replications, using Randomized Block Design (RBD) under organic farming system. Nursery sowing was done in June 2004. Seedlings of each germplasm were transplanted in a 20 m² (5 x 4 m²) plot. Transplanting was done after one month of sowing. During transplanting plant-to-plant distance was 15 cm and row-to-row distance was 20 cm. Observations for twenty traits were recorded during crop season taking data of five plants each in two replications for forty five genotypes.

The mean values of two replications were used for statistical analysis. The analysis of genetic divergence using D^2 -statistics of Mahalanobis (1936) as described by Rao (1952) and grouping of genotypes were done in to different clusters following Tocher's method (Rao 1952). The agro-morphological traits data was converted in to binary data and Dendrogram was prepared by Unweighted Pair Group Method Arithmetic Averages (UPGMA) based study using Jaccard Coefficient (Software Applied Math's 3.5 version). For cluster analysis Sequential Agglomerative Hierarchical Nestee (SAHN) was done.

Results and Discussions

Analysis of variance

The analysis of variance revealed the presence of significant variability among genotypes for all the characters studied. (Table 1)

Clustering pattern

All genotypes were grouped in 10 clusters using twenty agro-morphological traits. The clustering pattern is presented in Table 2. Twenty genotypes were accommodated in Cluster I, while cluster II accommodated 8 genotypes. There were 5 genotypes in cluster III and Cluster IV, cluster V, cluster VI, cluster VII and cluster VIII accommodated 2 genotypes each, while Cluster IX and X accommodated only one genotype each.

Intra and inter cluster divergence

The average intra and inter-cluster D^2 values and average genetic distance between and within cluster for agro-

morphological characters are presented in Table 3. The maximum intra-cluster divergence was observed for cluster VI (D^2 value of 2760.88, average distance 52.54) and least intra-cluster divergence was recorded for cluster IX and X (D^2 value of 0.00; and average distance of 0.00).

As far as the inter cluster divergence is concerned cluster IX and X were highly divergent, as indicated by maximum D^2 value of 15819.74 and average distance of 125.78 between them. The least inter-cluster divergence was recorded between cluster VIII and II as indicated by lowest D^2 value of 2499.51 and average distance of 50.00.

Cluster means for different characters

The cluster means of various agronomic traits are presented in Table 4. Cluster I consisting of 20 genotypes exhibited highest mean plant height (147.12 cm) and lowest mean for days to maturity (114.97 days) and filled grain/panicle (87.67). Cluster II having 8 genotypes and cluster III with 5 genotypes did not exhibit highest or lowest mean values for any characteristic. Cluster IV consisting of 2 genotypes exhibited highest mean value for panicle length (29.6 cm), panicle weight (3.65 g), filled grain /panicle (155.40) and lowest mean value for number of tillers/hill (9.70) and fertile tillers/hill (6.80). Cluster V, with 2 genotypes exhibited highest mean value for L/B ratio of flag leaf (27.07 cm) and lowest mean value for yield (33.30 q/h). Cluster VI with 2 genotypes exhibited highest mean value for panicle exersion (6.00) and total grains/panicle (170.75) and lowest mean value for plant height (90.40 cm). Cluster VII, with 2 genotypes exhibited highest mean value for flag leaf length (31.57 cm), flag leaf breadth (1.18 cm), ear bearing tillers/hill (9.42), days

Table 1. Analysis of variance for agro-morphological traits

		Mean Squares								
Source of variation	d.f.	Flag leaf length	Flag leaf breadth	L/B ratio of flag leaf	First leaf length	First leaf breadth	L/B ratio of first leaf	Tillers hill	E.B.T. hill	Panicle type
Replication	1	0.453	0.001	3.122	0.126	0.000	10.750	0.464	0.050	0.711
Treatment	44	22.74**	0.01**	16.72**	45.06**	0.02**	54.94**	12.34**	3.52**	10.32**
Error	44	0.048	0.000	0.215	1.495	0.000	2.266	0.206	0.090	0.711
C.D. at 1%		0.594	0.031	1.249	3.292	0.039	4.053	1.224	0.811	2.270

Table 1. contd.

		Mean Squares									
Source of variation	Panicle exersion	Days to 50% flowering	Days to Maturity	Plant height	Panicle length	Weight of panicle	Total grains panicle	Filled grains panicle	Unfilled grains panicle	1000 grain weight	Grain yield
Replication	0.000	7.534	44.080	7.086	-0.020	0.084	309.82	582.65	16.043	0.012	8.55
Treatment	5.95**	68.21**	91.30**	75.72**	11.29**	1.066**	2334.3**	1790.4**	110.4**	9.23**	195.5**
Error	0.272	1.965	1.986	1.409	0.215	0.006	15.53	107.54	12.635	0.060	0.47
C.D. at 1%	1.406	3.774	3.795	3.197	1.249	0.220	10.61	27.92	9.570	0.659	1.86

All values are significant at 1% level

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Table 2. Clustering pattern of 45 genotypes using agro-morphological traits

Cluster	Genotypes	Total number
I	Basmati 370, Basmati 3034, Dehradun Basmati 3020, Basmati Mohan 381, Hansraj 3086, Basmati 106, Basmati 122, Basmati 376, Basmati 134, Hansraj 3067, Basmati C 622, Hansraj 3074, Hansraj 3077, Basmati Sathi, Basmati 1-1 A, Basmati 6129, Type 3, Basmati 107, Taraori Basmati and Basmati 5836.	20
II	Hansraj 3074 (U), Basmati Uzearpka (U), Basmati 217, Basmati 124-10, Basmati 375 A, Basmati 43 A, Basmati 5875, Basmati 433.	8
III	Basmati 3317-1, Basmati 3065 AR 1409 (U), Basmati 3032 AR 575 (U), Dehradun Basmati 3020 (U), Hansraj 3072-1.	5
IV	Tilakchandani 3048, Kalanamak 3121.	2
V	Basmati 3085, Basmati 3065 AR 771 (U).	2
VI	Hansraj 3078, Basmati 127.	2
VII	Pokkali (U) & Hansraj 3072-2 (U).	2
VIII	Basmati 136 & Basmati sufaid 100.	2
IX	Hansraj 3072-2.	1
X	Basmati Nepal.	1

Table 3. Average intra and inter-cluster D² (bold) and D values (agro-morphological traits)

Cluster	1	2	3	4	5	6	7	8	9	10
1	2085.09 45.66	3120.07 55.86	6923.40 83.21	9839.01 99.19	3027.61 55.02	13149.76 114.67	6367.93 79.80	2739.39 52.34	13985.24 118.26	3440.11 58.65
2		1786.38 42.27	4367.21 66.08	5518.74 74.96	4186.51 64.70	7889.13 88.82	4570.34 67.60	2499.51 50.00	9117.61 95.49	4741.81 68.86
3			2207.82 46.99	4795.20 69.25	4832.23 69.51	4462.52 66.80	4165.84 64.54	6370.93 79.82	4126.55 64.24	8406.91 91.69
4				2603.46 51.02	9791.54 98.95	4515.60 67.20	7060.10 84.02	7763.13 88.11	2917.71 54.02	10945.94 104.62
5					2279.83 47.75	10968.51 104.73	4711.20 68.64	4800.54 69.29	11098.80 105.35	3672.67 60.60
6						2760.88 52.54	4618.93 67.96	12649.51 112.47	4221.49 64.97	12195.22 110.43
7							2538.50 50.38	7752.23 88.05	8411.66 91.72	4681.34 68.42
8								1149.75 33.91	11531.82 107.39	5306.65 72.85
9									0.00 0.00	15819.74 125.78
10										0.00 0.00

to 50 % flowering (107.50 days) and yield (54.62 q/h) and lowest mean value for panicle length (21.07 cm). Cluster VIII, with 2 genotypes exhibited highest mean value for panicle type (7.00) and lowest mean value for L/B ratio for flag leaf (20.50), L/B ratio for first leaf (41.15), panicle exersion (1.00), days to 50 % flowering (87.00 days), weight of panicle (1.57 g), total grains/panicle (89.25), unfilled grains /panicle (10.25). Cluster IX with 1 genotype exhibited highest mean value for L/B ratio of first leaf (58.00), number of tillers/hill (15.10), 1000-grain weight (23.50 g) and lowest mean value for flag leaf length (19.60 cm), flag leaf breadth (0.95 cm), first leaf length (38.00 cm), panicle type (1.00). Cluster X, with 1 genotypes exhibited highest mean value for first leaf breadth (1.05 cm), first leaf length (51.85 cm), days to maturity (140 days), unfilled grains /panicle (46.50) and lowest mean value for 1000 grain weight

(14.50 g).

Contribution of different characters towards genetic divergence

Contribution of different agro-morphological traits towards the genetic divergence among indigenous *Basmati* rice germplasm under study is presented in Table 5. It was observed that weight of panicle (32.6 per cent), plant height (21.0 per cent), 1000-grain weight, (18.9 per cent) and flag leaf length (13.9 per cent) were major contributing factors to genetic diversity among 45 aromatic rice genotypes. first leaf breadth (7.9 per cent), panicle length (3.2 per cent), unfilled grains/panicle (1.4 per cent), and tillers/hill (1.1 per cent) were moderate contributing factors to genetic diversity. Least contribution towards genetic diversity was of first leaf length (0.20 per cent), ear bearing tillers/hill (0.40 per cent), days to 50% flowering (0.40 per cent), days to maturity (0.30

Table 4. Cluster mean values for different agro-morphological traits

Cluster No.	Flag leaf length cm	Flag leaf breadth cm	L/B ratio of flag leaf	First leaf length cm	First leaf breadth cm	L/B ratio of first leaf	Tillers/hill	E.B.T./hill	Panicle type	Panicle exertion	Days to 50% flowering	Days to maturity	Plant height cm	Panicle length cm	Weight of panicle (g)	Total grains panicle	Filled grains panicle	Unfilled grains panicle	1000 grain weight (g)	Grain yield (q/ha)
I	28.26	1.08	26.17	45.99	0.92	50.18	12.35	8.03	6.80	1.35	88.85	114.90	147.10	25.41	1.95	98.65	87.67	10.90	20.98	36.02
II	26.43	1.14	23.05	43.98	0.99	44.08	13.63	8.13	6.25	1.20	88.75	116.20	142.20	26.68	2.71	136.70	119.80	16.80	20.84	37.90
III	26.99	1.06	25.81	40.70	0.84	47.50	13.62	8.32	5.00	2.20	90.00	116.00	108.80	27.21	2.50	119.30	103.40	15.90	22.66	38.56
IV	21.12	0.98	21.52	42.89	0.85	48.32	9.70	6.80	3.00	3.50	93.75	127.50	120.50	29.60	3.65	169.00	155.40	13.80	20.35	39.75
V	29.32	1.08	27.07	36.95	0.74	49.87	13.72	8.55	3.00	2.00	95.25	115.50	138.90	24.82	2.37	116.20	100.20	16.20	20.33	33.30
VI	27.60	1.13	24.05	46.05	0.98	46.70	13.00	7.90	4.00	6.00	97.00	121.70	90.40	26.70	3.37	170.70	154.00	16.70	20.53	40.95
VII	31.57	1.18	26.57	46.82	0.95	49.17	14.80	9.42	5.00	5.00	107.50	134.50	108.20	21.07	2.56	169.70	146.50	23.20	21.85	54.62
VIII	22.27	1.08	20.50	41.45	1.01	41.15	13.20	9.35	7.00	1.00	87.00	116.70	142.50	23.75	1.57	89.25	79.00	10.20	21.05	31.63
IX	19.60	0.95	20.60	38.00	0.65	58.00	15.10	8.30	1.00	3.00	98.50	117.00	101.90	28.00	3.39	154.00	92.00	12.00	23.50	50.00
X	29.65	1.18	25.10	51.85	1.01	51.05	12.70	8.80	5.00	5.00	94.50	140.00	135.00	23.25	1.80	158.00	111.50	46.50	14.50	36.55

Table 5. Per cent contribution of agro-morphological traits under study towards genetic divergence

S.No.	Character	Per cent contribution
1	Weight of panicle	32.8
2	Plant height	21.1
3	1000-grain weight	16.8
4	Flag leaf length	13.9
5	First leaf breadth	7.8
6	Panicle length	3.2
7	Unfilled grains/panicle	1.4
8	Tillers/hill	1.1
9	Total grains/panicle	0.5
10	Ear bearing tillers/hill	0.4
11	Days to 50% flowering	0.4
12	Days to maturity	0.3
13	First leaf length	0.2
14	Grain yield	0.1
15	Flag leaf breadth	0.0
16	L/B ratio of flag leaf	0.0
17	L/B ratio of first leaf	0.0
18	Panicle length	0.0
19	Panicle exertion	0.0
20	Filled grains/panicle	0.0

per cent), total grains/panicle (0.50 per cent) and yield (0.10 per cent). Traits like flag leaf breadth, L/B ratio of flag leaf, L/B ratio of first leaf, panicle type, panicle exertion and filled grains/ panicle showed no influence on genetic diversity among 45 rice genotypes.

Dendrogram Clustering

At 15 % similarity all genotypes were grouped in three major groups i.e. A group (6 genotypes), B group (36 genotypes) and C group (03 genotypes). The A major group was sub grouped in to A 1 and A 2 subgroups having 4 and 2 genotypes, respectively at 25 % similarity. The B group was further sub grouped in to B 1 and B 2 subgroups at 20 % similarity consisting of 4 and 32 genotypes, respectively. The B 2 sub group was further classified in to B 2-a and B 2 -b sub-sub groups consisting of 14 and 18 genotypes respectively. The C group comprised of 3 genotypes only.

The concept of “genetic distance” has been of vital utility (Arunachalam 1981). Several measures of distance have been proposed over the past two decades to suit

various objective of which Mahalanobis generalized distance (Mahalanobis 1936 and Rao 1952) has occupied a unique place in plant breeding. D^2 statistics has its several advantages over other methods. Firstly, it utilizes the multivariate normal distribution of the natural variation to construct the dispersion matrix, secondly, it recognizes the genotypes and environmental variation, thirdly, relative importance of characters is determined by the percentage of variation accounted by them, thus avoiding bias in choice, and lastly, the set of different populations or genotypes are classified in to distinct groups or clusters based on D^2 values. Usefulness of D^2 statistics as measure of genetic diversity will be dependent on stability over environment. The analysis of variance revealed highly significant differences among all the genotypes for the fourteen quality traits. This indicated the existence of significant amount of variability among the values for the characters studied.

Cluster prepared on the basis of D^2 statistics based on agro-morphological traits grouped, Tilak Chandan 3048 and Kalanamak 3121 in same cluster, was also confirmed by Dendrogram prepared by UPGMA based study using Jaccard Coefficient. All genotypes from usher soil (presented by “U” suffix) were clustered in same groups, i.e. Basmati 3065 1409 (U), Basmati 3032 AR 575 (U), Dehradun basmati 3020 (U) in cluster III and Pokkali (U), Hansraj 3072-2 (U) in cluster V.

Three genotypes i.e. Tilak Chandan 3048, Kalanamak 3121& Basmati Mohan 381 grouped in C group of Dendrogram, further Kalanamak 3121and Basmati Mohan 381 segregated together at 40 % similarity, though these two were groped in different groups by D^2 analysis. The reason was that there was quite similarity in Agro-Morphological traits of Kalanamak 3121& Basmati Mohan 381 with respect to Tilak Chandan 3048 which was as following. Flag leaf length (22.40 cm, 32.40 cm, 31.75 cm) L/B ratio of flag leaf (21.25, 27.0, 28.35) No. of tillers/hill (5.40, 9.40, 8.40) EBT/hill (5.40, 9.40, 8.40) and 1000 grain weight (20.50 gm, 21.30 g, 21.50 g) for Tilak Chandan 3048, Kalanamak 3121& Basmati Mohan 381 genotypes, respectively.

Bindali 3317, a medium grain genotype showed quite

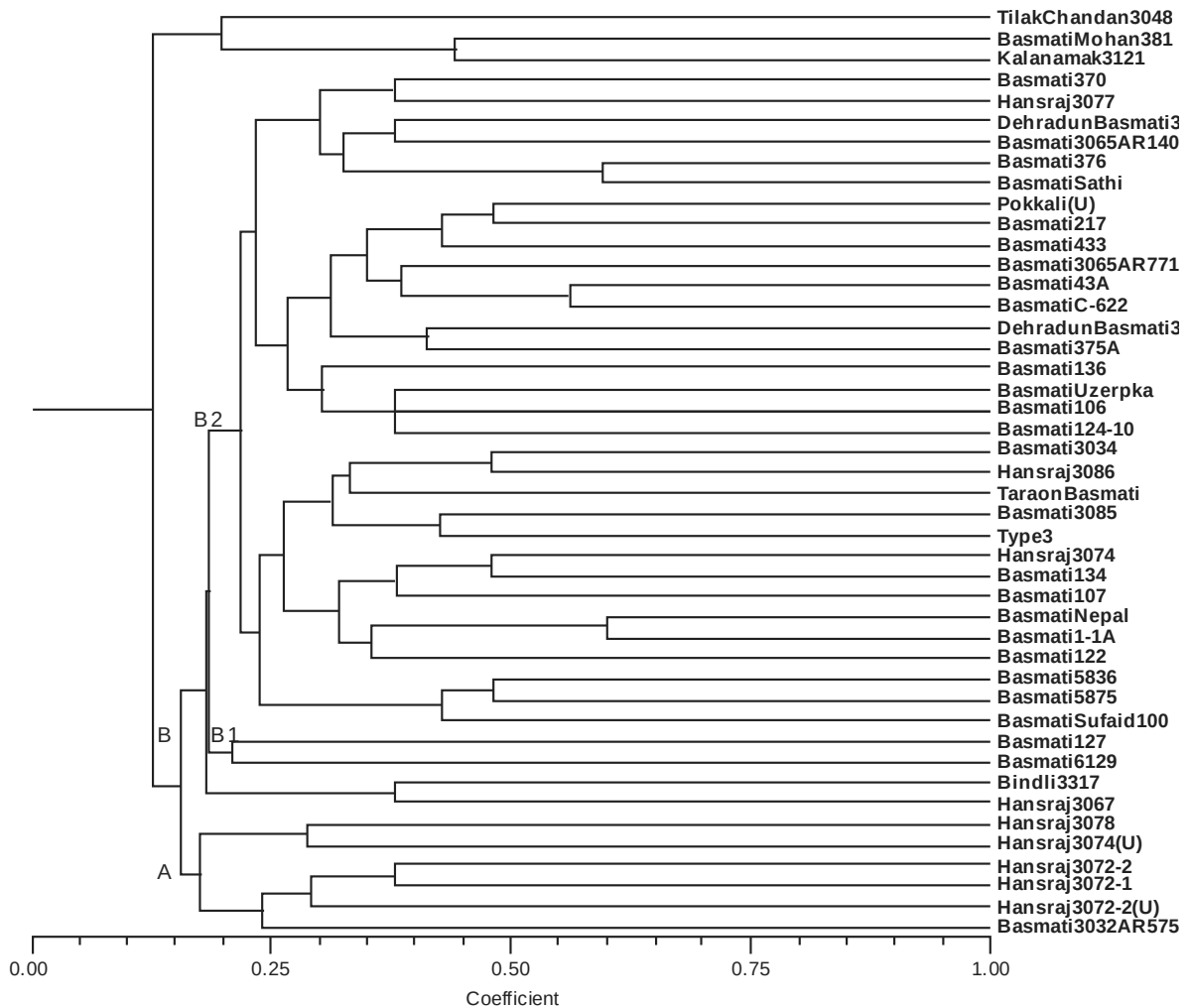


Fig. 1: Agro-Morphological trait based dendrogram

good resemblance to Hansraj 3067 a long grained genotype and segregated in B1 group of Dendrogram due to resemblance in agro-morphological traits as following. Flag leaf length (22.75 cm, 27.0 cm), L/B ratio of flag leaf (26.50, 26.85), first leaf length (39.0 cm, 40.0 cm), days to 50 % flowering (82.0 days, 82.0 days), days to maturity (106 days, 106 days) and 1000 grain weight (21.0 g, 21.0 g) for Bindli and Hansraj 3067 genotypes, respectively.

Basmati 3032 AR 575 (U) and Hansraj 3072 (U) genotypes clustered together due to resemblance in their adaptation of growing environment as both are adapted for usher soil environment. They showed resemblance in agro-morphological traits as following. Days to 50 % flowering (97.0 days, 98.5 days), days to maturity (117 days, 117 days) and plant height (102 cm, 101.9 cm) for Basmati 3032 AR 575 (U) and Hansraj 3072 (U) genotypes, respectively.

Present study indicated that different indigenous

varieties named after aromatic rice varied widely in their agro-morphological characteristics. However, a number of Dehradun Basmati and Hansraj selections showed high degree of similarity indicating that Hansraj which was once grown widely in districts Bijnore, Pilibhit and Bareilly of Uttar Pradesh and Udham Singh Nagar of Uttarakhand is *Basmati*. Probably *Basmati* lines grown in these districts were called as Hansraj.

As agro-morphological traits are influenced by environmental factors, hence there is need to use molecular markers like RAPD, and SSR in follow up of this study.

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Estimation of Genetic Divergence among Durum Wheat (*Triticum durum* L.) Genotypes for Yield and Yield Contributing Traits

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Selection of genetically distant parents is an essential step in hybridization. Twenty indigenous germplasm lines were evaluated to assess the genetic diversity and variability. The significant mean sum of squares for all the ten characters indicated the presence of variability. All the 20 genotypes were grouped into five clusters according to Tocher's method. Cluster I and IV evolved as large clusters comprising six genotypes each. The maximum inter-cluster distance was exhibited by genotypes of cluster V, while it was minimum in the genotypes of clusters III, suggesting that crossing between the genotypes included in these two clusters is expected to generate heterotic combinations and thus facilitate the isolation of desirable genotypes.

Key Words: Genetic diversity, Inter-cluster, Durum wheat (*Triticum durum* L.)

Durum wheat is next only to bread wheat in respect of area (1.5 million hectares) as well as production of 1.2 million tones (Anonymous, 2007). In breeding programme, selection of parents for hybridization is largely based upon genetic diversity, wide adaptation and high yielding potential. Genetic diversity for selecting parents plays a key role in genetic variability in varietal improvement programme for any crop. The germplasm consisted of large number of varieties, lines, genotypes, landraces and wild relatives available to breeder, serve as a reservoir for providing variability in different traits under consideration for improvement but a very limited number can be used in hybridization programmes. Hence, involvement of genetically diverse parents /lines based on desirable character combinations collectively is essential to obtain more heterotic recombinants in segregating generations and thus offers a scope for maximum improvement. The present study was, therefore, planned to assess genetic diversity in 20 genotypes of durum wheat using Mahalanobis D² statistics (1936) to cluster the genotypes in different groups based on genetic divergence.

Materials and Methods

Twenty genotypes, viz, MPO 1153(MOJO/AIRON), RAJ 6566(RAJ 6496/POW215), NIDW 309(YAVA ROS-79), NIDW 295(BHOOMI R33/P1A1A), RD 1093(T. POLonicum Lsp7/RD 75), AUKD 2(KYDRANASS A 30/SILVER5), AUKD 3(MAGH72/RUFO//ALG86/RU/3/ALTAR 84/ALD/4), HI 8591(HI 8144/NI 8652), UAS 2021(THB/CEP7780//2MUSK-4), RD 1008(PBW 34/RD

20), DBPY 02-3(RAJ1555/DCB 93), RD 1009(PBW 34/RD 20), HD 4713(SCOT 29/TARA 1//AJAIA2), UAS 404, HI 8638(SEL.BUTTAH), HI 8645(HI8185/MESSAP 10//HI 8381/MESSAPI0), PDW 300(PDW 2421/PDW 233/PDW 232), MASA 499, NIDW 37(PARRON 1/MRB 5895//PARRON 1) and DBPY 04-5(DUKEM 12/2RASCON 21//POW 233) of durum wheat of different agroecological origins were evaluated in randomized block design with three replications at the Field Experimentation Centre of the Department of Genetics and Plant Breeding, College of Agriculture, Allahabad Agricultural Institute, Allahabad during *rabi* 2007-08 to assess genetic diversity using Mahalanobis D² statistics (1936). Paired row plot of 3m length of each genotype was grown in each replication with row-to-row and plant -to-plant spacing of 25 and 5cm, respectively. Recommended package of practices were followed to raise a healthy crop. Ten randomly selected plants from each plot per replications were scored for recording observations on the following traits, viz., number of tillers per meter, number of tillers per plant, spike length (cm), number of seeds per spike, 1000 seed weight (g), biological yield per plant (g) and seed yield per plant (g). However, data on days to 50% heading, days to 50% flowering and days to maturity, were recorded on plot basis (the number of days taken from the date of sowing to 50 % head emergence/flowering/physiological maturity in each replication, respectively and were averaged). Mahalanobis D² statistics was used to assess genetic diversity. Genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952).

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Results and Discussion

Analysis of variance (Table 1) revealed significant differences among genotypes for all the characters studied indicating sufficient genetic variation among the genotypes for all the traits in the present study.

The twenty durum wheat genotypes were grouped into 5 clusters on the basis of their relative magnitude of D^2 values, in such a way that of D^2 values within the cluster were much lower than those between clusters (Table 2). As regards the distribution pattern of genotypes in different clusters, the cluster I and IV were the largest with 6 genotypes each, followed by cluster III with four genotypes, cluster II with three genotypes and cluster V with only one genotype. The clustering pattern indicated that there was little association of genetic diversity with ecogeographical distribution of genotypes. Genotypes with different ecogeographical origins were grouped into same cluster, which, suggested that geographical diversity does not necessarily represent genetic diversity.

These results are in agreement with the findings of Khumkar *et al.* (2000), Bergale *et al.* (2001), Gupta *et al.* (2002), Dwivedi and Pawar (2004) and Goel *et al.* (2005). However, to some extent the genotypes related by their place of origin have shown tendency to group in the different clusters, which may be because of dependence

upon the directional selection pressure that leads to evolve homeostatic mechanism that would favour consistency of the associated characters resulting in indiscriminate clustering as reasoned by Bergale *et al.* (2001) and Dwivedi and Pawar (2004). The clustering of genotypes from different ecogeographical locations into one cluster could be attributed to the frequent exchange of breeding material from one place to another and in further selection in different genotypic regions which could result in genetic drift as reasoned by Lad *et al.* (2002).

The genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selection other than ecological and geographical diversification. Therefore, selection of parents for hybridization should be based on genetic diversity rather than geographic diversity to get more heterotic recombinants and desired transgressive segregates. However, caution should be taken in selecting very divergent genotypes because such crosses may not yield proportionate heterotic response. Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high means for almost all component traits and further these divergent parents should have better combining ability to give results proportionate to heterotic response. Arunachalam (1981)

Table 1. Mean sum of squares obtained from the analysis of variance for various traits in durum wheat

Characters	Sources of variation		
	Replications	Genotypes	Error
d.f	2	19	38
Days to 50% heading	4.46	45.29**	1.62
Days to 50% flowering	1.05	59.17**	1.78
Days to maturity	4.51	28.91**	2.32
Number of tillers per meter	0.74	701.66**	1.77
Effective tillers per plant	0.73	2.84*	0.11
Spike length	0.02	3.80*	0.03
Number of grains per spike	0.90	33.34**	1.01
1000-grain weight	0.49	92.73**	0.27
Biological yield per plant	81.12	252.97**	4.64
Seed yield per plant	5.85	21.10**	2.13

** Significance at 1% level of significance

* Significance at 5% level of significance

Table 2. Clustering of 20 genotypes of durum wheat based on D^2 statistics

Cluster	Number of genotypes	Genotypes
I	6	MPO 1153, AUKD 2, HI 8638, PDW 300, RD 008, RD 1009
II	3	NIDW 309, HI 8591, RAJ 6566
III	4	HI 8645, MASA 499, DBPY 04-5, DBPY 02-3
IV	6	NIDW 295, USA 404, HD 4713, NIDW 37, RD 1093, USA 2021
V	1	AUKD 3

also observed that more diverse the parents within its overall limits of fitness, the greater are the chances of heterotic expression of F_1 's and a broad spectrum of variability in segregating generations.

The intra and inter-cluster average D^2 values given in Table 3. The magnitude of intra-cluster distances measures the extent of genetic diversity between the genotypes of the same cluster. Inter-cluster distance is a measure of genetic distance between two clusters. The intra-cluster distances ranged from 0.00 (cluster V) to 338.24 (cluster I) which indicated the presence of

sufficient amount of diversity among different clusters. The inter-cluster distances varied from 406.399 (between I and III) to 5744.840 (between III and V). The inter-cluster D^2 value was much higher than any intra-cluster average D^2 values. The maximum genetic diversity was observed between cluster III and V (5744.840) followed by that between cluster I and V (4719.071). Among these clusters, the cluster I, III and V performed outstanding on the basis of better cluster means for most of the characters. Out of three possible combinations from these selected clusters, most divergent cluster combinations were I and V as well as III and V. The involvement of genotypes belonging to cluster V with genotypes of clusters I and III in hybridization is advocated in order to achieve high transgressive segregates for grain yield, as these clusters showed maximum genetic diversity for grain yield and its components.

The mean values of different clusters for 10 characters are given in Table 4. The cluster means for different traits were reflections of genetic differences prevalent among the clusters. The clusters showed difference with each other for one or more traits. Cluster I took least time for days to 50% heading and days to 50% flowering. Cluster II took least time for days to maturity. Cluster III had highest mean values for number tillers per meter row and effective tillers per plant. The highest cluster mean for spike length was exhibited by cluster V, while number of grains per spike by cluster I. The cluster V exhibited the highest cluster mean value for 1000 seed weight, biological yield per plant and seed yield per plant. Thus cluster I, III and V performed outstanding on the basis of

better cluster means for most of the characters. Hence, the genotypes included in these clusters were divergent as well as had higher mean values for important yield component traits. Therefore, hybridization involving genotypes of clusters I, III and V is advocated in order to achieve high yielding segregates by utilizing the crosses between cluster I and V and III and V. The genotypes, viz., AUKD 3, PDW 300, RAJ 6566, HI 8638, DBPY 04-5 and MPO 1153 were found more divergent and having superior performance for most of the yield component traits can be utilized in crossing programme to generate useful genetic variability in segregating durum wheat populations.

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Table 3. Intra (diagonal) and inter-cluster D^2 (average) values among 20 durum wheat genotypes

Cluster number	I	II	III	IV	V
I	338.24	471.73	406.39	845.01	4719.07
II		266.28	422.86	427.24	3914.64
III			217.77	956.98	5744.84
IV				223.28	2573.89
V					0.0

Table 4. Mean values of different clusters for 10 characters in durum wheat

Cluster	Characters									
	Days to 50% heading	Days to 50% flowering	Days to maturity	Number tillers per meter	Effective tillers per plant	Spike length	Number of grains per spike	1000 grain weight	Biological yield per plant	Seed yield per plant
I	78.88	86.33	123.55	101.48	11.52	8.09	59.30	41.84	57.07	28.77
II	79.00	86.66	121.11	119.74	11.88	7.9	56.33	37.99	58.66	25.44
III	79.50	87.25	121.25	121.36	12.76	7.48	56.28	37.99	58.66	27.33
IV	81.83	89.88	124.61	111.29	11.87	8.18	57.19	36.41	57.90	27.05
V	80.00	87.33	123.33	101.69	11.27	8.55	57.87	48.61	65.67	33.67
GM	79.66	87.40	122.76	111.60	11.89	8.18	58.34	51.91	59.59	28.25
CV(%)	2.11	2.21	2.52	2.20	0.57	0.29	1.66	0.86	3.56	2.41

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Multivariate Characterization of Indian Bean [*Lablab purpureus* (L.) Sweet] Genotypes

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In Indian bean, PCV values were slightly greater than GCV, revealing very little influence of environment for their expression. High heritability was expressed by days to first flower, number of pods per plant, pod length and pod yield per plant. High value of heritability along with high genetic advance was observed for number of pods per plant followed by days to first flower and days to first picking. Genetic advance as per cent of mean was observed maximum for number of pods per plant and pod yield per plant. Pod yield per plant showed positive and significant association with number of pods per plant and significant negative correlation with days to first flower and days to first picking at both genotypic and phenotypic levels. Path analysis revealed that number of pods per plant, number of days taken to first picking; pod length, pod width, seed width and seed length had direct positive effect on pod yield per plant. Multivariate hierarchical clustering depicted the classification of 46 Indian bean genotypes in 2 groups with 17 and 29 genotypes. First group further divided into 2 groups with 7 (VRSEM-765 is genetically different from 6 other genotypes) and 10 genotypes, while 29 genotypes divided into 2 clusters with 13 and 16 genotypes, respectively.

Key Words: Indian bean, Variability, Correlation, Path Coefficient analysis, Hierarchical clustering

Introduction

Indian bean [*Lablab purpureus* (L.) Sweet] is an important vegetable crop of Indian origin (Deka and Sarkar 1990). It occupies unique position for vegetable purpose among the legume vegetable (Biju *et al.*, 2001). It is a good source of protein, minerals and vitamins (Basu *et al.*, 2002). The progress in breeding for the yield and its contributing characters of any crop is polygenetically controlled, environmentally influenced and determined by the magnitude and nature of their genetic variability (Wright, 1935 and Fisher, 1981). Genetic variability, character association and path coefficient are pre-requisites for improvement of any crop including Indian bean for selection of superior genotypes and improvement of any trait (Rai *et al.*, 2003). It is very difficult to judge whether observed variability is heritable or due to environment alone. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character in future generations. Knowledge of correlation between yield and its contributing characters are basic and for most endeavor to find out guide lines for plant selection. Partitioning of total correlation into direct and indirect effect by path coefficient analysis helps in making the selection more effective. Keeping in view the above facts, the present investigation was undertaken to know genetic divergence, correlation and path coefficient among yield and its contributing characters in 46 germplasms of Indian bean collected from Bihar.

Materials and Methods

The field experiment was comprised of 46 germplasm

accessions of Indian bean growing during *rabi*, 2006-2007 at Indian Institute of Vegetable Research, Varanasi in a randomized block design with three replications. All the recommended package of practices were followed to raise a good crop. For this study, the genetic divergence, correlation and path coefficient of yield contributing characters, viz., days to first flower, days to first picking, number of pods per plant, per cent of fruit set per cluster, pod length (cm), pod width (cm), number of seeds per pod, seed length (cm), seed width (cm), 100 seeds weight (g) and pod yield per plant (kg) were recorded on randomly selected five plants in each replication. The variability for different quantitative characters was estimated as per procedure for analysis of variance suggested by Panse and Sukhatme (1985), GCV and PCV by Burton and De Vane (1953) and heritability and genetic advance by Johnson *et al.*, (1955). Correlation coefficient was worked out as per Al-Jibouri *et al.*, (1958) and path coefficient of various characters was calculated by the formula given by Dewey and Lu, (1959). Multivariate clustering analysis was used to explain variability in genotypes which will help in choosing the parents for hybridization. This approach helps in reducing the large amount of data about the parental lines to manageable proportions (Peter and Martinalli, 1989).

Results and Discussion

Variability, heritability and genetic advance

Data presented in Table 1 showed that there was considerable variability in all the traits. Close relationship between GCV and PCV was found in all the characters and PCV values were slightly greater than GCV, revealing

very little influence of environment for their expression. More than 80% heritability values was observed for all the characters except number of seeds per pod and seed length which indicated very good scope of selection in this crop. High heritability expressed in days to first flowering, number of pods per plant and pod length. High heritability along with high values of genetic advance was observed for number of pods per plant followed by days to first flower and days to first picking. Genetic advance as per cent of mean was observed maximum for number of pods per plant, pod yield per plant, pod width, 100-seed weight and days to first flower. In present investigation, characters, namely, number of pods per plant, pod yield per plant and pod width had high values of GCV accompanied with high heritability indicated additive gene action and good scope for selection. Johnson *et al.*, (1955) also suggested that high GCV along with high heritability and genetic advance gave better picture for the selection of the genotypes. Similar results were also reported by Rai *et al.*, (2003), Lal *et al.*, (2005) in Indian bean and Lal *et al.*, (2007) in cowpea.

Correlation Coefficients

Genotypic correlations were observed to be higher than the corresponding phenotypic correlation coefficients for all the characters indicating the supervision of phenotypic expression under the influence of environmental factors (Table 2). Pod yield per plant showed maximum positive and significant association with number of pods per plant (0.80) at both genotypic and phenotypic levels. On contrary, pod yield per plant expressed significant negative correlation with days to first flower (-0.44) and days to first picking (-0.33). The number of days taken to first flower showed the positive correlation with days to first picking (0.79) and negative correlation with number of pods per plant. The number of days taken to first picking

showed negative correlation with number of pods per plant (0.55), whereas per cent fruit set per cluster showed negative correlation with pod length (0.38) and number of seeds per pod (0.46). The pod length showed positive correlation with number of seeds per pod (0.52), while seed length had positive correlation with seed width (0.72) and 100-seed weight (0.54). The seed width had positive correlation with 100-seed weight (0.59).

Path Coefficient Analysis

Path analysis revealed that number of pods per plant (0.921), number of days taken to first picking (0.336), pod length (0.299), pod width (0.246), seed width (0.066) and seed length (0.093) had positive direct effect on pod yield per plant (Table 3). Thus, selection for these traits may lead to an overall increase in pod yield per plant. These results are in close conformity with the findings of Baswana *et al.*, (1980), Biju *et al.*, (2001) and Lal *et al.*, (2005) in Indian bean. The highest indirect effect on pod yield per plant (0.799) was shown by number of pods per plant (0.921) through days to first flower (0.149), per cent fruit set per cluster (0.015) and number of seeds per plant (0.001). However, the highest indirect positive effect of days to first picking (0.336) on pod yield per plant was recorded through pod width (0.072), seed width (0.010) and seed length (0.003). A indirect positive effect of pod length (0.299) on pod yield (0.161) was obtained high through per cent fruit set per cluster (0.034), seed width (0.018) and seed length (0.017). Similarly, the pod width showed indirect positive effect (0.246) on pod yield (0.123) through days to first picking (0.100), seed width (0.010) and seed length (0.002). On contrary the, the number of days taken to first flower (-0.275), 100-seed weight (-0.124), per cent fruit set per cluster (-0.088) and number of seeds per pod (-0.078) had direct negative effect on pod yield per plant. Thus, path coefficient analysis

Table 1. Variability, heritability and genetic advance for the 11 characters in Indian bean

Characters	Range	Grand mean	Variability PCV	GCV	Heritability %	Genetic advance	Genetic advance as % of mean
Days to first flower	33.00 -136.60	110.268	18.30	18.29	99.9	41.52	37.65
Days to first picking	55.00 -165.00	141.82	12.03	12.00	99.4	34.95	24.64
Number of pods/ plant	45.33 -689.67	231.572	64.04	63.99	99.9	305.05	131.73
Per cent fruit set/ cluster	35.33 - 75.00	53.123	16.69	16.07	92.7	16.93	31.87
Pod length (cm)	7.25 - 12.82	9.78	14.05	14.02	99.5	2.82	28.83
Pod width (cm)	0.50 - 3.23	2.154	29.30	28.67	95.8	1.25	58.03
Number of seeds/ pod	3.67 - 5.67	4.522	13.78	10.33	56.2	0.72	15.92
Seed length (cm)	0.81 - 1.42	1.149	10.63	8.90	70.1	0.18	15.67
Seed width (cm)	0.50 - 0.93	0.781	11.07	10.07	82.8	0.15	19.21
100-seed weight (g)	14.67 - 42.33	27.789	24.72	23.65	91.6	12.96	46.64
Pod yield per plant (kg)	0.30 - 3.94	1.603	63.51	63.38	99.6	2.09	130.38

Table 2. Phenotypic and Genotypic correlation coefficients for 11 characters in Indian bean

Characters	Days to first flower	Days to first picking	Pods per plant	Fruit set per Cluster %	Pod length cm	Pod width cm	Seeds per pod	Seed length cm	Seed width cm	100 seed weight	Pod yield per plant
Days to first flower	P	0.792**	-0.543**	0.079	0.019	0.242	0.081	-0.009	0.067	-0.227	-0.435**
	G	0.793**	-0.543**	0.081	-0.020	0.247	0.107	-0.006	0.075	-0.237	-0.436**
Days to first picking	P		-0.554**	0.081	0.002	0.289	0.038	0.024	0.138	0.105	-0.332*
	G		-0.556**	0.083	0.002	0.296	0.052	0.035	0.157	0.112	-0.333*
Pods per plant	P			-0.156	-0.143	-0.140	-0.007	-0.104	-0.094	0.026	0.799**
	G			-0.165	-0.143	-0.142	-0.015	-0.127	-0.102	0.027	0.800**
Fruit set per cluster (%)	P				-0.366*	0.158	-0.310	0.010	-0.024	-0.139	-0.243
	G				-0.382*	0.165	-0.456**	-0.005	-0.026	-0.157	-0.255
Pod length (cm)	P					-0.043	0.384**	0.157	0.251	0.218	0.161
	G					-0.045	0.518**	0.180	0.273	0.230	0.162
Pod width (cm)	P						-0.024	0.012	0.124	0.038	0.123
	G						-0.007	0.017	0.150	0.041	0.126
Seeds per pod	P							0.023	-0.006	0.060	0.072
	G							0.019	0.019	0.049	0.087
Seed length (cm)	P								0.592**	0.421*	0.023
	G								0.721**	0.544**	0.026
Seed width (cm)	P									0.492**	0.101
	G									0.590**	0.117
100-seed weight (g)	P										0.177
	G										0.182

Table 3. Direct and indirect effects of different traits on yield in Indian bean

Characters		Days to first flower	Days to first picking	Pods per plant	Fruit set per Cluster %	Pod length cm	Pod width cm	Seeds per pod	Seed length cm	Seed width cm	100 seed weight (g)	Yield per plant Kg
Days to first flower	G	-0.275	-0.218	0.149	-0.022	0.005	-0.068	-0.029	0.002	-0.021	0.065	-0.435
flower No.	P	-0.232	-0.184	0.126	-0.018	0.005	-0.056	-0.019	0.002	-0.016	0.053	-0.436
Days to first picking	G	0.266	0.336	-0.187	0.028	0.001	0.100	0.018	0.012	0.053	0.038	-0.332
	P	0.229	0.289	-0.160	0.024	0.001	0.083	0.011	0.007	0.040	0.030	-0.333
Pods per plant	G	-0.501	-0.512	0.921	-0.152	-0.131	-0.131	-0.014	-0.117	-0.094	0.025	0.799
	P	-0.493	-0.503	0.909	-0.142	-0.130	-0.127	-0.007	-0.095	-0.085	0.024	0.800
Fruit set per cluster (%)	G	-0.007	-0.007	0.015	-0.088	0.034	-0.015	0.040	0.000	0.002	0.014	-0.243
	P	-0.005	-0.005	0.009	-0.059	0.021	-0.009	0.018	-0.001	0.001	0.008	-0.255
Pod length (cm)	G	-0.006	0.001	-0.043	-0.114	0.299	-0.014	0.155	0.054	0.082	0.069	0.161
	P	-0.005	0.001	-0.039	-0.100	0.274	-0.012	0.105	0.043	0.069	0.060	0.162
Pod width (cm)	G	0.061	0.072	-0.035	0.041	-0.011	0.246	-0.002	0.004	0.037	0.010	0.123
	P	0.057	0.069	-0.033	0.037	-0.010	0.237	-0.006	0.003	0.029	0.009	0.126
Seeds per pod	G	-0.008	-0.004	0.001	0.036	-0.040	0.001	-0.078	-0.001	-0.008	-0.004	0.072
	P	-0.002	-0.001	0.000	0.009	-0.011	0.001	-0.028	-0.001	0.000	-0.002	0.087
Seed length (cm)	G	-0.001	0.003	-0.012	0.000	0.017	0.002	0.002	0.093	0.067	0.050	0.023
	P	0.000	0.001	-0.006	0.001	0.008	0.001	0.001	0.053	0.032	0.022	0.026
Seed width (cm)	G	0.005	0.010	-0.007	-0.002	0.018	0.010	0.001	0.047	0.066	0.039	0.101
	P	0.004	0.008	-0.005	-0.001	0.015	0.007	0.000	0.035	0.058	0.029	0.117
100-seed weight (g)	G	0.029	-0.014	-0.003	0.019	-0.028	-0.005	-0.006	-0.067	-0.073	-0.124	0.177
	P	0.013	-0.006	-0.001	0.008	-0.012	-0.002	-0.003	-0.024	-0.028	-0.056	0.182

revealed the importance of characters such as number of pods per plant, pod length and pod width in selection of superior genotypes for pod yield per plant.

Multivariate Classification

The multivariate approach increases the precision and decreases the complexity introduced by increasing the number of variables. Multivariate hierarchical clustering was carried out for eleven different morphological characters (Fig. 1). Distance between all pairs of

genotypes was calculated using squared Euclidean distance method and genotypes were clustered based on Ward's method. Figure 1 the classification of 46 genotypes in 2 groups with 17 and 29 genotypes. First group further divided into 2 groups with 7 (VRSEM-765 is genetically different from 6 other genotypes) and 10 genotypes, while 29 genotypes divided into 2 clusters with 13 and 16 genotypes respectively. Actually, the group of individuals possessing similar characters mathematically gathered

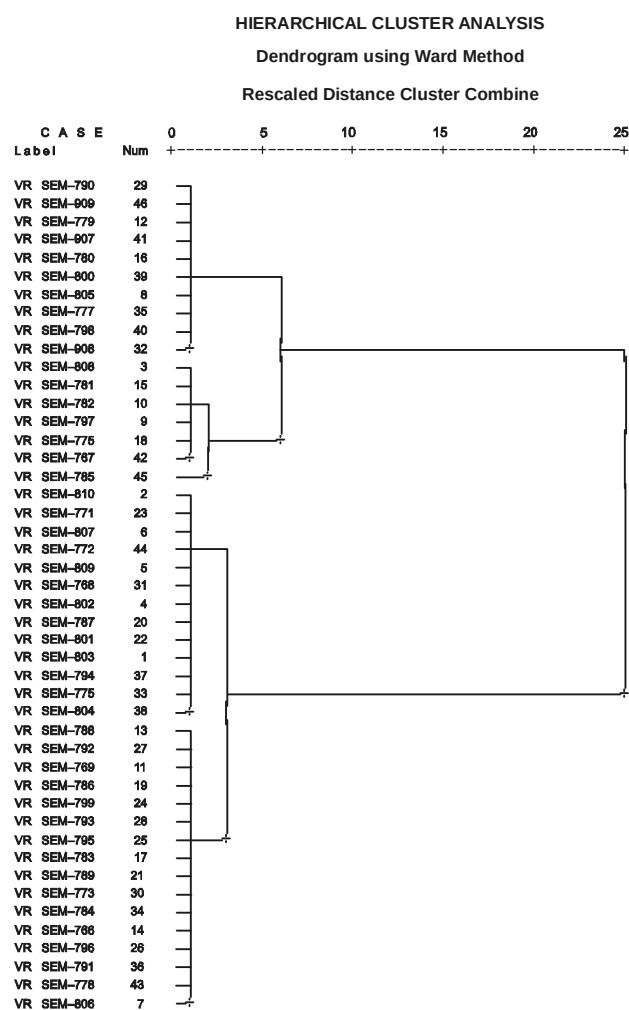


Fig. 1: Multivariate clustering of Indian bean genotypes based on Ward's method

into the same cluster and, all individuals of same cluster supposed to exhibit higher homogeneity. It is inferred from the present investigation that hybridization involving the inter-cluster representatives of clusters would be more useful in Indian bean breeding programme.

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Hill Wheat from Indian Himalayas: A Rich Source of Diversity

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Two hundred and sixty four hill wheat germplasm collections were grown at VPKAS Experimental Farm, Hawalbagh, Almora, for two consecutive years 2002-03 and 2003-04 in an augmented design. These were evaluated for 15 quantitative traits. All the genotypes were grouped into 15 clusters using non-hierarchical Euclidean analysis showing existence of high genetic diversity in the material. High coefficient of variability was observed for grain yield/plant, grain weight/spike and biomass/plant. First eight vectors explained more than 80% of the total variation. The highest intercluster distance was obtained between cluster X and XV (17.27). The intracluster distance was the maximum in cluster IV (4.73) and minimum in cluster V (2.30). Crossing between superior genotypes of diverse cluster is expected to generate transgressive segregants for grain yield, spike length, 1000-grain weight, effective tillers/plant, biomass/plant, early flowering and maturity.

Key Words: *Triticum aestivum*, Germplasm evaluation, Divergence, Hill wheat

Introduction

Wheat (*Triticum aestivum* L. em Thell.) is the most important crop of *rabi* (winter) season in North-Western Himalayas. The bread wheat (*Triticum aestivum*) is the most important species, occupying about 90% of the total wheat area. The genus *Triticum* is extremely variable and grows in habitats ranging from sea level to elevation of 3,500 m. Diverse agroclimatic conditions, different cultural practices and geographical conditions have generated substantial genetic diversity in this crop. Genetic diversity is the basic building block of any crop improvement programme (Kumar and Singh, 1997) as genetic variation among parents is highly essential to derive superior progeny (Chen *et al.*, 1994; Smell, 1995) and success of any hybridization programme depends upon selection of suitable parents of diverse origin (Selvarani and Chendirasekaran, 2000). Genetic divergence is one criterion for selecting parents to generate crosses that give transgressive segregant in subsequent generations. Multivariate analysis is a powerful tool in quantifying the degree of divergence present in the biological population at genotypic level. The use of multivariate analysis has been emphasized by many workers (Singh, 1994; Redhu *et al.*, 1995). Although several breeders in different crops have used D^2 statistics, but non-hierarchical Euclidean cluster analysis suggested by Beale (1969) and Spark (1973) is capable of overcoming the limitations of Mahalanobis D^2 statistics. These procedures characterize genetic divergence using the criterion of similarity and dissimilarity based on aggregates effect of a number of agronomically important

characters.

The pace and magnitude of genetic improvement generally depend on the extent of genetic variability in segregating generation which largely depends on the genetic diversity of the parents. It is, therefore, logical to assess the genetic divergence in the available germplasm for identification of diverse genotypes. The present investigation was, therefore, undertaken to study the nature and extent of genetic variability and genetic divergence in 264 germplasm lines using non-hierarchical Euclidean cluster analysis to identify the donor for yield and yield contributing characters.

Materials and Methods

Two hundred and sixty four hill wheat germplasm accessions were collected from the Uttarakhand hills of Indian Himalayas during different explorations. These accessions along with three checks, viz., Sonalika, VL Gehun 804 and HS 240 were evaluated under medium fertility (N: P_2O_5 : K_2O : 120: 60: 40 kg/ha), irrigated conditions at VPKAS Experimental farm, Hawalbagh (29°36'N, 79°40' E and 1250 msl) during *rabi* 2002-03 and 2003-04 in an augmented block design consisting of 6 blocks with each block having 47 plots and checks repeated in each block. Each plot comprised of two rows of 3 m length with inter and intra-row spacing 0.3 m and 0.1 m, respectively. The crop received 60 kg/ha N, 60 kg/ha P_2O_5 and 40 kg/ha K_2O as basal dose and 30 kg/ha N as a top dressing after first irrigation and at joining stage. Three irrigations (50 mm each) were provided to the crop in addition to 263.8 mm and 63.0 mm rainfall during *rabi* 2002-03 and 2003-04, respectively.

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Observations were recorded on fifteen quantitative characters, namely, days to 75% spike emergence, days to 80% maturity, flag leaf length, flag leaf width, peduncle length, plant height, effective tillers per plant, spike length, number of spikelets per spike, biomass per plant, number of grains per spike, grain weight per spike, grain yield per plant, 1000-grain weight and harvest index. Five competitive plants were randomly selected for recording observations. Genetic divergence was studied using non-hierarchical Euclidean cluster analysis (Beale, 1969; Spark, 1973). The SPAR 1 package developed by Indian Agricultural Statistical Research Institute (IASRI), New Delhi, was used for statistical analysis.

Results and Discussion

Genetic variability and divergence is of great interest to the plant breeder as it plays a vital role in framing a successful breeding programme (Mehetre *et al.*, 1994; Goel *et al.*, 2005). The greater the genetic heterogeneity, the more is the probability of getting diverse recombinants exhibiting high heterosis for the quantitative traits of economic importance.

A wide range of variation was observed for almost all the characters (Table 1). On the basis of pooled data promising genotypes were identified with respect to days to 75% spike emergence, days to maturity, plant height, effective tillers per plant, spike length, biomass per plant, number of grains per spike and grain yield per plant. Maximum range was observed for plant height (74.5 - 123.17 cm), while flag leaf width had the least range (0.86 - 2.09 cm). Genotype VHC (BD) 38B was the tallest (123.17 cm) and VHC (LK)-1 was the shortest (74.5 cm). These may be crossed with each other in order to develop semi, tall genotypes which is the requirement of hill farmers as fodder is an important component of hill farming. Accessions VHC (BD) 8, VHC (BD) 19 and VHC (BD) 20A had the highest spike length, grain yield and number of tillers, respectively (Table 2). Among the six best accessions, VHC 6314 had high spike length and high number of grains/spike and VHC (BD) 39 was the tallest with high biomass/plant. These accessions may be used as donors/parents for their respective characters in developing high yielding genotypes with desired traits. Wide range of variation for plant height, spike length, 100-seed weight and total tillers was also reported by Ajlouni and Jaradat (1997).

The coefficient of variability was the highest for grain yield/plant and lowest for days to maturity. Plant height, days to 75% spike emergence, days to maturity spike

length and number of spikelets/spike were the traits having CV value of less than 10%. On the contrary, rest of the traits had CV values above 10% ranging from 11.85% for 1000-grain weight to 36.58% for grain yield. It can be inferred that, in the present study, all characters except plant height, spike emergence, days to maturity, spike, length and number of spikelets per spike showed wide variations suggesting sufficient scope for further improvement for majority of characters. However, for improvement in plant height, spike emergence, days to maturity, spike length and number of spikelets per spike, there is need for introgressing the variability from outside sources.

Non-hierarchical Euclidean cluster analysis proved useful for estimating the genetic divergence in 264 wheat genotypes which were grouped into 15 different non-overlapping clusters. The grouping indicated a large amount of genetic divergence among the genotypes. The appropriate cluster arrangement as determined by F test revealed that the 15 clusters were the most suited in pooled analysis. Cluster V consisted of highest number of accessions (48) which showed the highest value for peduncle length (21.10 cm), plant height (118 cm), harvest index (44%) and days to 75% spike emergence (128) whereas, cluster X had the lowest number of accessions (1) and had maximum value for peduncle length (21.10 cm) and plant height (118 cm). Cluster XII had the highest value for days to 75% spike emergence (128), spike length (10.7 cm), number of spikelets/spike (25), therefore, may be important for developing early flowering genotypes with higher number of grains/spike. Cluster IV consisted of 5 accessions and had maximum value for flag leaf width (1.7 cm), number of grains/spike (62) and grain weight/spike (2.01 gm). This is an important cluster which can provide donors for number of grains/spike and grain weight, the two major yield attributes. Cluster VI showed the highest value for flag leaf length (20.78 cm), effective tillers/plant (14), biomass/plant (44.26 g) and grain yield/plant (20.71 g). This is most important cluster from yield point of view as the donors for effective tillers/plant, biomass/plant and grain yield/plant can be selected from this cluster. Cluster VII had 15 accessions and had highest value for days to maturity (166). Cluster XIII consisted of 24 accessions while cluster XIV contained 11 accessions which had the highest value for 1000-grain weight (37.53 g). This cluster can be useful in developing genotypes with higher grain weight. Interestingly, the grouped genotypes collected/originated from different

Table 1. Range, coefficient of variability and associated variance for various characters

S.No.	Characters	Season	Range	CV %	Eigen roots	% Variation
1	Days to 75% spike emergence	I	114.28-133.28	2.55	3.07	20.47
		II	114.83-134.17	2.77	3.53	23.53
		Pooled	118.78-131.78	2.03	3.199	21.32
2	Days to maturity	I	153.17-170.83	2.46	2.604	17.36
		II	154.39-170.72	1.85	2.508	16.72
		Pooled	157.44-169.11	1.51	2.438	16.25
3	Flag leaf length (cm)	I	10.76-27.52	13.32	1.963	13.09
		II	9.54-24.74	15.52	2.013	13.42
		Pooled	11.9-23.5	12.18	1.702	11.35
4	Flag leaf width (cm)	I	0.89-2.09	14.65	1.278	8.52
		II	0.62-2.09	20.17	1.295	8.64
		Pooled	0.86-2.09	15.25	1.395	9.3
5	Peduncle length (cm)	I	0.71-28.11	25.34	1.08	7.2
		II	3.4-22.9	25.19	1.092	7.28
		Pooled	2.24-25.18	23.15	1.048	6.99
6	Plant height (cm)	I	72.61-126.61	8.08	0.982	6.54
		II	60.67-130	9.35	0.907	6.05
		Pooled	74.5-123.17	6.75	0.928	6.19
7	Effective tillers/plant	I	4.72-17.39	24.72	0.843	5.62
		II	4.39-17.39	28.16	0.857	5.72
		Pooled	4.78-17.78	20.58	0.89	5.93
8	Spike length (cm)	I	5.68-12.52	10.86	0.686	4.57
		II	6.5-12.27	11.84	0.691	4.61
		Pooled	6.51-11.64	9.26	0.654	4.36
9	Number of spikelets/spike	I	10.94-38.94	11.05	0.608	4.06
		II	15.67-42	9.96	0.534	3.56
		Pooled	16.89-33.22	7.82	0.528	3.52
10	Biomass/plant (g)	I	7.62-44.97	28.67	0.487	3.25
		II	8.99-68.99	36.91	0.51	3.4
		Pooled	16.22-49.55	19.88	0.505	3.37
11	Number of grains/spike	I	34-68	13.82	0.411	2.74
		II	30.06-72.39	18.42	0.35	2.33
		Pooled	32.72-68.72	12.98	0.455	3.03
12	Grains weight/spike (g)	I	0.73-2.29	30.26	0.362	2.41
		II	0.56-3.62	21.55	0.319	2.13
		Pooled	0.97-2.48	20	0.391	2.6
13	Grain yield/plant (g)	I	2.98-17.32	34.15	0.332	2.22
		II	3.86-33.64	36.58	0.222	1.48
		Pooled	6.48-21.25	30.67	0.377	2.52
14	1000-grain weight (g)	I	20.11-43.65	14.96	0.273	1.82
		II	17.52-48.93	11.36	0.152	1.01
		Pooled	22.84-42.53	11.85	0.282	1.88
15	Harvest index%	I	16.08-74.4	21.61	0.02	0.13
		II	21.03-68.96	14.76	0.021	0.14
		Pooled	21.22-62.02	15.05	0.208	1.39

places falls into same cluster thus indicated their close affinity. Further, distribution of genotypes from same place into different clusters suggested that the geographical diversity may not necessarily be related with genetic diversity (Table 2). Redhu *et al.* (1995), Desmukh *et al.* (1999), Suri and Sharma (1999) and Bergale *et al.* (2001) also found no relationship between geographical and genetic distance. Further, the genotypes of the same cluster had little divergence from each other with respect of the aggregate effect of the fifteen characters examined. Therefore, the hybridization among the genotypes of the same cluster is not desirable for developing good segregates.

The estimates of inter and intra-cluster distances provide index of genetic diversity among and within the clusters. In pooled data, intra-cluster values ranged from 2.29 (cluster V) to 4.73 (cluster IV) indicating that cluster V and IV consisted individuals of minimum and maximum diversity, respectively (Table 3). Broadly, it can be concluded that relatively less divergence exists in cluster V, whereas individuals in cluster IV are more divergent. However, cluster XV showed zero intra-cluster distance since it had only one genotype. The inter-cluster distance of cluster X and XV was found the maximum (17.265), while cluster V and XIII had the least (2.29) suggesting wide diversity between the cluster X and XV

Table 2. Minimum and maximum values for morphological characters in hill wheat germplasm

Characters	Minimum				Maximum			
	Genotypes	Origin	Value	Group	Genotype	Origin	Value	Group
Days to 75% spike emergence	Noo1, Noo2, Noo34	Nepal	119	I, IX	VHC6206	Champawat	132	VII
Days to 80% maturity	VHC(BD)83, VHC6244	Uttarkashi Pithoragarh	157	X,V,IX	Noo3	Nepal	169	VII
	Noo75C	Nepal						
	VHC6102, VHC6248	Dwarahat Berinag						
Plant height (cm)	VHC(LK)-1	Namhole, Shimla	74.5	IV	VHC(BD)38B	Rudraprayag	123.17	XIV
Effective tillers per plant	VHC6149	Gairsain	5	III	VHC(BD)20A	Tharali	18	VI, XIII
Spike length (cm)	VHC6168	Karnprayag	6.51	V	VHC(BD)48	Tehri	11.64	VI, XII
	VHC6241	Berinag			VHC(BD)8	Almora		
Biomass per plant (g)	VHC6185	Lohaghat	6.22	I,III	VHC(BD)27	Rudraprayag	49.55	VI
	VHC6187	Barakot	25	V	VHC(BD)19	Tharali		
Number of grains per spike	VHC6409	Garur			VHC(BD)56	Tehri	68.72	IV
Grain yield per plant (g)	Noo31A	Nepal	6.48	XII	VHC(BD)19	Tharali	21.25	VI
1000-grain weight (g)	VHC(BD)56	Tehri	22.84	VIII	VHC(BD)75	Uttarkashi	42.53	XIV

Table 3. Average intra and inter-cluster distance D values in hill wheat germplasm

Season	Clusters	I	II	II	IV	V	VI	VII	VIII	IX	X	XI	XII	XII	XIV	XV
I	I	2.58														
II		2.69														
Pooled		2.97														
I	II	3.53	2.72													
II		5.04	2.57													
Pooled		5.28	2.90													
I	III	3.25	3.82	2.92												
II		3.92	4.81	3.25												
Pooled		3.54	3.21	2.50												
I	IV	6.18	3.26	4.75	2.97											
II		6.90	3.51	7.25	2.66											
Pooled		7.36	4.96	6.05	4.73											
I	V	2.98	2.40	4.46	5.24	2.72										
II		3.58	3.08	4.28	5.11	2.21										
Pooled		2.51	4.24	2.86	7.47	2.30										
I	VI	5.45	3.24	5.66	4.15	3.76	3.34									
II		5.51	4.33	6.37	4.46	3.83	2.41									
Pooled		7.73	4.26	6.45	5.82	6.49	3.49									
I	VII	2.33	2.86	3.70	5.13	3.10	4.19	2.38								
II		4.19	3.51	4.59	4.06	2.63	4.27	2.26								
Pooled		4.09	4.84	2.78	6.15	3.96	7.17	2.73								
I	VIII	4.17	3.34	3.94	4.00	4.85	4.39	2.50	2.63							
II		5.93	3.51	5.48	4.51	3.31	3.44	3.49	3.06							
Pooled		3.35	3.17	2.73	5.61	2.60	4.98	3.03	2.56							
I	IX	4.11	3.24	4.18	4.81	4.40	5.63	3.61	4.13	3.19						
II		4.01	4.36	4.17	5.99	3.02	4.72	3.91	5.17	2.66						
Pooled		3.74	2.77	2.60	6.64	2.73	5.98	4.49	3.03	2.35						
I	X	5.42	3.84	5.03	4.58	4.76	5.88	5.34	5.48	4.70	3.70					
II		4.61	3.12	6.04	4.06	2.47	4.43	3.17	4.36	4.20	2.30					
Pooled		11.87	9.38	10.69	11.47	11.53	10.97	12.15	11.03	9.73	0.00					
I	XI	14.08	13.56	12.86	13.36	14.38	15.04	14.32	14.04	13.15	13.64	0.00				
II		3.94	4.17	2.80	5.86	2.74	5.07	2.47	3.84	3.24	4.56	2.60				
Pooled		3.50	4.46	3.58	7.36	3.19	6.93	3.96	3.06	2.76	10.75	2.54				
II	XII	6.70	3.01	6.23	3.23	3.75	4.69	3.57	3.11	5.13	3.35	4.57	2.44			
Pooled		6.02	4.08	3.83	5.66	5.13	5.62	3.35	3.32	4.48	11.45	4.35	3.12			
II	XIII	5.42	3.91	5.02	6.17	2.54	4.11	4.54	2.93	4.05	4.35	3.89	4.24	2.70		
Pooled		4.04	3.25	3.33	7.09	2.29	4.90	4.88	2.63	2.52	10.64	3.72	4.86	2.45		
II	XIV	4.45	3.15	5.79	4.87	2.14	3.41	3.99	3.72	3.86	2.23	4.60	3.98	2.95	2.25	
Pooled		5.51	2.88	4.41	6.50	4.26	4.93	5.51	3.61	3.77	9.83	4.13	5.07	3.70	2.73	
II	XV	11.71	11.30	10.53	12.60	10.99	11.98	11.19	10.85	11.41	11.77	10.45	10.96	10.90	11.73	0
Pooled		11.13	12.36	11.61	13.48	11.10	13.11	10.90	10.74	11.30	17.27	10.03	10.25	12.02	11.98	0

Bold values denote intra-cluster distance

and a close relationship between cluster V and XIII. It may be inferred that intercrossing between the individuals of X and XV may give desirable segregants.

Cluster means for various characters exhibited significant differences. Maximum mean value for flag leaf length (20.78 cm), effective tillers/plant (14), biomass/plant (44.26 g) and grain yield/plant (20.71 g) were obtained in cluster VI which included nine genotypes. Cluster X which contained only one accession (NOO75C) showed maximum mean value for peduncle length (21.10 cm), plant height (118 cm), grain weight/spike (2.01 g) and harvest index (44%). Minimum mean value for spike length (8.56 cm) and number of spikelets/spike (19) was obtained in cluster I which included 13 genotypes. Cluster IV consisted of 5 genotypes which had minimum mean value for peduncle length (9.32 cm) and plant height (85 cm). Cluster VII showed minimum value for biomass/plant (22.88 g), while cluster XI showed minimum mean value for grain yield/plant (7.57 g). Cluster XV showed minimum value for flag leaf length (14.40 cm) and number of grains/spike (43). It is indicated that these genotypes are genetically divergent from other genotypes and exhibit superiority in aggregate performance of the above traits. These genotypes consisted of different combinations of traits individually.

On the basis of genetic divergence cluster III, IV and VI are important for yield and yield attributes. Therefore, the individuals of these clusters should be given utmost importance while framing a strategy for high grain yield. Similarly, for improving 1000-grain weight cluster XIV should get due importance. Hence, intercrossing the individuals of diverse clusters followed by pedigree or modified bulk pedigree may resort to developing superior recombinants in the segregating population.

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Studies on Genetic Variability, Character Association and Path Coefficient Analysis in Sesame (*Sesamum indicum* L.)

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Eighty two genotypes of sesame (*Sesamum indicum* L.) were evaluated in randomized block design during rainy season of 2006 at Agricultural Research Station, Mandor, Jodhpur to assess the variability and character association. The mean sum of squares were significant for all the characters studied except oil content, indicating the presence of variability. Characters like seed yield, primary branches per plant, capsules per plant and capsule bearing height exhibited high heritability coupled with high genetic advance revealing that these characters were controlled by additive gene action. Seed yield showed significant positive correlation with capsules per plant, oil content, test weight, capsule bearing height and primary branches per plant. The maximum positive direct effects on seed yield was observed by capsules per plant followed by test weight and plant height, while days to maturity, days to 50% flowering and capsule bearing height had negative effect. Thus, capsules per plant, test weight and plant height were the major components contributing to the seed yield in sesame.

Key Words: Sesame, Variability, Heritability, Correlation, Path coefficient

Introduction

Rajasthan is the major sesame growing state (314.9 thousand ha area) in India with a production of 126.9 thousand tonnes but the productivity (403 kg/ha) is low (Anonymous, 2007-08). In order to increase the potential of sesame genotypes for seed yield, an understanding of the relationship among different characters with seed yield and presence of variability is essential. Besides this, knowledge about the direct contribution of different characters to seed yield would be highly useful for formulating a selection criterion, which will combine high seed yield and other desirable traits such as oil content. Therefore, the present study was undertaken to know variability and characters association among sesame genotypes for seed yield with yield contributing characters.

Materials and Methods

The materials for present investigation comprised of 78 newly developed white seeded genotypes selected from F₆ generation of different crosses (Parents RT 3, RT 46, RT 73, RT 125, RT 127, RT 142, RT 156, RMT 34, RMT 40, RMT 50, RMT 117, RMT 123, TKG 20, TKG 55, ES 135, ES 187, GRT 8333, GRT 8368, JLT 8, TNAU 63, AT 8, C 6, TC 383, IS 158-2, IS 225-3 and IS 238) and four standard check varieties (RT 46, RT 54, RT 127 and TKG 22) of sesame (*Sesamum indicum* L.). A set of 82 entries/varieties of sesame was grown in randomized block design with three replications during *kharif* 2006 at research farm of Agricultural Research Station, Mandor, Jodhpur. Each genotype was sown in five rows of 4 m

length following crop geometry of 30 × 15 cm. The crop was raised under rainfed conditions and all agricultural operations were done as and when necessary. The data were recorded on five competitive plants taken from each replication for plant height (cm), capsule bearing height (cm), number of primary branches per plant and number of capsules per plant. Seed yield (kg/ha), test weight (g), oil content (%), days to 50% flowering and maturity were recorded considering whole plot. The data were subjected to analysis of variance following standard methods. Correlation coefficients were used to perform the path analysis of seed yield suggested by Dewey and Lu (1959) and the other genetic parameters such as variability, heritability and expected genetic advance as percent of mean were estimated using INDOSTAT software (Indostat Services, Hyderabad).

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters except oil content, indicating the presence of variability. The range, mean, coefficient of variability, heritability in broad sense and genetic advance (as per cent of mean) for yield and its component characters are given in Table 1. Wide variability was observed for seed yield (250-891 kg/ha) and other characters also. The high magnitudes of phenotypic as well as genotypic coefficient of variation for seed yield, primary branches per plant and capsules per plant indicated the presence of ample amount of variation for these characters. The high heritability (75-95%) combined with high genetic advance as percent of

Table 1. Estimates of genetic parameters of seed yield and its component characters in sesame

Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GA as per cent of mean
		Min.	Max.				
Seed yield (kg/ha)	571	250	891	25.4	26.0	95	50.9
Days to 50% flowering	42	38	45	3.2	3.6	82	6.0
Days to maturity	80	71	87	2.5	2.7	88	4.9
Plant height (cm)	127	95	145	5.4	6.2	75	9.7
Capsule bearing height (cm)	59	47	93	8.9	10.3	76	16.0
Primary branches/plant	2.9	1.0	4.4	18.7	20.4	84	35.4
No. of capsules/plant	45	28	62	13.9	15.2	84	26.2
Test weight (g)	2.66	2.44	2.95	3.7	4.1	83	7.0
Oil content (%)	45.7	38.4	49.2	1.9	3.9	22	1.8

GCV-Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation and GA- Genetic advance

mean for seed yield, primary branches per plant, capsules per plant and capsule bearing height revealed that these characters were controlled by additive gene action, suggesting that selection for these traits would be effective for crop improvement. These results are in agreement with those reported by earlier workers (Solanki and Gupta, 2004; Babu *et al.*, 2004).

The estimates of correlation coefficients between seed yield and other yield contributing characters in all possible combinations are presented in Table 2. Relative higher magnitude of correlation coefficients indicated a strong inherent association among various characters. Therefore, selection on the basis of the phenotype would be effective. Seed yield was found to be significantly and positively correlated with number of capsules per plant (0.56), oil content (0.48), test weight (0.31), number of primary branches per plant (0.26) and capsule bearing height (0.23), while days to maturity were significantly and negatively correlated with the seed yield (-0.42), which was a good sign for escaping drought in high yielding genotypes of sesame. Similar results were reported by Osman Khidir and Osman (1970) for plant height, branches number, capsules number and 1000-seed weight.

Among other characters number of capsules per plant had positive significant correlation with number of primary branches per plant (0.52) and capsule bearing height (0.45). Plant height also exhibited significant positive association with days to maturity (0.47), days to 50% flowering (0.43) and capsule bearing height (0.31). These results indicated that improvement in seed yield can be achieved by improving the characters like capsules per plant, test weight and primary branches per plant.

Dewey and Lu (1959) suggested that when more variables are considered in correlation matrix, path coefficient analysis becomes more useful in specifying the cause and also measures the relative importance of each character. The direct and indirect effects of various characters on seed yield are given in Table 3. Number of capsules per plant had the maximum direct effects (0.471) on seed yield followed by test weight (0.229) and plant height (0.051), while days to maturity (-0.330) showed maximum negative direct effect *i.e.* early maturing genotypes were also higher yielders.

Thus, it may be concluded from this study that number of capsules per plant, test weight, number of primary branches per plant and plant height are the most

Table 2. Correlation coefficients between seed yield and its component characters in sesame

Characters	Days to maturity	Plant height	Capsule bearing height	Primary branches/plant	No. of capsules/plant	Test weight	Oil content	Seed yield
Days to 50% flowering	0.328**	0.429**	-0.103	0.162	0.036	-0.265*	-0.045	-0.132
Days to maturity		0.479**	0.146	-0.301**	-0.273*	0.094	-0.112	-0.415**
Plant height			0.316**	-0.038	0.056	0.179	0.155	0.017
Capsule bearing height				-0.121	0.450**	0.253*	0.083	0.227*
Primary branches/plant					0.516**	-0.224*	0.234*	0.263*
No. of capsules/plant						0.098	0.167	0.561**
1000-seed weight							0.150	0.314**
Oil content								0.484**

*and ** significant at 5% and 1% level, respectively.

Table 3. Path coefficient analysis showing direct (diagonal) and indirect effects in sesame

Characters	Days to 50%	Days to maturity flowering	Plant height	Capsule bearing/height	Primary branches/plant	No. of capsules plant	1000-Seed weight	Oil content	Seed yield
Days to 50% flowering	-0.029	0.009	0.012	-0.003	0.005	0.001	-0.008	-0.001	-0.132
Days to maturity	-0.108	-0.330	-0.158	-0.048	0.099	0.090	-0.031	0.037	-0.415**
Plant height	0.022	0.025	0.051	0.016	-0.002	0.003	0.009	0.008	0.017
Capsule bearing height	0.005	-0.008	-0.017	-0.053	0.006	-0.024	-0.013	-0.004	0.227*
Primary branches/plant	-0.200	0.037	0.005	0.015	-0.121	-0.063	0.027	-0.028	0.263*
Capsules/plant	0.017	-0.129	0.026	0.212	0.243	0.471	0.046	0.078	0.561**
1000-seed weight	-0.061	0.022	0.041	0.058	-0.051	0.023	0.229	0.034	0.314**
Oil content	-0.016	-0.040	0.056	0.030	0.084	0.060	0.054	0.360	0.484**

Residual effect = 0.6321

important components for determining seed yield, as they recorded significant positive correlation coefficients and higher positive direct and indirect effects on seed yield.

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Occurrence, Distribution and *Ex Situ* Regeneration of Balsam Apple (*Momordica balsamina* L.) in India

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Momordica balsamina L. has a narrow distribution in India, confined to Rajasthan and Gujarat. *Ex situ* regeneration studies showed that it can be regenerated during October-April in Kerala, simulating the hot days and cool nights that occur in its home range. Even though pollination and seed dispersal by native fauna was observed, it could not naturalize in Western Ghats due to non-adaptability to the high rainfall monsoon period. Few reports of its occurrence and distribution in Kerala are obviously based on misidentification of a herbarium specimen as South India is far beyond its natural range.

Key Words: *Momordica balsamina*, Conservation, Distribution, Ecogeography

Introduction

M. balsamina L. is the type species for the genus *Momordica* L. The generic epithet *Momordica* is derived from the Latin word 'mordeo' meaning 'bitten' (Drury, 1864) for the jagged edges of the seeds (which look like 'bite' marks). Ironically, among the six species occurring in India, *M. balsamina* is unique for its seed shape, which is non-jagged. World distribution of the taxa is from North, East and South Africa, North and East Australia to West Asia extending to Pakistan and India (Hooker, 1871; Chakravarty, 1982; De Wilde and Duyfjes, 2002). It also occurs in Latin America as an introduced plant.

Known as balsam apple, it is a wild edible vegetable and medicinal plant in Tropical Africa and West Asia (Mishra *et al.*, 1986; Nayar and Singh, 1998; Jeffrey, 2001). Leaves and young fruits are cooked and eaten in Sudan, Senegal, Cameroon and southern Africa. Bright red fruit aril is eaten in Namibia. Ripe fruits are reported to be toxic, especially when consumed in large quantity. An infusion prepared from ripe fruits in olive oil is mentioned in ancient Arabic '*Materia Medica*' for the treatment of cracked heels (Nayar and Singh, 1998). It is used as an anthelmintic, antipyretic, hypoglycemic, abortifacient, aphrodisiac and lactogenic in African ethnomedicine (Watt and Breyer-Brandwijk, 1962; Burkill, 1985; Geidam *et al.*, 2007). Utilization is the best method for conservation of biodiversity. Its prospects as a new source of economic products, especially nutraceuticals and therapeutic agents, need to be investigated. Scope for introduction as an ornamental exists by virtue of its elegant foliage and beautiful scarlet

red fruits. It is used as camel fodder (Chakravarty, 1982), but there are no reports of its role in ecosystem functions in the desert.

As in the case of other *Momordica* species, there is lot of confusion in India regarding the correct botanical identity of balsam apple. There are several instances of misidentification and few reports of its (unlikely) occurrence in south India and Western Ghats (Subramanian, 1970; Sasidharan, 2004; Nayar *et al.*, 2006), far distant from its natural range. Besides, this taxon is poorly represented in the Indian National Genebank of NBPGR, New Delhi (personal communication, Chithra Pandey). Hence, it was considered appropriate to conduct a study on the natural distribution of *M. balsamina* and its field regeneration under *ex situ* conditions prevailing in Western Ghats.

Materials and Methods

Herbarium survey was carried out at CAL (Botanical Survey of India, Calcutta), BSIJO (Botanical Survey of India, Arid Zone Circle, Jodhpur), BSISH (Botanical Survey of India, Eastern Circle, Shillong), MH (Botanical Survey of India, Southern Circle, Coimbatore) and BSI (Botanical Survey of India, Western Circle, Pune) during 2002-2003. Based on the herbarium information, the first author visited Machia Safari Park, Jodhpur (one of the hotspots as per the survey) in October 2003 and could collect one accession (IC467683), besides carrying out *in situ* characterization. A representative seed sample was sent for conservation in the National Genebank of NBPGR (SBJ 03-135, Jodhpur, Kailana Lake Road, 24-9-2003,

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Joseph John K, RHK&NHCP). Seed regeneration was carried out at the Botanical garden of St. Berchmans' college, Changanacherry, Kerala during October 2003 (*Rabi* season) and June 2004 (*Kharif* season). Besides preliminary characterization, observations on interspecific crossability and phenology (flowering, fruiting, pollinators and dispersal agents) under *ex situ* situation were recorded. Soil samples from collection and regeneration sites were analyzed for major physical and chemical characters using standard analytical protocols.

Results and Discussion

Distribution and Occurrence

Natural distribution of *M. balsamina* is restricted to Rajasthan and Gujarat (Fig.1). There are altogether 45 herbarium sheets (eliminating duplicate sheets), 6 from Gujarat and 39 from Rajasthan at CAL (Botanical Survey of India, Calcutta) and BSIJO (Botanical Survey of India, Arid Zone Circle, Jodhpur). Districts of Ajmer, Pali, Ganganagar, Jalore, Bharatpur, Jaipur, Jodhpur and Churu in Rajasthan and Mehsana and Bharuch in Gujarat are the major areas of higher population in the wild. Its distribution in India is in continuation of that in Sindh province of Pakistan.

It is not known from South India or Western Ghats. The lone report of its occurrence in South India (Subramanian, 1970) is based on wrong identification of collection 77286 (Acc. No. 35124 of BSI, Pune), originally identified as *M. balsamina* (on 1-12-1961) and subsequently determined as *M. dioica* Roxb. (on 22-10-1962). Hence, the enumeration of *M. balsamina* in the floristic diversity of Kerala (Sasidharan, 2004; Nayar *et al.*, 2006) based on this report does not stand valid.

Vernacular names: Bara-karela (Rajasthan), Karelo-jangro (Sindhi)

Habitat and Ecology: Disturbed habitats in semi-arid and arid tropics, road sides, farm borders and fences on medium heavy soils with slightly acidic pH. *Prosopis cineraria* was the associated vegetation.

Morphology and Taxonomy

M. balsamina is distinguishable from the dioecious taxa by virtue of its monoecious, non-tuberos, annual habit. Unlike the other monoecious taxon (*M. charantia* L.), bracts of the male flowers are at the apex of the peduncle. Flowers are very distinct; the female flower is always smaller and male flower with red nectar guides. Fruits

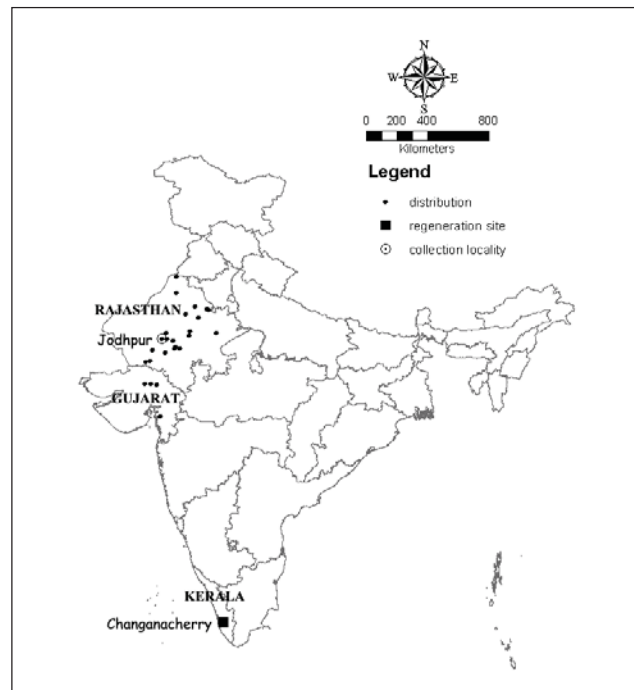


Fig.1: Map showing natural distribution, *in situ* characterization and *ex situ* regeneration sites

are non-pendant, small, bulged, distantly soft tubercled without any bumps or ridges. Seeds are very thin, flat and rugulose on surface, with a thinly grooved margin and finely tuberculate edges.

Herbarium records indicate September to March as fruiting season. Seeds germinate with monsoon showers in July-August (Rajasthan) and attain flowering and fruiting in September. Best time for seed collection is October when peak fruiting was observed in Machia Safari Park, Jodhpur.

Regeneration and Growth under Ex Situ Conditions

As soil and environmental features of native habitat and regeneration sites were different (Table 1), soil amendments by liming and adjusting the growth season to dry winter-summer months helped to get comparable plant growth. Though seeds sown in June germinated fast, they failed to grow beyond 4-leaf stage, due to heavy monsoon showers. October-sown seeds germinated on the fourth day and attained vine length up to 3 m. Germination was epigeal and roots non-tuberos as in the case of *M. charantia*. Plants took 69 days from seed to seed. Days to first male flower was 39 (range 35-42). Fruits took 9 days to attain full size and 22 days to colour

Table 1. Soil and climatic characteristics of natural and regeneration sites

Locality	Latitude	Longitude	Altitude	Soil colour	Soil type	Total N2 (%)	Available P (ppm)	Available K (ppm)	Soil pH	EC (us/cm)	Max. Temp. (°C)	Min. Temp. (°C)	Avg. rainfall (mm)
Jodhpur (in situ)	26.2833	73.0333	274	Brown	Calcareous sandy loam	0.063	90.8	257.8	8.5	160.3	41.5	10.0	2306
Changanacherry (ex situ)	9.750	76.5666	61	Red	Laterite	0.256	17.9	159.4	6.1	120.6	30.8	23.3	2874

breaker stage, 24 days to red stage and finally bursting open on 25th day.

Anthesis was between 4.30-5.00 AM. Small insects such as *Trigona iridipenis* (stingless honeybees), *Solenopsis* sp. (small red ant) and *Nomia* sp. (stingless metallic blue-white striped bees) were the floral visitors observed. As the male flower stalks are very fragile, it is not adapted to pollination by large bodied insects. Nearly 100 % natural fruit set was observed indicating efficiency of pollinators outside the home range of the species. Nectar, mild scent, and yellowish-orange petals with red spots at petal base act as floral rewards and nectar guides. Ripe fruits are orange red in colour and splits open exposing the carmine red seeds (aril) which remain adhered together. The fruit stalk is very short and not pendant unlike in the case of other *Momordica* species and *Pycnotus* sp. (red whiskered bulbul) was found to feed on ripe fruits. After ingestion of seed aril, the seeds are regurgitated effecting dispersal of seeds. Ripe fruits were mildly bitter whereas seed aril was sweet and slimy.

Growth performance of *M. balsamina* outside its home range was comparable to that of native habitat (Table 2). However, a reduction in plant height was observed. On an average, 40 fruits per plant (range 36-52) were obtained under Kerala conditions, which indicates need for raising about 40 plants per accession to get about 6,000 seeds for genebank storage.

As in the case of June-sown seeds, the soil seedbank (from the previous crop) also could not overcome the heavy monsoon climate occurring in the Western Ghats of Kerala. As the seeds do not have dormancy and being non-perennating, it cannot naturalize in the monsoon climate. However, by adjusting the growth season to dry winter-summer months, a simulated growth environment can be created permitting field regeneration. Curators can adapt and improve these methods with an aim to produce maximum seeds. Being an insect pollinated plant, maintenance of isolation distance or selfing is necessary in case of regeneration of more than one accession.

Response to Pests and Diseases and Interspecific Crossability

The plants were free from Ladybird beetle (*Epilacna septima*), red pumpkin beetle (*Aulocophora fevicolii*) and Cucurbit Yellow Mosaic, which are the main pests and diseases of bitter gourd in Kerala (Table 3). However, they were extremely susceptible to fruit fly (*Bactocera cucurbitae*). At its natural habitat also, severe fruit fly damage was observed.

Direct and reciprocal crosses with related taxa (*M. charantia* L., *M. dioica* Roxb., *M. sahyadrica* Joseph and Antony and *M. subangulata* ssp. *renigera* (G. Don) de Wilde) failed to set fruit. Though not coming in the primary genepool of bitter gourd (*M. charantia* L.), it is a potential source of many useful genes conferring resistance to several common pests, which can be

Table 2. Comparative growth performance of IC 467683 at in situ and ex situ situations

S.No.	Character	Ex situ site	In situ site
1	Plant height (m)	2.25 (1.5–3.0)	5 (3.0–6.0)
2	Inter node length (cm)	5.5	6
3	Petiole length (cm)	2	2.1
4	Lamina size (cm)	4 x 5	4 x 6
5	Tendril length (cm)	11.5	13.0
6	Male flower peduncle (cm)	0.3	0.4
7	Male flower pedicel (cm)	0.4	0.8
8	Male flower bract size (cm)	0.6 x 0.5	0.6 x 0.6
9	Male flower calyx (cm)	0.7 x 0.3	0.7 x 0.3
10	Male flower petal (cm)	1.3 x 0.9	1.5 x 1.0
11	Male flower diameter (cm)	2.5	2.9–3.0
12	Female flower peduncle (cm)	0.2	0.3
13	Female flower pedicel (cm)	0.4	0.6
14	Female flower bract size (cm)	0.3 x 0.3	0.4 x 0.4
15	Female flower petal (cm)	0.7 x 0.6	0.8 x 0.8
16	Female flower diameter (cm)	1.5	1.8
17	Ovary length (cm)	0.5	0.7–0.8
18	Fruit weight (g)	6.0	9.3
19	Fruit length (cm)	2.5–3.5	4.0–5.0
20	Fruit diameter (cm)	1.8	2.7
21	Fruit stalk (cm)	0.5	0.8
22	Seeds/fruit	3.0–5.0	4.0–7.0
23	100 seed weight (g)	8.7	9.0
24	Fruit wall thickness (mm)	1.5	1.5
25	Seed length (mm)	9.2	9.2
26	Seed width (mm)	6.5	6.5
27	Seed thickness (mm)	2.4	2.4

Table 3. Observations on tolerance/susceptibility of *M. balsamina* to common pests and diseases in comparison to other species

Biotic agent	<i>M. balsamina</i>	<i>M. charantia</i> var. <i>charantia</i>	<i>M. charantia</i> var. <i>muricata</i>	<i>M. dioica</i>	<i>M. sahyadrica</i>	<i>M. subangulata</i> ssp. <i>renigera</i>
Lady bird beetle (<i>Epilacna septima</i>)	1	5	3	5	5	5
Red pumpkin beetle (<i>Aulocophora fevicolii</i>)	1	3	3	7	3	3
Fruit fly (<i>Bactocera cucurbitae</i>)	9	5	3	3	1	5
Pumpkin caterpillar (<i>Margaronia indica</i>)	1	1	1	1	1	3
Gall fly (<i>Lasioptera falcata</i>)	1	3	3	1	3	5
Root knot nematode (<i>Meladogyne incognita</i>)	1	1	1	1	1	7
Cucurbit Yellow Mosaic	1	3	3	3	3	1
Little leaf disease	1	1	5	5	5	1

Scale: 1-9 (1=no visible sign of susceptibility; 3=low; 5=intermediate; 7=high; 9=highly susceptible)

transferred to the commercial bitter gourd varieties through modern biotechnological tools.

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Traditional Rice Landraces of District Bageshwar, Uttarakhand and their Conservation

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Farmers select varieties to suit their environmental, socio-economic and ethnic needs. The selection criteria and naming of folk varieties is based on certain desirable characteristics. Adoptability of these landraces to specific micro-niches provide the subsistence to the communities living in the remote areas of hilly region. In the present article, the importance of traditional rice landraces for sustainable development and their on-farm conservation by the farmers in district Bageshwar of Uttarakhand is discussed.

Key Words: Traditional knowledge, Traditional rice landraces, Farmers selection criteria, On-farm conservation

Introduction

Rice is the single most important food crop and 90% of it is grown and consumed in Asia (Khush and Brar, 2005). It contributes 26% in the world's food production (FAO 1996). It is well known that rice emerged as staple food in South-East Asia that proliferated and subsequently dominated the world food bowl along with other food crops (Paroda 2004).

Rice is the major food crop of the entire Kumaun region in general and particularly in Bageshwar district during *khariif* (May/June to September/October). Rice is grown since time immemorial in the region. Despite the spread of improved varieties, local landraces are still grown in the region because of their well adaptability in various agro-climatic conditions (Bisht *et. al.* 2005). More than 80% of the cultivable area in district Bageshwar is under rainfed. Local rice landraces are mainly confined to rainfed as well as semi-irrigated areas in the region. Farming communities in the interior localities are completely dependent on local cultivars, which are also suitable for their environmental, socio-economic and ethnic requirements.

Bageshwar is a remote district in Kumaun hills of Uttarakhand state and it is endowed with rich cultural heritage along with diverse vegetational wealth. It has a diverse geographical scenario comprising of rivers, valleys, medium gentle slopes, higher Himalayan peaks and glaciers. According to its diverse geographic and climatic conditions, farming communities have selected the diverse types of landraces of rice suitable to local conditions. The district Bageshwar is divided into four development blocks namely Bageshwar, Garur, Kapkote

and Kanda. Rice is the most important crop in the entire district. The old traditional rice landraces are also well documented in the Gazetteer of Himalayan provinces (Atkinson 1882). He had described 48 of them in the Uttarakhand Himalayas. Some other studies undertaken on old local cultivars are scattered in the literature (Pant and Negi 1992; Tiwari and Das 1996; Bhatt and Chauhan 1999). No systematic study has been undertaken. In order to document the traditional rice landraces in Uttarakhand, the district Bageshwar was selected in the first phase of our study since in the Bageshwar district, completely traditional farming is still practiced. Throughout the world, traditional farming system have served to preserve the diversity of local varieties along with the human knowledge and cultural practices that have shaped this diversity (Bellon 1996). Traditional farming systems are important *in-situ* conservation sites of crop diversity in the the United Nations Convention on biological diversity *in-situ* conservation "the conservation of ecosystems and natural habitats and the maintaining and recovery of viable populations of species in their natural surroundings and in the case of domesticated or cultivated species in surroundings where they have developed their distinctive properties." The present study was therefore undertaken with emphasis on utility of landraces for future needs vis-à-vis their conservation status (both *in-situ* and *ex-situ*) by farming communities themselves and government agencies.

Materials and Methods

Data on rice genetic diversity was collected from primary sources with the help of planned structured and un-structured questionnaires / interview schedules at

individual farm households level during 2002, 2006 and 2007 cropping seasons. Sample households were randomly selected from all four development blocks-Bageshwar, Garur, Kanda and Kapkote of Bageshwar district. Five to six villages were selected from each development block representing the distinct agro-ecological niches. In each selected village 5% households were randomly selected for interview. Lottery system was adopted for randomization. Thus, a total 58 respondent households were interviewed for documentation of rice landrace diversity. The detail of the number of households interviewed area wise is given in Table 1. During the survey of the district a non-participant observation method was also applied while recording the information.

Using Participatory Rural Appraisal (PRA), information was obtained on the erosion and shift in landrace diversity and changes in farming system. The collected information on current status of the landrace diversity was validated through observations on the fields under cultivation. The respondent households were also asked to fill a questionnaire for extracting information on their knowledge regarding distinctive properties and system of folk nomenclature of rice landraces etc.. All possible care was taken to determine the consistency in farmers naming and describing rice landraces by comparing information from farm households and different social groups. Information obtained was authenticated from knowledgeable elderly farmers and other secondary sources.

Results and Discussions

In the area under study, cropping pattern was built around two crop seasons, *Kharif* (April to October) and *Rabi* (October to April). Rice was the major crop of *kharif* sown in both conditions irrigated as well as rainfed. In the hill region, practice of mixed cropping was very common, however rice is grown as mono crop. More than 80% of the agricultural land was rainfed in the region. Rainfed rice in contour terraces on hill slopes was sown in the month of April by using broadcast method of sowing, however irrigated rice was grown with transplanting

Table 1. Number of development blocks, villages and households sampled for the study

Development blocks	No. of villages sampled	No. of households sampled
Garur	6	19
Bageshwar	4	12
Kapkote	6	17
Kanda	5	10
Total	21	58

method. In the present study it is revealed that more than 50 traditional rice landraces / cultivars were grown by the farmers three decades ago (Table 2). On the basis of irrigation requirement these landraces was classified into three groups – irrigated, rainfed and common (suitable for both irrigated as well as rainfed condition). A total of 44 landraces were still grown by the farmers of which; 14 were grown under irrigated conditions, 16 were grown under rainfed conditions and 14 were suitable for cultivation under both conditions. The landraces common for both agro- ecologies were widely adopted in the region. After the invent of the green revolution, some high yielding varieties (HYVs) entered into the region namely Tichung Native-8, China-4 and IR-24, consequently some of the traditional landraces were replaced by them (Table 3). Thus, the introduction of high yielding varieties was one of the major factors of the erosion of broad genetic base of crop diversity in the region. Over a period of three decades 13 (5.117%) traditional landraces of rice have eroded as replaced by 3 HYVs (Table 3). In this region, heterogeneity of topography, altitude, water regime, environment, temperature, soil type etc. was observed to be very high. This heterogeneity has created a large number of micro-eco-niches which in turn were responsible for creation of a large number of local landraces to suit varied environments. As the HYVs were adoptable to a wide environment they did not cater to the needs of the micro-eco-niches prevailing in such a heterogeneous environments. Perhaps, that is why, 81.03% of farm households still depended on traditional landraces in spite of the introduction of HYVs. The

Table 2. Local rice landraces still grown by farmers of district Bageshwar, Uttarakhand

S.No.	Common landraces/ cultivars grown in both irrigated & rainfed areas	Irrigated landraces/ cultivars	Rainfed landraces/ cultivars
1	Bakua	Baneti	Askoti
2	Banbasa	Ghesu	Banpas
3	Chotia/chotu	Jamali	Biraiya
4	Dalbadal	Jhadua	Boran
5	Dallu	Kashmiri	Chamadia
6	Jaulia	Katyuri	Dan nauli
7	Kapkoti	Muthmala	Jhumaria
8	Kavthuni	Panil	Jungai/Jungal dhan
9	Khazia	Prasad	Kavdhan
10	Madguri	Pyolia	Musoli
11	Nandhani	Punjabi	Paktoli
12	Naulia	Ratan	Patari
13	Sudia	Roti	Syont
14	Thapachini	Talpak	Taknoi
			Uskar
			Ut

cultivation of HYVs was confined to irrigated areas only. This has been noted elsewhere also that the large diversity of rice was managed by the farmers as an adaptable strategy to cope with heterogeneous and uncertain ecological and socio-economic environments including different soil types (Das and Das 2004). The adaptability of different landraces of rice to different agro-eco-niches was a major factor responsible for on-farm (*in-situ*) conservation of large number of landraces in the region. Another important factor responsible for cultivation of traditional landraces was land holding size of farm families. Around 66% farmers in Kumaon hills were marginal holders, holding with an average <0.5 ha. land (Bisht *et. al.*, 2005) scattered in different eco-niches, which compelled farmers to grow different landraces for different kind of lands. Since HYVs were successful only in valley areas, where assured irrigation facility was available, presently there was no serious threat to the remaining traditional landraces. Despite losing several landraces, the farmers were growing sufficiently large number of landraces. In the situation a meta population study would be interesting as the lost landrace populations though may be extinct locally, but be found again in the net work (Hanski and Gilpin 1996; Louette 2000).

The selection criterion applied by the farmers were influenced by different socio-economic and geographical factors viz., yield, quality, biomass yield, drought and damage by animal etc. Farming communities after a long observation and testing of landraces identified some of them to meet the subsistence needs. The landraces *Thapachini* and *Chotia* were found good yielding. However, *Jamai*, *Thapachini* and *Bakua* were considered good in taste. Hill agricultural is interlinked with animal husbandry and fodder is an important by-product of crop yield. *Thapachini* and *Uskar* were high biomass yielding landraces. Agriculture in the area was affected by the vagaries of rain, hence the drought tolerance was a major criteria of selection for rainfed cultivation. *Thapachini*, *Uskar*, *Chamadia*, *Kavthuni*, *Bakua*, *Boran* and *Dannauli*

were identified by the local farmers for rainfed cultivation. The damage caused by wild animals was also very common in the fields surrounded by forests. There were some awned and hard threshable landraces identified to minimize the damage. Traditional landraces-*Dannauli*, *Chamadia* and *Jungalidhan* are found suitable for this purpose. The most frequent landraces *Thapachini*, *Jamai* and *Chotia* occupied substantial area under rice cultivation in Bageshwar district of Uttarakhand for the last several decades (Table 4). A popular landrace *Thapachini* was the only variety, which was preferred for all purposes and suits to climatic conditions of the region.

The farmers often named the local landraces of rice, based on certain characteristics, which they possessed. (Lando and Mark 1994). In Bageshwar district of Uttarakhand 37.78% local varieties were named on the basis of morphological characters such as plant height, seed colours, vegetative traits, 28.89% named after environmental adaptation, soil type, micro-eco-niches, tolerance to biotic/abiotic stresses, cropping system etc., 8.89% based on agronomic traits viz. flowering and maturity time, earliness, growth habit, grain yield, 17.77% on the basis of their origin-region, village, farmer and 6.67% were named after their uses like type of recipes, taste ethno-medicinal values etc. The naming pattern of local landraces was much scientific since they possess and carry certain traits reflected in their names, and the landrace could be easily identified by such names (Table 5).

In rice, kernel characters were very important for determining its yield and market value. It is noticeable that there was a large amount of variability found in the kernel length, breadth and 100 kernel weight. The kernel length ranging between 0.56 to 0.88 with an average 0.69 cm and similarly breadth ranging between 0.22 to 0.37 with an average 0.29 cm and coefficient of variation (cv %) 9.53 and 9.80% respectively was numerically significant. The weight of 100 kernel also varied significantly between 1.63 to 2.99 gm with coefficient of variation 11.06% which was statistically significant (Table 6).

Traditional seed exchange and conservation system

It is evident from the study that there was no formal exchange system in the district, which was the limiting factor for continuous survival and on-farm conservation of local landraces, especially those grown by marginal farm holders. However, some seed flow of local landraces had taken place as farmers exchanged seeds among

Table 3. Effects of HYVs on traditional landraces in district Bageshwar, Uttarakhand

HYVs introduced	Traditional landraces replaced by HYVs	Percentage of traditional landraces replaced
Tichun Native-8 China-4, IR-24	Jiruli, Mangraj, Naulia Simanjari, Dhur basmati, Akadi Rajmati, Anjani, Musmar Kalpar, Hat, Makhur Sanwdhan	5.17

themselves within the same village, procured seeds or collected from other farmers or friends or relatives while visiting them or traveling. It is also observed in the study area that sometimes a married daughter would carry the seeds from parental house to her in-laws house and vice-versa. Similarly some service personnel like military men collected seed from far-flung areas like Kashmir, Punjab, Jorhat etc. after observing their performance. *Punjabi*, *Kashmiri*, *Kapkoti* and *Askoti* landraces were examples of such landraces in the study area. In the study area, 77.58% farmers arranged the seed material from their own harvest of last season. If, it falls short, 17.24% is arranged from neighborhood farmers or relatives and 5.18% procured from seed agencies (Table 7). The loss of the seed by the farmers was attributed to crop failure (particularly under rainfed condition) and consumption needs of the household in excess of production (Trip 2000). Several studies have documented the flow of local seed of different landraces among small farmers (Sperling and Loevinshon 1993). Farmers on the basis of performance and preference selected the varieties to be stored for the next season. Selection of seeds was done by old women folk from healthy crop fields. With their life long experience and testing, they were well equipped, to collect and store the seed material. Old women folk also imparted this traditional knowledge to their daughter-in-laws. It is carefully harvested and sun dried before storage. For safe storage, the leaves of Bach (*Acorus calamus*) and Timur (*Zanthoxylum armatum*) were mixed with cow dung ash and added so as to protect seeds from insect damage. Storage of each landrace was done

separately to facilitate their identification and collection from specific fields. The storage containers were made airtight by covering the mouth with straw and cloth plastered with cow dung and mud. Such storage systems have served farmers as their own gene banks, which have helped them to conserve the genes from centuries. An urgent need was felt to strengthen such community gene banks already occurring at the village level for *in-situ* (on-farm) conservation of crop diversity (Swaminathan 1998). Such repositories conserve the genes, which are adaptable in various agro-eco niches.

The Himalayan highlands, possesses various agro-climatic conditions and fragmented land holdings. For these various agro-eco-niches, local landraces of the crops were the only option for sustainability and subsistence of local communities. The various types of landraces and other local resources such as animal husbandry, surrounding, vegetation, soil types and traditional knowledge provided a complex production system in the region. Such regions were the reservoirs of traditional crop landraces and the farmers particularly marginal women farmers were the managers of the crop diversity for the centuries. For the sustainability of people the genes of traditional cultivars must be conserved for future generations so as to maintain the continuity of human society as well as the fragile environment in such areas.

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Table 4. Selection criterion and ranking of local varieties in Bageshwar district of Kumaun Himalaya

Ranking	Farmers criteria for variety selection					
	Area share	Good yield	Rice quality / taste	High biomass yield for fodder	Drought tolerant	To control animal damage
1	Thapachini	Thapachini	Jamai	Thapachini	Thapachini	Dan nauli
2	Jamai/Jamali	Chotia	Thapachini	Uskar	Uskar	Chamadia
3	Chotia	—	Bakua	—	Chamadia	Jungai
4	—	—	—	—	Kavthuni	—
5	—	—	—	—	Bakua	—
6	—	—	—	—	Boran	—
7	—	—	—	—	Dan nauli	—

Table 5. Farmers criterion for naming local rice landraces

Category	Agro-morphological criteria	No. of landraces (%)
Plant morphology	Plant height, seed colours, vegetative traits	17 (37.78)
Environmental adaptation	Type of soil, micro – econiches, tolerance to biotic/abiotic stress, cropping system	13 (28.89)
Agronomic traits	Flowering and maturity time, earliness, growth habit, grain yield	04 (8.89)
Origin/Source of material	Region, village, farmer	08 (17.77)
Uses	Type of recipes, taste, ethnomedicinal value	03 (6.67)

Table 6. Range, mean, standard deviation and coefficient of variation for kernel characters in rice germplasm collected from district Bageshwar, Uttarakhand

Characters	Range	Mean	Standard deviation (SD)	Coefficient of % variation (CV)
Kernel length (cm)	0.56-0.88	0.69	0.07	9.53
Kernel breadth (cm)	0.22-0.37	0.29	0.03	9.80
100 kernel weight (g)	1.63-2.99	2.38	0.26	11.06

Table 7. Sources of the seed material of farming communities in district Bageshwar, Uttarakhand

S.No.	Source of seed material	No. of farmers	Percentage (%)
1	Own field	45	77.58
2	Neighborhood farmers and relatives	10	17.24
3	Own seed agencies	3	5.18
	Total	58	100.00

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Evaluation of Genetic Stock of Desi Cotton (*Gossypium arboreum*)

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A total of 138 accessions of *Gossypium arboreum* of diverse origin were evaluated for seven morphological traits i.e. days to first flower, plant height (cm), number of monopods, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), and ginning per cent. The genotypes Ac 64 was observed as earliest (64 days to first flower) along with good number of bolls (118), seed cotton yield (185 g per plant) and ginning out turn (40.8 %). The genotypes FFS-1 had recorded highest seed cotton yield (250 g per plant) whereas, HD 328 had recorded highest boll weight (2.7 g) among these lines. Based on this study, it is advocated that these lines could be used in crossing programme for improvement of *diploid* cotton.

Key Words: Evaluation Genetic stock, Desi Cotton, *Gossypium*

Introduction

Cotton is the most important commercial crop of India. Although cotton is grown for fibre but its seeds are also an important source of food oil and the meal is a protein rich by-product used as feed for ruminant livestock. Out of 51 species, four lint bearing species of genus *Gossypium*, viz., *hirsutum* and *G. barbadense* are tetraploid known as New World Cottons ($2n=4x=52$) and *G. arboreum* and *G. herbaceum* are diploid ($2n=2x=26$) and cultivated. *G. hirsutum* is commonly known as Upland cotton or American cotton, *G. barbadense* as Egyptian or Sea Island cotton whereas diploids *G. arboreum* and *G. herbaceum* commonly known as *desi* or Old World cottons.

In Haryana, farmer's preference is for American cotton particularly after the availability of Bt. cotton hybrids since last 3-4 years. Bt. cotton hybrids had less incidence of bollworms particularly *Helicoverpa* and secondly frequent picking of cotton is required in *desi* cotton. Availability of pickers is becoming a big problem in North zone. In spite of such problems there is sizeable (about 15%) area under *G. arboreum* in Haryana. The *desi* cotton species are inherently resistant to sucking pests and cotton leaf curl virus disease. As cotton leaf curl virus disease is transmitted by white fly and *desi* cotton are being resistant to sucking pests (white fly, jassid and aphids).

Germplasm is the basic raw material for any crop improvement programme. Conservation and use of genetic resources have great significance. It may either be introduced from other sources and may be developed by concerned breeder from his own material. The availability of genetic variability in germplasm and its proper use is

very important (Singh and Mohan, 1999; Sangwan *et al.*, 2004; Van Esbroeck and Bowman, 1998). For maintaining adequate variability the germplasm should include land races, obsolete varieties, varieties and parents of hybrids, breeding lines with genetic markers and other morphological variants, wild forms and their relatives. Hence, collection, evaluation, maintenance, categorization and utilization of germplasm have special significance. The precise evaluation of genetic stock and dissemination of findings is important for their utilization in breeding programme. The systematically evaluated genetic resources of crop plays pivotal role in crops improvement. In the present study, germplasm of *G. arboreum* was evaluated for some traits of economic importance and identified the superior lines for future use in breeding programme.

Materials and Methods

The experimental material consisted of 138 accessions of *G. arboreum* of diverse origin, grown in a single row of 6 m length during *Kharif* 2007. The spacing between rows was 67.5 cm and plants in a row were kept 30 cm apart. Recommended agronomic and plant protection measures were adopted. The season remained by and large favorable for cotton crop. Diseases attack was negligible and incidence of boll worms was also low. Observations were recorded on seven traits i.e. days to first flower, plant height (cm), number of monopods, number of bolls per plant, boll weight (g), seed cotton yield/plant (g), and ginning per cent. Some morphological traits like plant body colors, leaf shape and flower colors were also observed. All the data were recorded on randomly selected five competitive plants and averaged.

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Table 1. Overall mean and range of different characters in germplasm of desi cotton

Character	Range	Mean values
Days to first flower	64-97	80
Plant height (cm)	90-225	164
Number of monopods/plant	0-13	3.3
Boll number per Plant	13-167	65.7
Boll wt (g)	1.4-3.1	2.0
Seed cotton yield/plant (g)	18-250	102
Ginning per cent	26.1-46.3	37.3

Results

Wide range of variability was observed for different traits and their range and mean values are given in Table 1. The findings of the present study for different traits are discussed individually.

Days to first flower

Earliness is an important agronomic trait. Typically, it is measured by number of days to first flower (when data is to be recorded on individual plant basis) or days to 50% flowering (data to be recorded in a population or a plot) meaning that first flower had appeared in about 50% plants of a particular plot. Early maturing genotypes have a great advantage in cases where terminal drought is common occurrence. It also escapes high pest or disease incidence, abnormal weather conditions and field is timely vacated for sowing of next crop. It is not necessary that early flowering genotype will also mature early as cotton plant has indeterminate growth habit. Therefore, date of commencement of flowering or peak flowering or date of bursting of the first boll can be regarded as only

indication of earliness. The number of days to 50% flowering ranged from 64 (AC 41) to 97 (30822 BLL) days after sowing with mean value of 80 days (Table 1). Earliest flowering genotypes were AC 41 (64), D 462 P4 (68), B 4 (70), FFS 15 (70), HD 123 (72), D 462-P5 (72) (Table 2) and these genotypes can be utilized in crossing programme for reducing the days to flowering.

Plant height

The role of plant height is not very clear in cotton. Requirement of plant height may vary according to the objective. For machine picking, the sympodial variety with less height will be more desirable. Under poorly managed conditions tall genotypes with more monopods will be more suitable. In general plant height around 150 cm is most appropriate. The plant heights ranged from 90 (Jubli) to 225 cm (Vira) with mean value of 164 cm (Table 1).

Number of Monopods per Plant

Monopods are the vegetative branches and they do not bear the bolls directly on them. However, they bear sympods which are fruit bearing branches. Varieties/hybrids having more monopods have great advantage as most of the farmer's unable to maintain the proper plant stand. Monopodial varieties under such situations compensate the vacant space to some extent by using this space with more monopods. Secondly, the seed of cotton hybrids are more costly so monopodial hybrids can be sown on wider spacing, thus seed requirement will be less and ultimately reduce the production cost. The

Table 2. Superior genotypes for seed cotton yield (single plant basis) among germplasm of desi cotton with other traits

SNo.	Genotype	Days to 50% flowering	Plant height (cm)	Mono pods	No of bolls per plant	Seed wt (g)	GOT yield/plant (g)	Remarks (%)
1	FFS-1	95	165	13	167	2.2	250	38.6
2	HD 408	80	160	5	155	2.1	220	38.5
3	HD 372	86	180	4	147	2.3	208	37.8
4	FFS-16	77	180	4	135	1.9	210	40.1
5	AC 3028	92	175	3	108	2.9	200	36.1
6	NGPA 1-9-1	77	185	2	127	1.8	195	40.2
7	HD 328	82	210	3	90	2.7	190	42.4
8	CAD 306	82	150	5	102	2.3	190	35.2
9	DS 5	76	120	4	110	2.0	186	38.0
10	302	82	160	3	120	1.7	185	39.0
11	HD404	82	195	5	110	2.4	185	38.2
12	HD 20	87	190	4	95	2.3	185	39.9
13	AC 41	64	185	3	116	1.8	185	40.8
Mean	82	173	4.5	122	2.1	199	38.7	
	HD123 (check)	72	145	4	28	2.5	59	38.7
	Mean of all accessions	80	164	3.3	65.7	2.0	102	37.3

number of monopods per plant ranged from 0 (H476-5) to 13 (BH 05 VIII) with mean value of 3.3 (Table 1). Maximum number of monopods were observed in the genotypes namely FFS 1 (13), HD 369 (10), DS 5-2 (8), AKA 9410 (8), CISA 317, 2204 and P 248/98 (7).

Number of Bolls per Plant

The number of bolls per plant were observed to be the major yield contributing trait. It is the net outcome of flower produced and flower or bolls shed. Emphasis should be given on the selection of genotypes with more number of effective bolls. The deterioration of lint yield and quality may be caused by environmental factors and incidence of pests and diseases. The number of bolls per plant ranged from 13 (BH 05 VIII) to 167 (FFS 1) with mean value of 65.7 (Table 1). This character besides genotypic differences may also be widely influenced by environmental factors like high attack of boll worms, spacing, moisture at flowering and boll development stage, weather conditions etc. Number of bolls is not a stable character in different environmental conditions. The genotypes identified with maximum numbers of boll per plant are listed in (Table 3).

Boll weight

Final seed cotton yield is directly proportional to boll weight, as larger bolls weight increases the seed cotton yield with same number of small or medium bolls. Larger bolls were observed advantageous as they can be easily picked up and had less trash content. In the present time, farmers are more receptive to a variety/hybrid with larger boll size, even they sacrifice little yield advantage of smaller boll variety or hybrid. Picking rates are more expensive in varieties/ hybrids having smaller bolls and

availability of pickers is also a problem in such cases because of difficulty in picking. The boll weight, in the present study, ranged from 1.4 (AC 3377) to 3.1 g PL 375 and the mean for this character was 2.0 g (Table 1). In general, boll size in North zone is smaller than South and Central zone because of short boll development period in this zone. Most of the released *desi* varieties/hybrids have boll size between 2.2-2.6 g. There is urgent need to give more emphasis for improvement of this character. The germplasm needs to enrich with accessions having boll weight around 3.5 g so that future varieties/hybrids may have boll size of at least 2.7 to 3.0 g and hence more acceptable to the farmers. Good boll entries were PL 375 (3.1 g), HD 248 and AC 3028 (2.9 g), HD 453 (2.8 g), HD 328, PA 464 and AH 11 (2.7 g) as given in Table 3 and use of these entries to improve boll size is advocated.

Seed cotton yield

Yield in cotton is a very complex character and has different meaning for farmers, ginners and textile owner. As the farmers wants more seed cotton yield, ginners are more interested in higher ginning per cent, where as textile owners requirement is better quality fibres. Keeping all in mind, a cotton breeder had to satisfy all the above three categories to some extent. Primary components of yield in cotton are: number of plants per unit area, number of bolls per plant and boll weight. As low as 18 g (BH 05 VIII) seed cotton yield per plant was observed and maximum yield was 250 g (FFS 1) with a mean value of 102 g yield/plant (Table 1). The genotypes which are having high seed cotton yield are listed in the (Table 3).

Ginning Percent

Table 3. Elite germplasm lines for different traits of desi cotton

SNo.	Characters	Name of germplasm line
1	Days to 50% flowering	AC 41 (64), D 462 P4 (68), B 4 (70), FFS 15 (70), HD 123 (72), D 462-P5 (72)
2	Monopods/plant	FFS 1 (13), HD 369 (10), DS 5-2 (8), AKA 9410 (8), CISA 317, 2204 and P 248/98 (7)
3	Number of bolls/ plant	FFS 1 (167), AC 3347 (164), HD 408 (155), HD 372 (147), DS 5-2 and FFS 16 (135), NGPA 1-9-1 (127), AKA 9410 (122), 302 (120), AC 41 (116), 3031 (111), HD 404, PL 375-1, DS 5, FFS 12 and G, cot 19 P1 (110),
4	Boll wt (g)	PL 375 (3.1), HD 248 and AC 3028 (2.9), HD 453 (2.8), HD 328, PA 464 and AH 11 (2.7)
5	Seed cotton yield/plant (g)	FFS 1 (250), HD 408 (220), FFS 16 (210), HD 372 (208), AC 3028 (200), NGPA 1-9-1, HD 328, and CAD 306 (190), DS 5 (186), 302, HD 404, HD 20 and AC 41 (185)
6	Ginning per cent	0479 (46.3), RG 255 (46.0), HD 302 (45.7), LD 327 and LD 805 (45.4), DS 5 (44.8), FFS 14 (44.4)

Values in parentheses are mean value of a particular genotype

Note: GBW denotes for Green Broad White; GNW denotes for Green Narrow White; RNP denotes for Red Narrow Pink; GDNW denotes for Green Deep Narrow White; RNR denotes for Red Narrow Red; GNY denotes for Green Narrow Yellow; RBP denotes for Red Broad Pink

This is a character of economic importance and it is the lint percent to that of total seed cotton yield. In general ginning percent is inversely proportional to the fibre quality in cotton. As cotton is mainly grown for lint, so, higher ginning per cent is a big advantage. The lowest ginning per cent was 26.1 (AC 3233) and highest was 46.3 (0479) and average was 37.3 (Table 1) for this character. Thirty five accessions have ginning per cent 40 or more indicating very good material for this character. Seven lines having highest ginning per cent *i.e.* 44.4 or more are given in Table 3. Such lines can be utilized for the development of variety with high ginning percent. To improve ginning per cent use of genotypes, namely, 0479 (46.3), RG 255 (46.0), HD 302 (45.7), LD327 and LD 805 (45.4), DS 5 (44.8), FFS 14 (44.4) is advocated.

Morphological Observations

The observations were also recorded for morphological characters *i.e.* plant body color, lobing of leaves and flower color. Out of 138 accessions, 115 accessions had green plant body color and 23 had red plant body color. With respect to lobing of leaves, 114 had narrow lobes or okra type or normal leaves, 4 had deep narrow lobes and 20 accessions had broad lobes. Large variations was observed for flower color *i.e.* white (58), cream (4), pink (15), red (4) and yellow (54). Out of 13 best yielding genotypes, 10 had green plant body and 3 had red plant body color, 11 genotypes had narrow/deep narrow lobes and 7 accessions had white, 3 yellow, 2 pink and 1 red petal color. Among the top yielding accessions for seed cotton yield on morphological basis we can conclude that it is the green plant body color having narrow lobed leaves with white petal colour is most common.

Discussion

The mean seed cotton yield of best yielding 13 genotypes was 199 g per plant as compared to 102 g of mean of all accessions and 59 g of local check (LC) variety HD 123 (Table 2). The average number of bolls per plant in these genotypes was 122 as against 65.7 of mean of all accessions and far less than that of local check. With regard to boll weight, there was large variation among these highest yielding genotypes *i.e.* 1.7 g to 2.9 g with average boll weight of 2.1 g almost similar to that mean of all accessions (2.0 g) and much lower than local check (2.5 g). The perusal of Table 2 indicated that it is number

of bolls per plant which played more role towards higher seed cotton yield rather than boll weight. Mean number of days to first flower of selected genotypes was 82 almost similar to that of general mean and local check was 10 days earlier in flowering. Mean plant height of best yielding genotypes was 173 cm as compared to 164 cm mean of all accessions and 145 cm of local check. This indicated that optimum plant height in desi cotton is around 170 cm. Mean number of monopods per plant of good yielding accessions was 4.5 as against 3.3 of mean of all accessions. This indicated that better seed cotton yield genotypes had more numbers of monopods. Best yielding genotypes had ginning per cent 38.7 same as that of local check and better than mean of all accessions (37.3). This is mainly because all these 13 accessions had coarse fibre and such genotypes are more adopted in North Indian conditions. Coarse genotypes in general had more ginning per cent and vice versa.

Conclusion

We can conclude that some of the accessions had very good seed cotton yield potential and such accessions can be tried for their direct exploitation in larger plot and in different environments. As cotton crop is very sensitive to change in environmental conditions. Many a times data recorded for seed cotton yield on single plant basis may give contradictory results compared to data of per plot or per hectare basis. The results described in this paper are based on the data of one year so it can be considered as a preliminary study of superior accessions for a particular trait.

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Heterosis over Superior Parents under Diallel Cross in Linseed/Flax (*Linum usitatissimum* L.)

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A heterozygous individual resulting from the cross of two unlike parents is a hybrid which is usually vigorous. This increased vigour is often referred as hybrid vigour or heterosis. In general considerable amount of heterosis over superior parent was observed for almost all the characters. Forty crosses showed positive and significant heterosis for seed yield per plant and 13 crosses for fibre yield per plot while nine crosses showed heterosis in both seed yield per plant and fibre yield per plot.

Key Words: Heterosis, Seed yield, Fibre yield

Introduction

Linseed/Flax (*Linum usitatissimum* L.) is an oilseeds crop grown in winter (*rabi*) season in India mainly for industrial oil purpose. Besides oil, linseed is an excellent fibre producing crop with immense medicinal properties. India is one of the major linseed growing countries but its utilization is confined to only industrial oil purpose. The importance of this crop needs great attention to popularize the diverse use of linseed for better reaps of harvest. It is a highly self-pollinated crop. The scope for exploitation of hybrid vigour in genetically diverse population depends on direction and magnitude of heterosis and type of gene action. Techniques of hand emasculation and crossing have been standardized in this crop and the studies on the extent of heterosis for yield and its components were carried out through diallel mating design.

Materials and Methods

Experimental materials comprised of ten varieties, namely, Shubbra, Garima, Shekhar, Janki, J-23, T-397, Gaurav, Belinca, Rasmi and Nagarkot. The above varieties crossed in diallel mating design (without reciprocal) thus 45 F_1 were produced which were advanced to get the sufficient seeds for F_2 generation, the 10 Parents along with 45 F_1 s and 45 F_2 s were grown in a randomized block design with three replications at Oilseeds Farm CSA University of Agriculture and Technology, Kalyanpur, Kanpur, during *Rabi* 2002-2003. In 5 x 2 sq m plot size, row-to-row and plant-to-plant distance were maintained at 45 and 30 cm, respectively. The crop protections and other cultural operation were carried out as required to raise a good crop. The data were recorded on 5 randomly selected plants on

thirteen characters, namely, days to 50% flowering, plant height (cm), technical plant height (cm) days to maturity, stem diameter (mm), number of capsules/plant, number of tillers/plant, seed yield/plant (g), oil content (%), fibre length (cm), fibre strength (Tax), fibre fineness (g/Tax) and fibre yield/plot (kg.) Magnitude of heterosis was calculated as per cent of F_1 performance in favorable direction over superior parent as suggested by Hays *et al.* (1955)

Results and Discussion

For all the characters under study, F_1 crosses varied in magnitude and direction of heterosis (Table 1). This can be ascribed to the presence of genetic diversity among parents for all characters. The main cause of heterosis is dominant effect. The negative heterosis, which is desirable for days to 50% flowering, plant height, technical plant height and days to maturity was common in most of the crosses. The high negative heterosis over superior parent was observed in T-397 x Nagarkot, J-23 x Nagarkot, T-397 x Gaurav, Janki x Belinca, and T-397 x Rasmi for days to 50% flowering, T-397 x Gaurav, Shekhar x Janki, Garima x Belinca, Shekhar x Belinca, and Janki x Belinca for plant height, for technical plant height Garima x Rasmi, T-397 x Rasmi, J-23 x Nagarkot and Garima x Belinca. Likewise for days to maturity, T-397 x Nagarkot, Garima x Nagarkot and Shekhar x Nagarkot were found to name negative heterosis over superior plants. These results are in conformity with the findings of Singh *et al.* (1981), Singh and Srivastava (1987), Thakur and Bacteria (1991) for plant height and days to maturity.

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Table 1. Percent heterosis over superior parent for 13 characters of a 10 x 10 diallel crosses of Linseed/Flax

Crosses	Days to 50% flowering	Plant height	Technical Plant height	Days to maturity	Stem dia	Number of capsules plant	Number of tillers plant	Seed yield plant	Oil content	Fibre length	Fibre strength	Fibre fineness	Fibre yield/plot
Shubhra x Garima	6.36**	5.72**	28.94**	4.49**	-2.02**	-4.84	0.25	-11.95**	3.14**	14.55**	26.32**	7.01**	18.34**
Shubhra x Shekhar	-0.89	10.44**	25.17**	0.72	4.67**	6.57*	14.17**	-15.15**	5.73**	-9.12**	24.15**	10.85**	-2.70**
Shubhra x Janki	-11.20**	1.77	-0.83	-5.79**	23.96**	72.20**	15.73**	26.11**	3.07**	-14.26**	4.73**	14.12**	26.76**
Shubhra x J-23	7.83**	23.61**	22.55**	5.27**	8.11**	20.87**	16.99**	16.13**	0.98*	1.50	3.44**	15.30**	74.45**
Shubhra x T 397	3.69**	21.16**	29.41**	2.60*	50.56**	20.48**	50.00**	34.67**	6.64**	-3.90**	6.23**	3.55**	8.28**
Shubhra x Gaurav	2.71*	-8.87**	-22.60**	-1.66	35.35**	12.02**	29.71**	13.04**	6.26**	-11.32**	-5.90**	-19.19**	-15.22**
Shubhra x Belinca	-5.06**	-6.58**	-10.97**	-7.30**	4.81**	38.07**	-13.04**	34.05**	1.02**	-16.70**	-4.40**	-3.87**	-29.71**
Shubhra x Rasmi	-5.95**	-2.76	-15.75**	-3.53**	21.87**	-17.42**	21.66**	16.66**	8.75**	-26.81**	-6.03**	7.10**	-22.43**
Shubhra x Nagarkot	-15.22**	-13.36**	-16.73**	-9.53**	18.02**	37.79**	10.23**	77.49**	0.59	-24.18**	0.77	-2.41**	-29.87**
Garima x Shekhar	-3.35*	-3.67*	1.35	-2.31*	8.41**	-12.65**	-9.63**	-4.74**	5.50**	-23.24**	-2.58*	14.12**	-1.09**
Garima x Janki	-2.73	-6.28**	-9.00**	-4.40**	3.12**	17.84**	-3.93**	35.14**	2.77**	-25.84**	0.29	15.83**	24.66**
Garima x J-23	1.55	5.87**	9.47**	2.98**	-15.32**	-4.62	10.46**	17.63**	4.40**	-17.48**	8.26**	4.15**	22.36**
Garima x T 397	5.17**	2.37	-3.30	4.56**	6.74**	-18.53**	1.35**	13.71**	3.67**	-4.52**	3.34**	16.68**	-0.32
Garima x Gaurav	-3.18*	-10.62**	-26.32**	-3.17**	-17.17**	8.59**	4.35**	1.07**	0.78*	-4.64**	1.81	-29.89**	-19.14**
Garima x Belinca	-13.14**	-21.49**	-38.05**	-8.44**	2.88**	34.86**	-7.61**	56.75**	-2.10**	-22.09**	7.45**	-17.44**	-39.81**
Garima x Rasmi	4.29**	-7.92**	-53.99**	-6.17**	-20.83**	2.97	16.98**	30.03**	3.62**	-42.12**	-11.61**	-11.93**	-49.07**
Garima x Nagarkot	-12.26**	-13.35**	-31.17**	-10.99**	-37.84**	74.92**	15.91**	103.96**	-2.79**	-28.87**	5.74**	-0.47**	-36.29**
Shekhar x Janki	-9.78**	-25.46**	-32.57**	-5.55**	-22.92**	22.97**	12.36**	40.14**	13.61**	-15.77**	34.10**	2.16**	-13.01**
Shekhar x J-23	2.91*	5.77**	-6.94**	6.39**	-24.32**	3.62	34.64**	30.70**	5.21**	7.33**	6.61**	0.55**	67.57**
Shekhar x T 397	1.29	-8.31**	-27.67**	1.11	-11.24**	-19.31**	8.78**	45.15**	-0.43	3.90**	18.84**	5.53**	1.94**
Shekhar x Gaurav	2.43	-14.44**	-8.75**	-0.46	-24.24**	-1.77	23.19**	16.83**	4.89**	21.05**	14.94**	-5.93**	27.58**
Shekhar x Belinca	-4.70**	-21.05**	-26.05**	-6.90**	-25.96**	11.48**	-20.65**	45.78**	-6.07**	10.99**	15.01**	-14.56**	-7.87**
Shekhar x Rasmi	-4.71**	-8.83**	-21.74**	-3.45**	-17.71**	0.08	23.66**	23.48**	4.07**	8.23**	-9.26**	-10.38**	-10.28**
Shekhar x Nagarkot	-11.19**	-16.91**	-33.42**	-10.45**	-28.83**	49.57**	-4.55**	56.91**	5.12**	-2.72*	10.59**	-7.48**	-23.90**
Janki x J-23	5.29**	-3.44*	-20.35**	4.95**	-15.32**	4.46	29.41**	17.91**	6.67**	-4.32**	10.19**	2.30**	62.16**
Janki x T 397	6.43**	-9.44**	-31.97**	3.02**	-13.48**	-13.77**	26.35**	27.55**	4.84**	-7.19*	25.23**	9.38**	1.29**
Janki x Gaurav	-3.87**	-11.88**	-1.93	-2.98**	-32.32**	5.94	29.71**	16.26**	1.10**	9.72**	23.86**	-21.54**	-6.15**
Janki x Belinca	-16.36**	-20.86**	-30.88**	-8.98**	-30.77**	42.30**	0.00	41.84**	1.56**	8.73**	9.82**	0.00	-25.62**
Janki x Rasmi	-6.99**	-7.89**	-33.14**	-2.31*	-30.21**	11.64**	9.63**	13.03**	-2.25**	-3.58**	13.62**	-8.83**	-21.50**
Janki x Nagarkot	-10.52**	-8.70**	-14.28**	-8.08**	-30.63**	60.90**	11.36**	45.51**	-8.88**	2.18	23.60**	11.84**	-24.20**
J-23 x T 397	0.83	-1.49	-23.65**	2.73**	2.25**	-10.19**	27.03**	12.46**	3.00**	11.70**	24.47**	-2.50**	-15.05**
J-23 x Gaurav	-5.57**	-19.48**	1.26	-1.87	-22.22**	55.89**	55.07**	36.89**	10.44**	37.59**	18.55**	-15.75**	-5.12**
J-23 x Belinca	-3.80*	-12.66**	-32.50**	-6.05**	-35.58**	50.51**	-1.09*	42.96**	-0.40	10.24**	16.59**	-12.81**	-13.35**
J-23 x Rasmi	-7.71**	-14.25	-32.52**	-2.24*	-19.79**	19.52**	45.72**	28.36**	-2.16**	10.02**	5.36**	-6.65**	-13.46**
J-23 x Nagarkot	-19.16**	-12.21**	-38.53**	-10.11**	-22.52**	56.42**	-1.70**	48.79**	7.82**	-12.31**	31.25**	-15.81**	-32.48**
T 397 x Gaurav	-17.72**	-34.31**	-28.33**	-4.49**	2.02**	50.34**	50.72**	34.24**	-6.16**	12.92**	11.69**	3.74**	-31.31**
T 397 x Belinca	-12.59**	-15.67**	-28.13**	-4.82**	-21.15**	30.94**	-11.41**	34.43**	4.56**	1.08	22.01**	-18.27**	-24.53**
T 397 x Rasmi	-16.24**	-17.43**	-44.28**	-3.57**	1.04**	-2.89	14.30**	7.87**	3.16**	-6.80**	0.83	-4.10**	-8.60**
T 397 x Nagarkot	-20.34**	-18.57**	-21.78**	-11.65**	-0.90**	80.84**	10.23**	66.57**	6.93**	-16.99**	23.72**	-14.41**	-42.70**
Gaurav x Belinca	-5.51**	-15.67**	-21.63**	0.83	21.15**	38.79**	-8.70**	38.27**	6.16**	8.80**	21.44**	-21.30**	-12.65**
Gaurav x Rasmi	4.79**	-16.78**	-21.28**	0.39	5.21**	-6.88**	12.97**	-2.30**	5.08**	29.59**	7.92**	-8.83**	7.10**
Gaurav x Nagarkot	-8.89**	-18.47**	-25.76**	0.46	-15.32**	75.05**	6.82**	51.30**	-0.81*	6.10**	36.22**	5.30**	-7.49**
Belinca x Rasmi	8.38**	5.81**	-8.38**	6.37**	25.00**	-18.86**	3.61**	-14.70**	6.74**	16.59**	19.31**	29.96**	33.51**
Belinca x Nagarkot	-1.97	5.67**	-5.14**	3.31**	21.62**	28.04**	3.41**	26.28**	2.93**	0.98	36.86**	-1.40**	11.46**
Rasmi x Nagarkot	-12.68**	-4.45**	-6.26**	-2.18*	-15.32**	61.22**	0.00	59.71**	2.36**	6.54**	23.85**	-9.35**	-27.93**

* Significant at 5% per cent level; ** Significant at 1 per cent level

The range of heterosis over superior parents is given in Table 3. The results indicated that seed yield/plant, fibre yield, stem diameter, technical plant height and fibre length, heterosis was maximum for seed yield/plant up to 103.96% as observed over superior parents.

Positive heterosis, which is desirable for stem diameter, number of capsules/plant, number of tillers/plant, seed yield/plant, oil content, fibre length, fibre strength, fibre fineness and fibre yield. High positive heterosis over superior parents was observed and T-397 x Nagarkot for seed yield/plant, T-397 x Nagarkot, Gaurav x Nagarkot and Garima x Nagarkot for no. of capsules/plant, Shubhra x J-23, Shekhar x J-23 and Jaki x J-23 for

fibre yield, Shubhra x T-397, Shubhra x Gaurav, T-397 x Gaurav and Shubhra x T-397 for no. of tillers/plant. For oil content the crosses, Shekhar x Janki, J-23 x Gaurav and Shubhra x Rasmi showed low heterosis percentage of over superior parents. The results were in agreement with those of Kansal and Gupta (1981) Singh *et al.* (1983), Dakhore *et al.* (1987) and Rao *et al.* (1987) for seed yield and no. of capsules/plant.

Conclusion

The studies on diallel (10 x 10 parents) without reciprocal analysis were carried out linseed during *rabi* (winter) season 2002-03 to work out in the extent of heterosis for yield and its contributing traits. Garima, T-397, Nagarkot,

Table 2. Crosses showing maximum heterosis for 13 characters in Linseed/Flax

S. No.	Characters	Crosses	Heterosis (%)
1.	Days to 50% flowering	T-397 x Nagarkot	-20.34
		J-23 x Nagarkot	-19.16
		T-397 x Gaurav	-17.72
		Janki x Belinca	16.36
2.	Plant height	T-397 x Rasmi	-16.24
		T-397 x Gaurav	-34.31
		Shekhar x Janki	-25.46
		Garima x Belinca	-21.49
3.	Technical plant height	Shekhar x Belinca	-21.05
		Janki x Belinca	-20.86
		Garima x Rasmi	-53.99
		T-397 x Rasmi	-44.28
4.	Days to maturity	J-23 x Nagarkot	-38.53
		Garima x Belinca	38.05
		T-397 x Nagarkot	-11.65
		Garima x Nagarkot	-10.99
5.	Stem diameter	Shekhar x Nagarkot	-10.45
		Shubhra x T-397	50.56
		Shubhra x Gaurav	35.35
		Belinca x Rasmi	25.00
6.	Number of capsules/plant	T-397 x Nagarkot	80.84
		Gaurav x Nagarkot	75.05
		Garima x Nagarkot	74.92
		J-23 x Gaurav	55.07
7.	Number of tillers/plant	T-397 x Gaurav	50.72
		Shubhra x T-397	50.00
		Garima x Nagarkot	103.96
		Shubhra x Nagarkot	77.49
8.	Seed yield/plant	T-397 x Nagarkot	66.59
		Shekhar x Janki	13.61
		J-23 x Gaurav	10.44
		Shubhra x Rasmi	8.75
9.	Oil content	J-23 x Gaurav	37.59
		Gaurav x Rasmi	29.59
		Shekhar x Gaurav	21.05
		Belinca x Nagarkot	36.46
10.	Fibre length	Gaurav x Nagarkot	36.22
		Shekhar x Janki	34.10
		J-23 x Nagarkot	31.25
		Belinca x Rasmi	29.96
11.	Fibre strength	Gamma x Janki	15.83
		Garima x T-397	15.68
		Shubhra x J-23	74.45
		Shekhar x J-23	67.57
12.	Fibre fineness	Janki x J-23	62.16
13.	Fibre yield/plot		

Table 3. Range of heterosis for 13 characters in Linseed/Flax

S.No.	Characters	Range in heterosis (%)
1	Days to 50% flowering	-20.34-8.33
2	Plant height	-34.31-23.61
3	Technical plant height	-53.99-29.41
4	Days to maturity	-11.65-6.39
5	Stem diameter	-37.84-50.56
6	Number of capsule/plant	-19.31-80.84
7	Number of tillers/plant	-20.65-55.07
8	Seed yield/plant	-15.15-103.96
9	Oil content	-8.88-13.61
10	Fibre length	-42.12-37.59
11	Fibre strength	-11.61-36.46
12	Fibre fineness	-29.89-29.96
13	Fibre yield/plot	-49.07-74.45

Table 4. Estimates of SCA effects for 13 different characters in a 10 x 10 diallel cross of Linseed/Flax

Crosses	Days to 50% flowering	Plant height	Technical plant height	Days to maturity	Stem dia	Number of capsules/plant	Number of tillers/plant	Seed yield/plant	Oil content	Fibre length	Fibre strength	Fibre fineness	Fibre yield/plot
	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i
Shubhra x Garima	1.08	-3.06**	5.80**	3.72**	-0.64**	8.47**	0.43	-0.68**	0.96**	4.93**	0.03	0.19*	6.20**
Shubhra x Shekhar	-0.47	3.14**	2.77**	3.11**	-0.02	12.26**	0.73*	-0.65**	1.01**	-0.57	-0.03	-0.11	4.65**
Shubhra x Janki	-4.69**	2.79**	-0.07	-3.09**	0.36*	22.28**	0.35	0.30	-1.52**	0.41	-0.05	0.09	-1.83*
Shubhra x J-23	1.63	1.84	1.63	1.04	0.18	0.78	-0.53	-0.20	-1.78**	-0.13	0.25**	0.08	-1.15
Shubhra x T 397	1.27	2.76**	3.12*	-0.66	0.56**	20.19**	1.16**	0.86**	1.57**	-0.59	-0.13*	0.02	-1.84*
Shubhra x Gaurav	4.88**	3.55**	-8.77**	-0.87	0.53**	-14.10**	-0.15	-0.15	0.48	-2.38**	-0.16**	-0.16*	-2.70**
Shubhra x Belinca	2.73**	6.98**	6.82**	-3.41**	-0.44**	-5.71**	-0.74*	-0.09	-0.71**	-0.41	0.31**	-0.22**	-2.18**
Shubhra x Rasmi	-0.56	3.54**	2.88*	-1.88**	0.06	-25.09**	-0.05	0.11	1.47**	-2.88**	0.39**	-0.12	-0.16
Shubhra x Nagarkot	-3.32**	-3.73**	-0.03	-3.94**	0.31	-17.23**	-0.02	0.81**	-1.11**	-0.75	0.18**	-0.09	-1.97*
Garima x Shekhar	-1.30	-0.91	2.21	1.27	0.98**	-1.58	-0.34	-0.20	1.65**	-2.06**	0.17**	0.07	-1.61
Garima x Janki	4.37**	2.24	4.16**	1.05	0.51**	-8.73**	-0.41	0.50*	-0.89**	-1.47	0.11	0.23**	-2.55**
Garima x J-23	-2.00*	-2.99**	4.92**	0.41	0.13	-14.59**	-0.46	-0.36	0.35	-2.25**	0.02	-0.11	0.32
Garima x T 397	3.74**	-2.39*	0.88	4.04	0.08	-13.98**	-0.83**	-0.44*	1.06**	0.55	0.40**	0.10	-2.11**
Garima x Gaurav	0.56	7.43**	-3.05*	-0.74	-0.89*	-11.47**	-0.91**	-0.94**	-0.98**	0.40	-0.54**	-0.06	-0.26
Garima x Belinca	-4.25**	-3.82**	-5.53**	-2.88**	0.31	-1.72	0.01	0.48*	-1.27**	-0.83	-0.18**	-0.30**	1.62
Garima x Rasmi	2.34**	4.82**	-14.16**	-3.55**	-0.49**	-3.32**	0.13	0.52**	0.16	-5.91**	-0.20**	-0.43**	-1.52
Garima x Nagarkot	1.09	1.84	-1.79	-3.91**	0.94**	7.33**	0.73*	1.49**	-1.76**	-0.94	0.37**	-0.07	-0.36
Shekhar x Janki	-3.57**	-10.51**	-6.72**	-2.34**	-0.20	0.96	0.45	0.57**	2.90**	-3.67**	-0.26**	-0.36**	3.66**
Shekhar x J-23	-2.42*	-1.26	-1.53	2.86**	-0.08	-3.46**	0.67*	0.09	0.23	-2.05**	-0.06	-0.02	-1.73*
Shekhar x T 397	-0.81	-6.68**	-7.45**	-2.11**	-0.33	-10.48**	-0.57	0.99**	-1.12**	-2.28**	0.07	-0.09	-0.42
Shekhar x Gaurav	4.24**	5.59**	5.19**	1.21	0.50**	-14.21**	-0.14	-0.37	0.02	2.10**	0.58**	0.48**	1.72*
Shekhar x Belinca	2.91**	-1.55	2.39	-2.39**	-0.56**	-10.32**	-0.90**	-0.07	-3.38**	5.21**	-0.03	0.26**	2.21**
Shekhar x Rasmi	0.46	5.27**	5.74**	-1.37*	-0.27	-1.29	0.36	0.04	-0.11	3.96**	-0.11	0.04	-2.47**
Shekhar x Nagarkot	0.73	0.17	-4.20**	-5.36**	-0.48**	-1.20	-0.58*	-0.30	1.02**	2.86**	0.10	-0.01	-0.75
Janki x J-23	-0.37	-9.03**	-7.37**	1.23	0.40*	-0.51	0.27	-0.08	2.24**	-3.39**	-0.09	0.08	-1.20
Janki x T 397	3.43**	-9.71**	-10.11**	0.46	-0.26	-2.57*	0.16	0.54**	2.51**	3.36**	0.11	0.01	0.64
Janki x Gaurav	-1.38	5.64**	7.40**	-2.12**	-0.62**	-6.73**	0.02	0.04	0.11	0.22	-0.22**	0.07	3.85**
Janki x Belinca	-8.98**	-3.73**	-2.53*	-5.32**	-0.59**	8.93**	0.24	0.23	1.21**	5.22**	0.53**	0.04	0.33
Janki x Rasmi	-1.56	3.76**	-2.99*	-0.41	-0.52**	10.02**	-0.47	-0.02	-1.23**	1.38	-0.14*	-0.02	4.02**
Janki x Nagarkot	1.61	5.75**	6.94**	-1.61*	-0.40*	6.78**	0.22	-0.26	-3.29**	5.08**	0.84**	0.12	2.31**
J-23 x T 397	2.12*	-1.36	-5.13**	-1.46*	0.00	-4.13**	0.22	-0.12	0.54*	-0.97	-0.15*	-0.08	0.48
J-23 x Gaurav	0.18	2.23*	11.52**	0.78	-0.49**	21.98**	1.21**	1.11	2.66**	5.94**	0.17**	0.15*	-2.39**
J-23 x Belinca	7.14**	9.09**	-1.28**	0.41	-0.96**	8.24**	0.19	0.88	0.81**	5.01**	0.09	0.32**	2.34**
J-23 x Rasmi	0.86	1.71	-0.13	1.87**	-0.40*	11.29**	1.35**	0.82**	-2.40**	4.50**	0.06	0.18*	1.56
J-23 x Nagarkot	-4.34**	6.17**	-6.44**	2.86**	-0.31	-0.72	-1.52**	-0.03	2.34**	-0.04	-0.22**	-0.01	4.32**
T 397 x Gaurav	7.62**	-0.64	-1.76**	0.22	14.49**	1.27*8	0.68**	-4.36**	2.21**	0.88**	-0.26**	1.53	
T 397 x Belinca	0.25	10.07**	5.27**	3.34**	-0.55**	-6.29**	-0.18	-0.23	0.92**	4.11**	-0.33**	0.06	4.98**
T 397 x Rasmi	-5.17**	3.07**	-4.42**	1.10	0.18	-10.33**	0.04	-0.46*	-0.61*	1.74*	-0.02	0.28**	1.10
T 397 x Nagarkot	-3.36**	4.29**	7.80**	-4.10**	0.40*	7.93**	0.44	0.27	1.63**	0.47	-0.34**	-0.22**	3.40**
Gaurav x Belinca	-1.63	-6.94**	-3.08*	4.16**	0.89**	10.19**	0.11	0.45*	2.71**	0.21	-0.86**	-0.08	1.22
Gaurav x Rasmi	5.92**	-13.35**	-2.70*	-0.98	0.28	-1.32	0.10	-0.40*	1.28**	5.85**	-0.59**	0.12	-0.22
Gaurav x Nagarkot	0.54	-12.63**	-7.94**	6.59**	-0.16	17.13**	0.36	-0.41	0.98	0.11	0.13	3.07**	
Belinca x Rasmi	3.82**	-4.72**	-4.13**	2.88**	0.78**	-1.60	-0.32	-0.44*	1.44**	-1.71*	0.75**	0.22**	1.50
Belinca x Nagarkot	1.12	-1.43	-4.24**	6.59**	1.07**	2.46*	0.21	-0.01	0.62*	-4.01**	-0.26**	0.14	1.56
Rasmi x Nagarkot	-5.93**	-2.04	2.47*	3.18**	-0.07	11.25**	-0.04	0.52**	1.09**	0.54	-0.21**	-0.31	0.35
SE (S _{ij}) ⁺	0.968	1.066	1.246	0.648	0.171	1.172	0.295	0.197	0.268	0.764	0.0595	0.074	0.828
SE (S _{ij} -S _{ijk}) ⁺	1.088	1.126	1.143	0.909	0.241	1.318	0.413	0.276	0.376	1.056	0.0834	0.104	1.065

* Significant at 5% per cent level; ** Significant at 1 per cent level

Table 5. Estimates of GCA effect of the parents for 13 different characters in F₁s of linseed/Flax

Crosses to 50% flowering	Days height	Plant height	Technical maturity	Days to	Stem dia capsules plant	Number of tillers plant	Number of yield plant	Seed content	Oil length	Fibre strength	Fibre fineness	Fibre yield/plot	Fibre
F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i	F _i
1. Shubhra	-1.53*	0.43	1.34**	-1.72**	0.74**	11.48**	0.35**	0.15	0.82	-4.32	-2.27	-0.11	-0.11
2. Garima	-2.82**	-5.12**	-6.33**	-3.96**	-0.08	5.72**	-0.06	0.39	0.08	-5.56	-2.57	0.21	-0.28
3. Shekhar	-1.34*	-6.91**	-5.39**	-2.14**	-0.20*	1.42	0.05	0.55	0.53	-1.36	-0.92	-0.24	-0.06
4. Janki	-1.52*	-4.53**	-4.02**	-2.31**	-0.34**	-0.83	0.18*	0.11	-0.88	-2.08	-0.58	-0.16	-0.20
5. J-23	-4.64**	-8.35**	-6.48**	-3.68**	-0.14	4.40**	0.16*	0.00	0.32	-1.40	-0.59	-0.28	-0.26
6. T 397	-6.85**	-12.65**	-90.79**	-4.77**	-0.05	8.12**	-0.10	0.31	0.67	-3.34	-1.63	-0.10	-0.27
7. Gaurav	2.36**	4.38**	3.35**	2.84**	-0.02	-4.02**	-0.22**	-0.23	-0.46	8.31	1.96	0.29	0.17
8. Belinca	7.93**	16.59**	13.12**	7.35**	0.11	-13.14**	-0.27**	-0.79	0.04	6.64	8.64	0.38	0.57
9. Rasmi	3.75**	7.29**	5.68*	2.25**	-0.12	5.13**	-0.23**	-0.18	-0.66	3.79	1.45	-0.02	0.14
10. Nagarkot	4.65**	8.84**	8.52**	6.15**	0.10	-8.02**	0.14	-0.32	-0.47	4.42	1.53	0.45	0.30
SE _{ij}	0.29	0.35	0.37	0.19	0.05	0.58	0.08	0.06	0.08	0.22	0.25	0.01	0.02
SE (gi-gj) +	0.49	0.52	0.55	0.28	0.08	0.86	0.13	0.09	0.11	0.33	0.37	0.03	0.03

* Significant at 5 per cent level; ** Significant at 1 per cent level

Shekhar and Shubhra were observed to be best performing parents for seed yield and earliness. Shubhra, Shekhar, Janki and J-23 were observed good parents for fibre yield but not for other fibre quality characters like fibre strength and fibre fineness. Appreciable heterosis were found over superior parents for all the characters of desirable directions. Parents Subhra, Janki, J-23 are observed to be good parents for fibre yield and oil content and Shubhra is good parent for seed yield, fibre yield and oil content, while Belinca, Rasmi, Gaurav, and Nagarkot good parents for fibre quality character.

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Autumn Joy-A New Variety of Chrysanthemum for Garden Decoration

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A field experiment was conducted during 2003-07 at the research farm of department of Floriculture and Landscaping. The objective was to develop varieties suitable as cut flower, loose flower, pot culture and garden decoration. The recently released variety Autumn Joy (hybrid of White Bouquet X Flirt) had medium height (57.63 cm) and spread (62.66 cm) of plants. It exhibited 11.73 number of sprays per plant and 25.33 flowers per spray. The total number of flowers was reported to be 283.46 per plant. On the other hand, the length of spray was observed as 48.46 cm. Autumn Joy had pink decorative flowers with creamy yellow centre. It took 101.26 days for flowering (from transplanting) and was an early bloomer with long duration of flowering (35.81 days). The size and weight of flowers was reported to be 6.60 cm and 3.90 g, respectively.

Key Words: Chrysanthemum, Variety, Autumn Joy

Introduction

Chrysanthemum, belonging to family *Asteraceae*, is popular as cut or loose flower, for garden decoration and pot culture. It ranks second among the top ten flowering plants of the world owing to its attractive flowers of different shapes with wide spectacle of colours. In India, it occupies third position with jasmine and rose standing first and second respectively (Kolavalli *et al.*, 1991). A lot of varieties in the market. Also, commercial success of any crop depends upon the availability of suitable cultivars to fulfill the needs of the consumers. Since chrysanthemum is a cross-pollinated crop, a lot of scope lies in development of varieties through conventional breeding programme. An added advantage of the asexual propagation makes it quicker and easier for breeders to release the variety. Hence, it is necessary to assess the earlier germplasm and find out the suitable parents for establishing strong breeding programme by hybridization.

Materials and Methods

A field experiment was conducted during 2003-07 at the research farm of Floriculture and Landscaping. The objective of breeding was to develop varieties suitable as cut flower, loose flower, pot culture and garden display. The 18 parents were used for crossing, namely, Ajay, Reagan White, Reagan Emperor, Major Bosshardt Wit, Rage, Vyking, Flirt Jaya, Mother Terrace, White Bouquet, Puncho, Bindiya, Gul-e-Sahir, Sharad Shingar, Sadbhawna, Regal Times, Ratlam Selection and Baggi. These were selected on the basis of quantitative and qualitative characteristics (plant height, spread, number of flowers per plant, flowering behaviour, duration of

flowering, flower size, shape, type and colour) to be utilized in breeding programme. These varieties were selected as per their suitability for cultivation as cut or loose flowers, for garden decoration and pot culture. Various reciprocal crosses were made among these varieties. Apart from this, open pollinated seeds of the germplasm available at the centre was also collected and sown. As a result, 1,500 hybrids and 1,700 open pollinated seedlings were studied for various growth and flowering characters (Poonam and Kumar, 2006). Out of these, 15 open pollinated seedlings and 27 hybrids were selected on the basis of flower type, colour, shape, floriferousness, earliness and duration of flowering and rest were discarded. Among these, four hybrids and two open pollinated seedlings were further short listed as they were having better traits with respect to growth and flowering parameters. Next year, the terminal cuttings of selected plants were made, treated with IBA (100 ppm) and transplanted in pots during 1st week of July. The experiment was laid out in Complete Randomized Block Design with 3 replications. The recommended cultural practices were followed. The data on various vegetative (plant height, spread, number of sprays per plant, length of spray) and floral characters (number of flowers per spray, number of flowers per plant, number of days to flowering, duration of flowering, size and weight of flowers) were recorded. The pooled analysis was carried out as per method suggested by Panse and Sukhatme (1967).

Results and Discussion

The hybrids generated from these crosses were screened

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for various qualitative and quantitative characters. As a result, the hybrid 'Autumn Joy', an outcome of cross between White Bouquet and Flirt was found promising with respect to growth and flowering parameters.

The pooled data of 3 years (2004-07) presented in Table 1 and 2 revealed that variety Autumn Joy had medium height (57.63) and spread (62.66 cm) of plants. It exhibited 11.73 number of sprays per plant having 25.33 flowers per spray per plant. The length of spray was recorded to be 48.47 cm. It is highly floriferous in nature having 283.46 flowers per plant. Autumn Joy has decorative flowers of pink colour with creamy yellow centre (68 A as per Royal Horticultural Society, London, Colour Charts). It belonged to early maturity group *i.e.* it took 101.26 days to mature. It had long duration of flowering *i.e.* 35.81 days, which is a desirable trait for suitability of any variety for garden decoration. The size and weight of flowers were reported to be 6.60 cm and 3.90 g, respectively.

The data presented in Table 3 revealed that the recently released variety Autumn Joy was superior over the parents *i.e.* Flirt and White Bouquet and also over other varieties for garden decoration available at the research farm for most of the growth and flowering parameters.

The variety Autumn Joy had medium height of 52.63 cm, which was at par with height of White Bouquet (51.33 cm), but slightly dwarf than Flirt (66.46 cm). However, Autumn Joy exhibited more plant spread (62.66 cm) than the parents (42.39 cm in White Bouquet and 46.16 cm in

Flirt) and all other varieties. On the other hand, variety White Bouquet had 4.63 sprays per plant with 10.56 flowers per spray. This indicated that the number of flowers per plant in White Bouquet was 48.69 while in Flirt it was 90.24. The variety Autumn Joy exceeded in all the three parameters over the parents and other varieties *i.e.* it had 11.73 sprays per plant with 25.33 flowers per spray resulting in 283.46 flowers per plant. It made this variety highly floriferous and suitable for garden decoration. Further, the length of spray of Autumn Joy was 48.46 which was at par with the spray length of parents (47.48 cm in White Bouquet and 39.00 cm in Flirt) and also some of other varieties.

White Bouquet is an early flowering variety taking 108.46 days for flowering, whereas, on the contrary, Flirt belonged to late maturity group, which took 120.26 days from transplanting to flowering. Autumn Joy was a very early blooming variety, which flowered in early October taking 101.26 days for flowering after transplanting. The flowering duration of Autumn Joy was 35.81 days which was at par with White Bouquet having flowering duration of 35.80 days but significantly higher than Flirt (26.20 days) and all other cultivars. The flower size (6.60 cm) and weight (3.90 g) of Autumn Joy was in between the flower size and weight (4.58 cm and 2.28 g, respectively) in White Bouquet and (7.56 cm and 3.68 g, respectively) in Flirt. The variety White Bouquet had pure white pompon flowers, Flirt had decorative maroon flowers, while flowers in Autumn Joy were decorative type and colour was pink with creamy yellow centre (Table 4).

Table 1. Performance of Autumn Joy during 2004-2007

Year	Plant height (cm)	Plant spread (cm)	Number of sprays per plant	Number of flowers per spray per plant	Number of flowers per plant	Length of spray (cm)
2004-05	62.20	68.70	15.20	31.40	250.20	45.20
2005-06	55.30	71.70	11.40	21.00	302.00	48.60
2006-07	55.40	47.60	8.60	23.60	298.21	51.60
Pooled Mean	57.63	62.66	11.73	25.33	283.46	48.47

Table 2. Performance of Autumn Joy during 2004-2007

Year	Number of days to flowering	duration of flowering (days)	Flower size (cm)	Flower weight (g)	Flower type	Flower colour
2004-05	100.20	36.60	6.50	3.42	Decorative	Pink with creamy Yellow centre
2005-06	105.60	35.60	6.80	4.00	Decorative	Pink with creamy Yellow centre
2006-07	98.00	35.24	6.50	4.30	Decorative	Pink with creamy Yellow centre
Pooled Mean	101.26	35.81	6.60	3.90	-	-

Table 3. Evaluation of different varieties of chrysanthemum (for garden decoration) for growth and flowering parameters

Variety	Plant height (cm)	Plant spread (cm)	Number of sprays per plant	Number of flowers per spray per plant	Number of flowers per plant	Length of spray (cm)
Autumn Joy	52.63	62.66	11.73	25.33	283.46	48.46
Flirt	66.46	46.16	7.56	9.58	90.24	39.00
White Bouquet	51.33	42.39	4.63	10.56	48.69	47.48
Jaya	63.99	47.72	8.60	11.60	106.22	38.52
Ravi Kiran	57.53	50.16	4.80	12.90	68.28	50.00
Ratlam Selection	61.76	59.74	1050	16.26	172.90	52.60
Sadbawna	54.72	53.62	7.58	10.59	88.62	41.30
Baggi	65.78	48.55	8.96	9.88	85.60	55.58
Basanti	55.56	46.48	7.50	10.52	80.40	47.64
CD _(0.05)	2.50	2.72	1.10	1.90	20.50	2.10

Table 4. Evaluation of different varieties of chrysanthemum (for garden decoration) flowering parameters

Variety	Number of days to flowering	Duration of flowering (days)	Flower size (cm)	Flower weight (g)	Flower type	Flower colour
Autumn Joy	101.26	35.81	6.60	3.90	Decorative	Pink with creamy
Yellow centre						
Flirt	120.26	26.20	7.56	3.68	Decorative	Deep maroon
White Bouquet	108.46	35.80	4.58	2.28	Pompon	White
Jaya	118.20	29.66	5.72	3.37	Decorative	Maroon
Ravi Kiran	116.66	28.98	6.78	2.05	Decorative	Rusty red
Ratlam Selection	105.90	28.40	8.16	4.60	Decorative	Creamy White
Sadbhawna	102.82	25.66	6.62	1.06	Korean single	Peach
Baggi	103.69	30.22	5.99	2.92	Pompon	White
Basanti	110.80	28.80	6.70	3.33	Decorative	Yellow
CD _(0.05)	1.78	2.00	0.56	0.48	-	-

Therefore, it is concluded that Autumn Joy due to its early flowering; medium height; highly floriferous variety with long duration of flowering and pink (creamy yellow centre) decorative flowers is suitable for cultivation for garden decoration.

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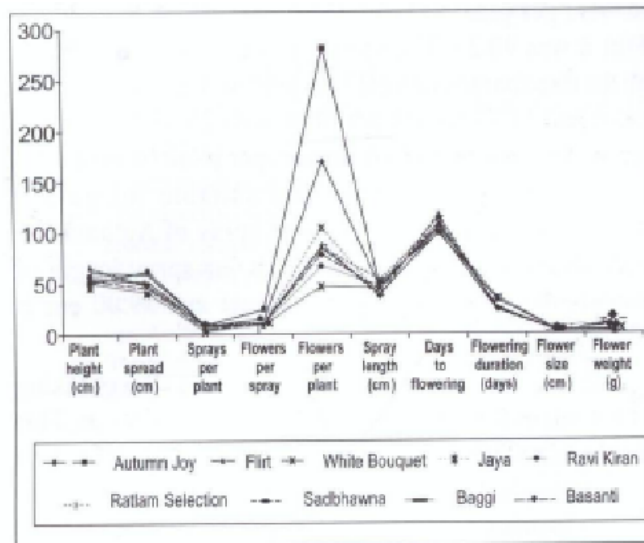
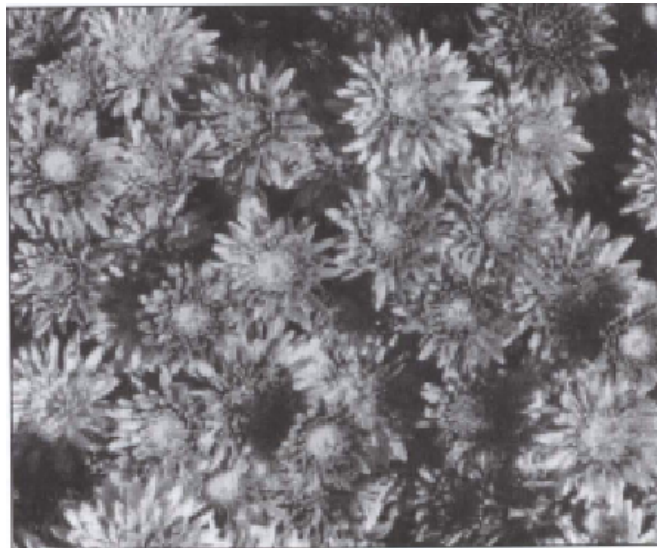


Fig. 1: Evaluation of different varieties of chrysanthemum for growth and flowering parameters



Autumn Joy

Association Studies for Salinity Tolerance in Sorghum [*Sorghum bicolor* (L.) Moench]

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A laboratory experiment was conducted to determine the effect of salinity stress (0 dSm⁻¹, dSm⁻¹, 6 dSm⁻¹ and 9 dSm⁻¹) on germination and seedling growth of 100 germplasm lines of sorghum (*Sorghum bicolor*), collected from different agroclimate zones of Rajasthan. The analysis of variance for all the traits revealed considerable variability in the experimental material and environments. In present study, the trend of genotypic and phenotypic correlation was similar between different characters. Three genotypes, viz., Raj 27, Raj 30 and Raj 4 could be identified for salinity tolerance as they were stable and having bi>I and high germination percentage at the highest (9 dSm⁻¹) salinity level. Another genotype Raj 42 though was not stable but it exhibited higher mean performance in all salinity levels for fresh weight of root per seedlings, coleoptile length, germination percentage and ratio of fresh weight of shoots to roots.

Key Words: Germplasm, Sorghum, Salinity, Variability

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench] is an important cereal crop of the country primarily grown for food, feed, forage and industrial raw material. Soil salinity, in arid and semiarid regions of the world, is a major detrimental factor for crop production. In India, nearly 10 million area is salt affected, out of which 17, 8716 ha area is in Rajasthan (Govt. of India, 2002-03). Plant resistance in context of salinity is not a simple reaction but it is a complex interaction between the plant and operating due to the extent and the constant increase in salt affected areas. Sorghum has been considered relatively more salt tolerant than maize and has potential as a grain and fodder crop for salt affected areas, and also has shown to contain variability for salinity. Breeding of salt tolerant crop varieties for such soils, as proposed by Epstein (1972) is an attractive possibility in combination with appropriate management programme. The development of high yielding salinity tolerant sorghum varieties is the best option to increase the productivity in saline soils. So the present investigation was undertaken to study the variability in germination and seedling traits at various levels of salinity and to identify sorghum genotypes for tolerance to salinity at germination and seedling stage.

Materials and Methods

Seeds of 100 germplasm of sorghum (*Sorghum bicolor*), collected from different agroclimatic zones of Rajasthan were evaluated in four salinity levels (0 dSm⁻¹, 3 dSm⁻¹, 6 dSm⁻¹ and 9 dSm⁻¹). Four types of test solution having salinity levels 0, 3, 6, 9 dSm⁻¹ were prepared artificially

by the addition of requisite amount of NaCl, CaCl₂, MgSO₄ & NaHCO₃ to Hoagland solution and used for watering the test crops as per need arise. Twenty seeds of each germplasm were surface sterilized with 0.1% HgCl₂ solution for 5 minutes followed by at least three washings with distilled water and placed in autoclaved petridishes. The whole experiment was replicated three times. The petridishes were watered with 5 ml of sterile test solution after draining out the previous day's solution, during the first five days. After 5th day each petridish was watered with 10 ml of the test solution. All the petridishes were kept in dark for 72 hours, later the dishes were exposed to artificial light (10 hrs/day) achieved by the use of fluorescent lamps and incandescent bulb. On the 11th day, observations were recorded for various germination and early seedling growth traits, viz., germination percentage, seedling height, coleoptile length, fresh weight of shoot per seedling, fresh weight of root per seedling, dry weight of shoot per seedling, dry weight of root per seedling, ratio of fresh weight of shoots to roots and ratio of dry weight of shoots to roots. Data on different characters were subjected to the appropriate statistical analysis.

Results and Discussion

Mean sum of squares due to genotype was significant for all the characters at all the salinity levels (Table 1). Similarly, difference among salinity levels and interaction of genotypes with environments were also significant for all the characters. In fact, variation in whole plant biomass responses to salinity was considered to provide the best means of selection (Krishnamurthy *et al.*, 2007). Variation

for germination percentage and seedling characteristics at different salinity level were widely reported (Khalvati *et al.*, 2001; Khan *et al.*, 2003). The salinity gradient adversely affected the mean value of all the characters. The *per se* performance decreased with increasing the salinity. Such effects were also noticed by (Mcharia *et al.*, 1995; Kumari and Pillai, 1997). Comparison of mean performance of genotype in different salinity levels revealed that genotype Raj 42 exhibited higher values for various traits, viz., germination percentage, coleoptile length and fresh weight of shoot per seedling.

In the present investigation, the magnitude of phenotypic coefficient of variation (PCV) was higher than Genotypic coefficient of variation (GCV) in all the four salinity levels for all the characters, however, magnitude

of both moved together (Table 2). In the present study, high GCV was observed for dry weight of root per seedling and ratio of dry weight of shoots to dry weight of roots in all the four salinity levels. Besides these traits, some characters had high GCV in specific environment like dry weight of shoot per seedling in S_0 and S_1 and ratio of fresh weight of shoots to fresh weight of roots in S_3 . Similar type of results of high GCV for one or the other aforesaid character were reported by Mehdi and Ahsan (2002).

In present study, heritability was high for fresh weight of root per seedling, dry weight of root per seedling, fresh weight of shoot per seedling and ratio of fresh weight of shoots to fresh weight of roots in all the four salinity levels. It indicated that heritability of these characters was less

Table 1. Mean squares for different characters in different salinity levels in sorghum

S.No.	Characters	Salinity levels	Genotype [99]	Error [200]
1	Germination Percentage	S_0	232.15**	5.33
		S_1	248.98**	5.00
		S_2	252.29**	5.42
		S_3	376.27**	5.92
2	Seedling height (cm)	S_0	24.42**	0.06
		S_1	14.63**	0.32
		S_2	14.66**	0.01
		S_3	23.44**	0.02
3	Coleoptile length (cm)	S_0	4.08**	
		S_1	3.60**	0.02
		S_2	4.68**	0.04
		S_3	11.48**	0.02
4	Fresh weight of shoot per seedling (g)	S_0	0.27**	6.433e-05
		S_1	0.23**	3.633e-05
		S_2	0.22**	4.934e-05
		S_3	0.21**	4.234e-05
5	Fresh weight of root per seedling (g)	S_0	0.03**	3.45e-07
		S_1	0.03**	4.15e-07
		S_2	0.03**	2.5e-08
		S_3	0.03**	6.5e-08
6	Dry weight of shoot per seedling (g)	S_0	0.03**	1.633e-05
		S_1	0.05**	6.5e-08
		S_2	0.02**	6.5e-08
		S_3	0.01**	6.5e-08
7.	Dry weight of root per seedling (g)	S_0	0.01**	6.5e-08
		S_1	0.02**	2.65e-07
		S_2	0.01**	4.15e-07
		S_3	0.01**	5.2e-07
8	Ratio of fresh weight of shoot to fresh Weight of root	S_0	62.69**	0.001
		S_1	66.24**	0.002
		S_2	44.54**	0.001
		S_3	64.78**	0.001
9	Ratio of dry weight of shoot to dry Weight of root	S_0	37.91**	0.01
		S_1	77.32**	0.48
		S_2	29.86**	0.02
		S_3	32.72**	0.26

Table 2. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H) and genetic gain (GG) for different characters in sorghum

S.No.	Characters	Salinity Level	GCV	PCV	H2	GG
1	Germination percentage	S ₀	10.87	11.25	93.35	21.63
		S ₁	11.86	12.23	94.15	23.72
		S ₂	12.84	13.27	93.76	25.62
		S ₃	18.06	18.49	95.38	36.33
2	Seedling height (cm)	S ₀	19.27	19.34	99.25	39.54
		S ₁	17.19	17.77	93.59	34.27
		S ₂	22.17	22.19	99.83	45.62
		S ₃	39.85	39.91	99.72	81.98
3	Coleoptile length (cm)	S ₀	29.31	29.71	97.28	59.54
		S ₁	23.56	23.75	98.35	48.13
		S ₂	20.27	20.54	97.32	41.92
4	Fresh weight of shoot per seedling (g)	S ₀	26.67	26.68	99.93	54.92
		S ₁	27.64	27.65	99.95	56.93
		S ₂	29.29	29.30	99.93	60.31
		S ₃	31.72	31.72	99.94	65.31
5	Fresh weight of root per seedling (g)	S ₀	57.47	57.48	100.00	118.40
		S ₁	58.59	58.59	100.00	120.69
		S ₂	55.84	55.84	100.00	115.04
		S ₃	53.37	53.37	100.00	109.95
6	Dry weight of shoot per seedling (g)	S ₀	72.60	72.65	99.85	149.44
		S ₁	89.89	89.89	100.00	185.17
		S ₂	75.17	75.17	100.00	154.85
		S ₃	64.81	64.81	100.00	133.51
7	Dry weight of root per seedling (g)	S ₀	118.99	118.99	100.00	245.11
		S ₁	146.31	146.31	99.99	301.38
		S ₂	116.79	116.80	99.98	240.56
		S ₃	103.45	103.47	99.96	213.07
8	Ratio of fresh weight of shoot to fresh weight of root	S ₀	53.57	53.57	99.99	110.34
		S ₁	62.40	62.40	99.99	128.53
		S ₂	64.14	64.14	99.99	132.11
		S ₃	85.47	85.47	99.99	176.06
9	Ratio of dry weight of shoot dry weight of root	S ₀	79.83	79.86	99.93	164.39
		S ₁	102.03	102.99	98.15	208.23
		S ₂	75.45	75.53	99.80	155.27
		S ₃	83.63	84.63	97.65	170.25

affected by salinity levels. Whereas some characters had high heritability in specific environment such as seedling height in S₀, S₁ and S₃ and for ratio of dry weight of shoots to dry weight of roots in S₀ and S₂ which indicated that the inheritance of these traits was affected by salinity. These results were in accordance with the finding of Maiti *et al.* (1994).

The ultimate aim of studying the variability and heritability of any trait is to have an idea about the efficiency with which it can be improved by selection. The genetic gain was high for dry weight of root per seedling in all the four salinity levels, whereas, it was high for ratio of dry weight of shoots to dry weight of roots in S₁.

On the basis of above discussion about GCV, heritability and genetic gain, it can be concluded that the experimental material of this study possessed potential for improvement in dry weight of root per seedling as the estimates of GCV, heritability and genetic gain were high in this character in all the four salinity levels. Therefore, selection is amicable in all the four salinity levels. Whereas, for ratio of dry weight of shoots to dry weight of roots, it is amicable only in S₁ as estimates of these three parameters, viz., GCV, heritability and genetic gain were higher in S₁ salinity level only.

Salinity tolerance, being complex character, is difficult to improve by direct selection. The efficiency of selection can be increased by simultaneous selection for

Table 3. Correlation matrix for different traits in sorghum

S.No.	Character	Correlation coefficient (r)	Seedling height	Coleoptile length	Fresh weight of shoots per Seedling	Fresh weight of roots per seedling	Dry weight of shoot per seedling	Dry weight of roots per seedling	Ratio of fresh weight of shoots fresh weight of roots	Ratio of dry weight of shoot
1	Germination percentage	g p	0.23* 0.12	-0.09 -0.09	0.35** 0.23*	0.09 0.04	0.39** 0.09	0.25* 0.08	-0.00 0.02	0.16 -0.05
2	Seedling height	g p		-0.39** -0.44**	0.24* 0.14	0.07 0.04	0.14 0.10	0.11 0.4	0.18 -0.01	-0.02 0.04
3	Coleoptile length	g p			-0.13 -0.08	-0.03 0.03	-0.08 -0.04	-0.16 -0.03	-0.07 -0.03	-0.13 -0.02
4	Fresh weight of shoots per seedling	g p				0.25* 0.19	0.76** 0.40**	0.09 0.04	0.43** 0.26**	0.58** 0.25**
5	Fresh weight of roots per seedling	g p					0.15 0.19	0.03 0.06	-0.06 -0.62**	-0.13 0.03
6	Dry weight of shoots per seedling	g p						0.03 -0.00	0.40** -0.01	0.73** 0.64**
7	Dry weight of roots per seedling	g p							0.02 -0.07	-0.38** -0.24**
8	Ratio of fresh weight of shoot to fresh of root	g p								0.47** 0.19

g=Genotypic Correlation Coefficient , p=Phenotypic Correlation Coefficient

few correlated characters. In present study, the trend of genotypic and phenotypic correlation was similar between different characters (Table 3). However, the genotypic correlation coefficients were slightly higher than the corresponding phenotypic correlation coefficients. This indicated the role of environment on the association between characters.

Perusal of correlation across the environments showed that germination percentage was positively and significantly correlated with fresh weight of shoots per seedling, dry weight of shoot per seedling and dry weight of roots per seedling; seedling height with fresh weight of shoots per seedling, fresh weight of shoots per seedling with fresh weight of roots per seedling, dry weight of shoots per seedling, ratio of fresh weight shoots to fresh weight of roots; germination percentage and fresh weight of shoot per seedling was positive in all the four salinity levels. While seedling height was negatively and significantly correlated with coleoptiles length; fresh weight of roots per seedling with ratio of fresh weight of shoots to fresh weight of roots; and dry weight of roots per seedling to ratio of dry weight of shoots to dry weight of roots.

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SHORT COMMUNICATION

NRCG CS-148: A New Large Seeded Genotype of Groundnut**SK Bera, K Hariprasanna and Vinod Kumar***National Research Centre for Groundnut, P.B. #5, Ivnagar Road, Junagadh-362001, Gujarat, India***Key Words: Groundnut, Large seed, Disease resistance, Confectionery**

Groundnut (*Arachis hypogaea* L.) is a principal oilseed crop in India accounting for more than 25% of the total area under oilseed production in India. Though India accounts for largest area under groundnut, it does not contribute much to the global production and trade, particularly due to the high level of fluctuation in the productivity due to different abiotic and biotic stresses. Development of genotypes endowed with tolerance to different biotic and abiotic yield limiting factors together with high reproductive potential is an important aspect in groundnut improvement. Apart from use for oil extraction, groundnut is also consumed directly because of its high food value owing to protein (22%), carbohydrate (10%), minerals (3%), niacin (17mg/ 100g) and vitamin B especially thiamin (1mg/ 100g) content (Rajgopal *et al.*, 2000). The groundnut, which is used for direct consumption both in domestic and international market, is generally referred as large seeded groundnut or hand picked selection (HPS) groundnut and confectionery groundnut depending upon the quality attributes like chemical, nutritional or sensory properties (Dwivedi and Nigam, 2005).

Large kernel size, elongated shape, uniformity of kernel mass and shape, high proportion of sound mature kernels and testa colour are some of the physical attributes that exemplify the confectionery groundnut (Chuni Lal and Hariprasanna, 2004). A maximum count of 44 kernels per 25 g of the material (Reddi, 1988) or in other words 100-kernel weight of 57 g or more is essential for a groundnut sample to qualify for grading as HPS groundnut. Confectionery groundnut with premium edible grade has a great demand all over the world. Indian groundnut is very popular in the international market for the table purpose, due to its characteristic natural nutty flavour, taste and crunchy texture and also relatively longer shelf life. Therefore, with the growing consumer taste world over for organic food with natural flavour, Indian groundnut has better export opportunity (Nautiyal, 2002). In spite of the immense export potential, only limited genotypes have been bred with an aim to obtain HPS or confectionery groundnuts in India. Considering

all these facts, attempts were made to develop large seeded groundnut genotypes with appropriate attributes. A number of interspecific derivative breeding lines have been developed at the National Research Centre for Groundnut (NRCG), Junagadh.

A set of 301 groundnut genotypes developed at NRCG was evaluated in an augmented design with checks during rainy season of 2003 and 2004 at the experimental farm. Each genotype was planted in 3 rows of 3 m. length with recommended spacing. Observations on pod yield/ plant and 100-kernel weight were recorded at harvest. The genotypes NRCG CS-148 and 219 recorded higher 100-kernel weight than the best check TKG 19A among the 35 promising genotypes during 2003 (Table 1). Similarly, NRCG CS-148 showed highest 100-kernel weight (Table 2) among the 15 genotypes, which recorded 100-kernel weight more than 44g in spite of severe drought condition the crop faced during reproductive stage resulting in poor pod and kernel yields/ plant and shelling percent.

The genotype NRCG CS-148 was also evaluated in a separate replicated large seeded groundnut trial along with three checks during rainy season of 2005 at NRCG (Table 3). Data on days to 50 per cent flowering, number of pods/ plant, pod and kernel yields, 100-kernel weight, sound mature kernel percent, shelling percentage, harvest index and oil content were recorded. There was not much difference in days to 50 per cent flowering among NRCG CS-148, GG 20 and TKG 19A indicating equal crop duration of NRCG CS-148 and elite large seeded cultivars. The genotype NRCG CS-148 performed better than all the checks for pod yield, kernel yield, 100-kernel weight, sound mature kernel per cent and shelling per cent. The oil content was also slightly better than all the checks.

Thirty three selected genotypes based on their performance during 2003 and 2004, were further evaluated during rainy season of 2006 along with four checks at KVK, Mundra, Gujarat, where soil conditions

Table 1. Promising large seeded advance cultures during rainy season 2003

Genotype	Pod weight/ plant (g)	Kernel weight/ plant (g)	100-kernel weight (g)	Shelling percent (%)	Harvest Index (%)
NRCG CS-7	8.1	5.9	46.4	72.84	24.58
NRCG CS-8	13.8	10.5	46.8	76.09	32.21
NRCG CS-12	12.6	9.4	47.7	74.60	31.23
NRCG CS-13	9.0	6.2	48.8	68.89	29.81
NRCG CS-18	14.6	9.9	58.9	67.81	25.19
NRCG CS-60	9.4	6.6	48.6	70.21	20.75
NRCG CS-67	2.7	1.6	47.6	59.26	10.00
NRCG CS-74	10.5	7.5	50.0	71.43	24.75
NRCG CS-76	6.3	4.7	46.1	74.60	24.10
NRCG CS-85	9.0	6.7	46.6	74.44	24.45
NRCG CS-86	9.1	6.8	49.4	74.73	23.53
NRCG CS-89	9.3	6.6	48.0	70.97	24.09
NRCG CS-97	13.3	9.3	47.7	69.92	22.57
NRCG CS-103	8.9	6.6	54.6	74.16	31.88
NRCG CS-115	8.6	6.2	55.3	72.09	21.02
NRCG CS-116	11.0	8.0	48.0	72.73	22.60
NRCG CS-123	6.6	4.7	51.2	71.21	18.80
NRCG CS-126	7.8	5.2	47.7	66.67	16.10
NRCG CS-130	7.1	5.1	53.0	71.83	20.00
NRCG CS-131	12.3	8.6	46.5	69.92	26.06
NRCG CS-132	13.0	9.7	63.6	74.62	28.12
NRCG CS-133	11.4	7.9	51.5	69.30	22.38
NRCG CS-138	11.7	8.1	52.0	69.23	22.07
NRCG CS-145	7.8	5.1	49.8	65.38	19.54
NRCG CS-148	8.0	5.4	73.2	67.50	13.50
NRCG CS-161	10.3	7.3	46.2	70.87	21.86
NRCG CS-164	7.2	5.3	51.1	73.61	25.48
NRCG CS-165	10.5	7.4	49.4	70.48	32.31
NRCG CS-178	9.2	6.9	46.8	75.00	29.87
NRCG CS-198	9.3	6.4	47.8	68.82	20.58
NRCG CS-201	12.1	8.5	46.3	70.25	38.99
NRCG CS-218	12.0	9.1	56.4	75.83	35.00
NRCG CS-219	10.1	7.6	68.3	75.25	28.68
NRCG CS-223	10.5	6.9	46.2	65.71	32.55
NRCG CS-241	9.2	6.7	47.4	72.83	25.67
TKG 19A	14.5	10.2	67.0	70.34	28.20
BAU 13	10.8	7.6	66.5	70.37	30.40
SEm	2.5	1.8	7.2	3.6	6.0
CD (0.05)	5.2	3.8	14.9	7.4	12.4

Table 2. Promising genotypes with higher 100-kernel weight during rainy season 2004

Genotype	Pod yield/ 10 plants (g)	Kernel yield/ 10 plants (g)	100-kernel weight (g)	Shelling percentage (%)
NRCG CS-148	60	33.5	48.5	50.77
NRCG CS-138	22	8.6	48.1	51.13
NRCG CS-283	62	36.2	47.0	51.48
NRCG CS-18	57	15.0	46.6	57.25
NRCG CS-122	32	20.9	44.2	52.90
NRCG CS-266	75	17.7	43.7	46.06
NRCG CS-126	58	20.9	43.1	53.33
NRCG CS-123	46	15.4	42.4	52.90
NRCG CS-276	35	22.0	42.3	48.98
NRCG CS-184	53	26.5	41.4	48.54
NRCG CS-189	61	45.0	41.0	46.67
NRCG CS-218	46	33.0	40.9	45.76
NRCG CS-118	38	23.2	40.3	52.79
NRCG CS-108	86	9.0	40.1	54.17
NRCG CS-132	74	36.5	40.1	52.90
BAU 13	9.4	5.5	32.3	59.3
TKG 19A	11.0	7.4	40.6	67.3
SEm	21.8	11.6	3.6	5.3
CD (0.05)	45.4	24.2	7.4	11.0

Table 3. Performance of NRCG CS-148 during rainy season 2005 in a replicated trial

Genotype	Days to 50% flowering	No. of pods/ plant	Pod yield/ plant (g)	Pod yield (kg/ha)	Kernel yield (kg/ha)	100- kernel weight (g)	Sound mature kernels (%)	Shelling percentage (%)	Harvest Index (%)	Oil Content (%)
NRCG CS-148	28.7	9.7	13.9	2398.3	1760.0	66.6	54.0	73.5	37.1	51.8
GG 20	27.7	18.0	17.6	2163.0	1401.3	38.6	39.3	64.6	42.6	51.7
M 13	29.3	13.3	15.5	2292.0	1527.7	44.5	40.5	66.7	57.1	50.5
TKG 19A	26.0	15.0	14.9	2299.3	1309.7	36.5	32.0	56.8	40.9	49.3
SEm	0.3	1.8	2.3	308.1	207.1	5.3	6.1	2.5	4.4	0.6
CD (0.05)	0.9	5.0	6.4	875.5	NS	15.1	NS	7.1	12.4	1.8

Table 4. Performance of large seeded genotypes at Mundra, Gujarat during rainy season 2006

Genotype	Pod weight/ plant (g)	100-kernel weight (g)	Shelling percentage (%)	Sound mature kernels (%)
NRCG CS-148	16.7	60.2	68.0	64.0
NRCG CS-285	29.3	46.9	56.0	79.1
NRCG CS-241	18.2	46.5	63.0	79.9
NRCG CS-219	20.5	46.2	62.5	82.1
NRCG CS-188	17.4	46.5	71.5	70.6
M 13	26.6	43.0	55.5	65.2
TKG19A	29.1	50.2	62.5	67.3
B 95	20.4	41.9	51.0	84.4
BAU 13	17.5	46.5	52.5	80.9
SEm	4.8	8.9	7.4	9.7
CD (0.05)	9.9	18.6	15.5	20.1

are highly conducive for development of large seed size in groundnut. The experiment was undertaken in a randomized block design with two replications and recommended management practices for groundnut were followed to raise a good crop. The observations on pod weight, 100-kernel weight, shelling percentage and sound mature kernel were recorded at harvest (Table 4). Among the 33 genotypes, NRCG CS-148 recorded the highest 100-kernel weight (60.2g), while among the checks TKG 19A (50.2g) had highest kernel size. Genotype NRCG CS-148 recorded kernel size higher than all the checks and also recorded shelling percentage higher than all the checks though pod yield and sound mature kernel percentage were comparatively lower.

The genotype NRCG CS-148 was also screened for reaction to foliar diseases like early leaf spot (*Cercospora arachidicola*), late leaf spot (*Phaeoisariopsis personata*) and rust (*Puccinia arachidis*) on a 1 to 9 scale over two years at NRCG in the field condition during rainy season. Mean scoring showed moderately resistant reaction for late leaf spot and rust compared to the susceptible check, GG 20 (Table 5).

The pods of the genotype are bold, two seeded with moderate reticulation and a slight beak (Fig. 1). The kernels are elongated to elongated-oval in shape with tapering ends and rose testa colour. The genotype is semi-spreading in growth habit. The seed size and other physical

Table 5. Mean disease reaction of NRCG CS-148 against foliar fungal diseases

Year	Genotype	Early leaf spot	Late leaf spot	Rust
2006	NRCG CS-148	3.8	1.5	1.0
	GG 20*	4.3	3.0	1.0
	NRCG CS-352	5.3	2.8	1.0
	NRCG CS-296	4.5	4.8	1.2
	NRCG CS-176	4.8	2.8	2.2
2007	NRCG CS-148	7.2	3.7	4.8
	GG 20*	8.2	4.7	6.2
	NRCG CS-272	8.5	5.8	4.3
	NRCG CS-337	7.8	3.8	7.0

(*Susceptible check; the highest score recorded for each disease is given in bold face along with the name of the genotype)

**Fig. 1: Pods and kernels of NRCG CS-148**

attributes make NRCG CS-148 an ideal donor parent for quality improvement and hence, the genotype can find its place in future breeding programmes aimed at development of large seeded and confectionery type groundnut.

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SHORT COMMUNICATION

Genetics of Quantitative Traits in Indian Mustard [*Brassica juncea* L. Czern and Coss]**RK Singh¹ and Pallavi Dixit**

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36 F₁s, 36F₂s and 9 parents were evaluated during rabi seasons 2003-2004 in randomized block design replicated thrice. The observation were recorded on ten metric traits and analyzed excluding reciprocals. The presence of epistasis was revealed for plant height, main raceme length, primary and secondary branches, siliquae on main raceme, seed yield and oil content per plant in F₁ and for day to flower, plant height, primary branches and siliqua length in F₂. The analysis of components of genetic variance revealed that the additive component (D) was significant for all the characters except primary and secondary branches in F₁. The two measures of non-additive components, $\sigma^2_{1/2}$ and $\sigma^2_{2/4}$ were significant for all the characters. Positively significant h^2 for different traits indicated that the average direction of dominance was positive and hence the characters were controlled by dominance genes in positive direction. The proportion of $\sigma^2_{1/2}$ / $\sigma^2_{2/4}$ & $\sigma^2_{2/4}$ / $\sigma^2_{1/2}$ for most of the traits in both F₁ and F₂ population indicated nearly symmetrical distribution of positive and negative alleles among the parents. The proportion of dominant to recessive gene (KD/KR) exhibited an excess of dominant genes controlling most of the traits. The estimates on h^2 / $\sigma^2_{1/2}$ & $\sigma^2_{2/4}$ varied from 0.05 (day to flower) to 3.74 (siliquae on main raceme) in F₁ indicating that siliquae on main raceme is governed by 3 to 4 genes or group of genes. In F₂ estimate of $\sigma^2_{1/2}$ / $\sigma^2_{2/4}$ & $\sigma^2_{2/4}$ / $\sigma^2_{1/2}$ were lower than unity for all the characters and thus the number of dominant genes controlling the traits were underestimated.

Key Words: Indian mustard, Diallel, Genetic components, Epistasis, Dominance

Indian mustard (*Brassica juncea* (L.) Czern & Coss) is an important oilseed crop of the country covering more than six million hectares during the rabi season and yielding about 4.3 million tones of seeds. The country accounts for 13% of the world's oilseeds area and 7% of production. Oil seeds form the second largest agricultural commodity after cereals sharing 14% of the country's gross cropped area and accounting for nearly 5% of the gross national products and 10% value of all agricultural products [Hegde *et al.*, 2004]. The present average yield of Indian mustard in our country is low (<1000 kg/ha) as compared to the world average of more than 1333 kg/ha [Yadav *et al.*, 2000]. As a result, production of edible oils in India, is grossly short of the requirements. Consequently large quantities have to be imported for making up the short fall, which in turn, is a heavy drain on foreign exchange resources. It, therefore, becomes essential to breed a variety having high yield potential. Hence, the present study was undertaken to understand gene action for seed yield, its contributing characters and oil content through diallel analysis, so that an effort could be made in right direction for the genetic improvement of mustard crop.

Nine diverse genotypes of Indian mustard, viz., T-59, RH-30, Pusa Bold, RL-1359, JGM-01-15, RW-351,

CS-52, RK-1418 and Pant Rai-16 were selected as basic experimental material from breeding materials officially collected in October 2001 from National Research Centre on Rapeseed-Mustard, Sewar, Bharatpur (Raj.). During rabi 2002-2003, the nine strains cultivated in different states of India were grown and crossed in diallel mating design excluding reciprocals. The nine parents along with their 36F₁s and 36F₂s were grown during 2003-2004 and 2004-2005 in a randomized block design with three replications at the Agricultural Research Farm of Narain P.G. College (affiliated to Dr. BR Ambedkar University, Agra), Shikohabad (U.P.). The parents and F₁s were sown in single row and F₂s in three rows each of 4m length with 45 cm spacing between rows and 10-15 cm between plants. A fertilizers dose of 40 N : 20P : 20 K kg/ha was applied and normal cultural practices were followed for raising a good crop. Ten healthy vigorous plants in the parents and F₁s and 20 plants in F₂ populations were selected randomly for recording observations on 10 characters namely, days to first flower (mean in days on plot basis), plant height (cm), length of main raceme (cm), number of primary branches, number of secondary branches, number of siliquae on main raceme, siliqua length (cm), 1000-seed weight (g), seed yield/plant (g) and oil content/plant (%). The mean values of each

observation were used to determine genetic components of variation as per Hayman, (1954).

The estimates of components of genetic variances ($\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, $\hat{F}$ and E) alongwith their standard errors and its different proportions for F_1 s and F_2 s are presented in Table 1. The estimated values of the components of variation due to additive effect of gene ($\hat{D}$) were highly significant for most of the characters in both F_1 and F_2 generations except for primary and secondary branches and seed yield per plant in F_1 generation. The magnitudes of $\hat{D}$ estimates in both the analysis were almost similar except for plant height. The estimates of dominance components, $\hat{H}_1$ and $\hat{H}_2$ were highly significant for most of the characters in F_1 and F_2 analysis. The relative magnitude of these components was higher for all the traits in the F_2 s when compared with the F_1 s except for the number of primary branches. The results are in agreement with the reports of Labana *et al.* (1984). It showed that both additive and non-additive gene action were important for the traits under study. The role of both additive and non-additive gene action to seed yield, its component characters and oil content in Indian mustard was also reported by Yadav *et al.* [1981] and Trivedi and Mukherjee [1986]. Components $\hat{H}_1$ and $\hat{H}_2$ were found higher than $\hat{D}$ for most of the traits which confirmed predominance of non-additive genetic variance. The observed positive values of $\hat{H}_1$ and $\hat{H}_2$ for all the traits of interest, indicated that there were unequal frequencies of alleles, i.e. $u \neq v$, at all the loci, where u is proportion of positive genes in the parents and v is proportion of negative genes in the parents.

Further proof for the unequal distribution of alleles over loci was obtained by the ratio of $\hat{H}_2/4\hat{H}_1$, which is the estimate of uv . In the present study, the uv estimates were in the range of 0.17 to 0.23, which is less than its maximum value of 0.250 (Table 1). The maximum value of 0.250 arises, when $u = v = 0.5$ i.e., the increaser (positive) and decreaser (negative) alleles at all these loci are in equal proportion in the parents. But, the low estimates of uv indicated that the positive and negative alleles at loci exhibiting dominance were not in equal proportions in the parents of interest. However, these estimates did not permit a determination as to which type of allele occurred more frequently. The proportion of positive and negative alleles ($\hat{H}_2/4\hat{H}_1$) were unequal. The positive F values showed that parents studied had more dominant alleles than recessive ones for these characters. Indeed, the proportion of dominant to recessive genes

$$(KD/KR) \text{ i.e. } \frac{(\hat{4DH}_1)^{0.5} + F}{(\hat{4DH}_1)^{0.5} - F}$$

confirmed the above mentioned fact. The ratios were more than one for most of the characters except plant height where ratios were less than one in both the generations. Hence, it can be said that the nine parents used for study, carried more dominance than recessive genes and it was in conformity with the findings of Yadav *et al.* [1981].

The estimate of $\hat{h}^2$ were positive and significant for most of the characters in F_1 analysis except days to flower. In F_2 analysis, siliquae on main raceme, test weight, seed yield per plant and oil content per plant were the traits which recorded positive significant estimates of $\hat{h}^2$. This indicated that the direction of dominance for there characters was positive and dominance effect expressed as the algebraic sum over all loci in heterozygous phases in all the crosses. The estimates of degree of dominance, as revealed by the ration of ($\hat{H}_1/\hat{D}$) 0.5 were higher than unity for all the characters except days to first flower in F_1 s suggested that analyzed characters were under the influence of over dominance while days to first flower indicated partial dominance. The magnitude of the estimates of degree of dominance for most of the characters increased in the F_2 s as compared with the F_1 s except for number of primary branches, indicated an increase in the dominance effects and decrease in the additive effects in the selfed generation.

The ratio of $\hat{h}^2/\hat{H}_2$ denotes an approximate number genes or group of genes controlling the characters, exhibiting dominance were analyzed. The estimates ranged from 0.01 to 3.70 and therefore, indicated that at least 1 to 4 genes or groups of genes showing dominance were present for all the traits in F_1 s except for days to flower and secondary branches. But in F_2 , the estimates were less than one for all the characters, which is most likely an under estimation. This may be attributed to unequal effects of dominant genes in intensity and dependent on their direction as well as cancellation effects. Yadav *et al.* [1981], Trivedi and Mukherjee [1986] and Kant and Gulati [2001] also arrived at the same conclusion. According to Jinks [1954] non random distribution of genes may bring about this discrepancy. The lower values of the estimate would not mean absence of genes exhibiting dominance for the character as this estimate has no connection with Mather's [1949] definition of effective factors.

Table 1. Estimates of genetic components of variation and their proportions in F₁ and F₂ diallel progenies for 10 characters in Indian mustard

Characters	Populations	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{h}^2$	$\hat{F}$	E	$\left(\frac{\hat{H}_1}{\hat{D}}\right)^{\frac{1}{2}}$	$\left(\frac{\hat{H}_2}{4\hat{H}_1}\right)^{\frac{1}{2}}$	$\frac{KD}{KR}$	$\frac{\hat{h}^2}{\hat{H}_2}$
Days to first flower	F ₁	31.79**	29.36**	22.96*	1.08	11.14	0.72	0.96	0.19	1.44	0.05
	SE	±3.47	±7.67	±6.59	±4.41	±8.10	±1.09				
	F ₂	31.77**	123.80	89.65**	1.53	36.85*	0.74	1.97	0.18	1.89	0.02
	SE	±2.88	±25.42	±21.86	±3.66	±13.43	±0.91				
Plant height (cm)	F ₁	180.00**	186.20**	170.80**	494.43**	-130.30*	22.53*	1.01	0.22	0.47	2.85
		±21.62	±47.72	±41.03	±27.48	±50.44	±6.83				
	F ₂	201.20**	401.20**	323.50	52.19	-72.15**	1.46	1.41	0.20	0.76	0.01
		±13.68	±120.84	±103.88	±17.39	±63.86	±4.32				
Main raceme length (cm)	F ₁	83.39**	216.30**	176.80**	575.64**	93.24	00.08	1.61	0.20	2.06	3.24
		±24.97	±55.12	±47.38	±31.74	±58.25	±7.89				
	F ₂	82.25	543.50**	390.40	36.74	172.10	1.22	2.57	0.17	2.35	0.09
		±13.22	±116.73	±100.34	±16.80	±61.68	±4.18				
No. of primary branches	F ₁	0.62	6.66**	6.29**	8.30**	0.06	0.01	3.26	0.23	1.03	1.32
		±0.50	±1.11	±0.95	±0.64	±1.17	±0.15				
	F ₂	0.62*	5.17*	4.75*	0.14	0.87	0.01	2.88	0.22	1.64	0.03
		±0.21	±1.85	±1.59	±0.26	±0.98	±0.06				
No. of secondary branches	F ₁	2.22	14.41**	12.83**	7.96**	-0.07	0.02	2.97	0.22	0.98	0.62
		±1.38	±3.05	±2.62	±1.75	±3.22	±0.43				
	F ₂	2.17**	20.38**	15.79**	0.55	4.09	0.03	3.05	0.19	1.88	0.04
		±0.38	±3.35	±2.88	±0.48	±1.77	±0.02				
No. of siliquae on main raceme	F ₁	14.05*	107.20**	92.76**	347.14**	14.35	0.25	2.76	0.20	1.43	3.70
		±5.18	±11.44	±9.84	±6.59	±12.09	±1.64				
	F ₂	14.07*	233.30**	174.30**	20.63**	24.58	0.24	4.07	0.17	1.52	0.12
		±4.34	±38.30	±32.95	±5.51	±20.26	±1.37				
Siliqua length (cm)	F ₁	0.15**	0.35**	0.30**	0.92**	0.09	0.0007	1.48	0.22	1.52	2.94
		±0.02	±0.04	±0.04	±0.02	±0.05	±0.007				
	F ₂	0.15**	1.51**	1.19**	0.02	0.21	0.0007	3.09	0.19	1.56	0.02
		±0.02	±0.23	±0.20	±0.03	±0.12	±0.008				
Test weight (g)	F ₁	0.32**	0.42**	0.37**	1.22**	0.13*	0.001	1.14	0.21	1.43	3.28
		±0.02	±0.04	±0.04	±0.02	±0.05	±0.007				
	F ₂	0.32**	1.39**	1.17**	0.22**	0.18	0.002	2.07	0.21	1.31	0.19
		±0.02	±0.25	±0.22	±0.03	±0.13	±0.009				
Seed yield/plant (g)	F ₁	1.67	19.19**	16.61**	50.72**	-1.24	0.27	3.38	0.21	0.81	3.05
		±2.08	±4.60	±3.95	±2.65	±4.86	±0.65				
	F ₂	1.91**	24.68	21.05**	10.42**	2.90	0.02	3.58	0.21	1.51	0.47
		±0.37	±3.34	±2.87	±0.48	±1.76	±0.11				
Oil content (%)	F ₁	3.42**	31.23**	30.45**	65.36**	10.45	0.45	3.02	0.23	1.65	3.45
		±1.36	±5.18	±4.75	±6.75	±7.05	±0.26				
	F ₂	3.15**	45.22**	33.23**	8.24**	16.25	1.01	3.79	0.22	2.12	0.35
		±1.84	±6.22	±2.48	±2.55	±4.15	±0.76				

*, ** significant at 5% and 1% level of probability, respectively.

Our results from diallel experiment demonstrate that seed yield, oil content and major yield components showed the significance of both additive and non-additive type of gene action in different cross combinations for different characters in mustard. Therefore, further improvement in important traits in this crop is not possible by simple pureline selection or modified pedigree methods. Continuous improvement can be obtained through recurrent selection like diallel selective or bi-parental mating.

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SHORT COMMUNICATION

Evaluation of Tomato Genotypes for High Temperature Tolerance**R Borgohain and A Swargiary***Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat-785013, Assam, India*

Twenty tomato genotypes were evaluated for heat tolerance by comparing six heat influenced traits under normal and elevated temperature regime. Stigma exersion, reduction in pollen fertility, increased flower drop, decreased fruit numbers, fruit weight and fruit yield were observed under high temperature in all the genotypes. However, the yield loss due to high temperature was comparatively lesser in genotypes LP-1, CLN2001A, BL1174, CLN2366A and CLN2413R.

Key Words: Tomato, High temperature tolerance, Stigma exersion, Pollen fertility

High temperature is a major production constraint of tomato in tropical and subtropical regions. Temperature regime higher than 32-33°C/20-22°C (day/night) or exposure of tomato plants for a period of four hours at 36-38°C causes blossom drop in most of the cultivars (Hall, 1992). At high temperature the whole plant and the reproductive parts in particular are adversely affected resulting in poor fruit set (Kuo *et al.*, 1979, Peet *et al.*, 1997). Stigma exersion, poor pollen fertility/germination, poor pollen tube growth and carbohydrate stress are some of the manifestations of high temperature reducing fruit set in tomato (Lohar and Peet, 1998; Sato *et al.*, 2004). Therefore, high temperature restricts the cultivation of tomatoes in the tropics and subtropics to the relatively cooler winter season only. To extend tomato cultivation into the off-season in these areas, heat tolerance in tomato varieties is the most important prerequisite.

The present investigation was aimed at evaluation of heat tolerance of 20 tomato genotypes, 17 of which were collected from AVRDC, Taiwan and three were from India. Some of them were advance breeding lines while others were established varieties from different countries (Table 1). To assess the heat tolerance of the genotypes, we compared several traits like stigma exersion (%), pollen fertility (%), flower drop (%), fruit weight (g), number of fruits/plant and fruit yield/plant (g) under favourable temperature and at elevated temperature during 2005-06 at Assam Agricultural University, Jorhat. For evaluation of the genotypes under normal temperature regime, the genotypes were grown under field condition during Nov.-Feb. (average day/night temperature was 26°/18°C). Evaluation under high temperature regime was done in a green house maintained at a temperature of 33±2°C day/24±2°C night during entire reproductive phase. In each

temperature regime, the genotypes were grown in two replications and each of the genotypes were grown in two 5 rows. The data were analyzed as a randomized block design.

A stigma was considered exerted when it was out of the antheridial cone due to heat stress and was recorded on the flowers of first three clusters of 3 selected plants of each genotype and from each replication on the day of anthesis.

Pollen fertility was recorded in two flowers taken from each of the 3 plants from each genotype and replication. One anther from each flower was squashed in a drop of 2% acetocarmine solution on a slide. After placing the cover slips, the slides were allowed to stain for 2 minutes. Five fields were then observed under a compound microscope for each slide and percentage of fertile grains was calculated. Well filled and stained pollen grains were scored as fertile while shrunken, deformed, unstained and partially stained grains were considered sterile. Flower drop was recorded in first three clusters of 3 selected plants of each genotype from each replication.

Analysis of variance revealed significant variation among the 20 cultivars for the six characters. The mean values of the characters under normal and high temperature regime are presented in Table1. Exersion of stigma from the antheridial cone under high temperature hampers the pollination process in tomato. It was observed that under high temperature all the genotypes exhibited stigma exersion which ranged from 4.25-94.42%. LP-1, Saladette, CLN2001A and CLN2413R exhibited relatively low stigma exersion. Similarly, pollen fertility was high under normal temperature but it was adversely affected under high temperature. LP-1, CLN2001A,

Table 1. Mean performance of 20 tomato genotypes under normal (26° C day/18° C night) and high temperature (33° C day/24° C night)

Genotypes	EC No	Origin	Flowers with exerted stigma (%)		Pollen fertility (%)		Flower drop (%)		No. of fruits/plant		Fruit wt (g)		Yield/plant (g)		Yield reduction over normal temperature (%)
			NT	HT	NT	HT	NT	HT	NT	HT	NT	HT	NT	HT	
PI120277	-	Turkey	00.00	40.50	88.26	48.75	5.25	57.32	22.75	11.27	56.34	54.00	1735.33	856.50	50.64
PI205009	-	USA	00.00	66.45	87.00	20.65	2.00	86.50	27.50	10.45	47.22	43.21	1875.50	435.37	76.78
H7996	-	Taiwan	00.00	55.00	90.54	52.33	4.00	58.33	15.25	7.23	75.33	69.75	1026.00	457.50	55.40
H7997	-	-do-	00.00	60.23	87.26	50.60	4.25	52.45	28.00	12.00	62.45	54.78	1321.00	573.45	56.58
BL1174	-	-do-	00.00	37.25	92.35	66.03	3.83	29.50	47.25	35.59	30.25	29.59	1400.33	1095.00	21.80
BL1176	-	-do-	00.00	45.35	83.20	58.00	2.33	65.23	27.79	10.29	55.71	47.84	1200.12	475.50	60.37
CLN2264F	-	-do-	00.00	50.50	89.33	60.00	3.00	66.75	32.12	11.33	35.42	32.85	1081.35	382.45	64.63
CLN2264G	-	-do-	00.00	38.67	93.00	57.67	1.05	55.62	38.20	12.36	62.93	59.00	1826.00	822.50	54.95
CLN2413R	-	-do-	00.00	25.52	89.00	68.75	3.24	49.05	25.36	11.00	39.95	37.50	886.20	570.67	35.60
CLN2366A	-	-do-	00.00	33.25	82.25	50.83	2.75	27.70	26.82	19.00	43.76	42.30	1205.09	880.00	26.97
CLN1621L	-	-do-	00.00	30.00	80.00	53.44	1.23	36.95	24.25	14.25	40.44	38.67	876.33	507.35	42.10
CLN2001A	-	-do-	00.00	21.01	90.75	71.42	3.05	23.77	54.75	45.27	24.22	24.00	1235.45	992.00	19.70
Saurav	-	India	00.00	94.42	86.33	32.87	2.89	77.10	34.18	13.25	68.67	62.09	2210.45	453.52	79.49
Arka Aloak	-	India	00.00	71.75	85.73	20.00	4.75	91.33	29.00	3.56	94.33	86.00	2354.20	150.75	93.59
Saladette	EC501581	Netherlands	00.00	17.00	82.50	68.79	2.00	48.50	20.00	10.00	48.63	45.22	962.50	465.67	51.61
Severnian	EC501579	USSR	00.00	40.75	70.20	36.00	5.45	59.66	22.00	7.50	57.23	50.15	1200.33	375.25	68.73
Walter	EC501584	USA	00.00	55.25	91.00	50.25	2.15	48.33	20.20	9.00	70.75	68.00	1206.67	576.45	52.22
Avalance	EC501583	Netherlands	00.00	57.33	95.00	30.50	2.65	80.00	21.33	3.25	61.00	58.00	1098.18	247.58	77.45
LO6035 (L. Cheesmanii)	EC501584	Taiwan	00.00	67.28	87.75	45.50	3.00	88.69	35.36	5.26	10.25	10.00	800.66	202.25	74.22
LP-1 (L. pimpinellifolium)	-	India	00.00	4.25	95.66	75.23	1.75	10.33	130.45	101.23	7.00	6.85	780.25	661.00	15.28
Mean± S. Em			00.00	45.24± 2.45	87.35± 5.22	50.88± 3.10	3.03± 0.16	55.65± 3.30	34.13± 9.22	17.65± 1.86	49.59± 2.89	45.99± 2.35	1314.09± 40.35	554.04± 24.75	-
C.D (p=0.01)			-	9.34	7.33	5.26	1.12	4.65	4.86	2.85	13.05	3.34	80.12	26.33	-

*NT= Normal Temperature, HT= High Temperature

Saladette, CLN2413R and BL1174 however recorded relatively higher pollen fertility even under high temperature. The highest flower drop under normal temperature was only 5.45% (Severnian) while, under high temperature, flower drop scaled up to 91.33% (Arka Aloak). Genotypes LP-1, CLN 2001A, CLN2366A and BL1174 exhibited comparatively low flower drops even under high temperature. No remarkable change was observed for fruit weight under both the temperature regimes. However, a uniform trend was recorded that invariably in all the genotypes fruit weight was observed to be higher under normal temperature to those harvested from plants raised under high temperature condition. This clearly depicts the adverse effect of high temperature on fruit weight. Similar observation was also reported by Levy *et al.* (1978). Yield under normal temperature ranged from 780.25 g (LP-1) to 2354.20 g (Arka Aloak) while under high temperature, it ranged from 150.75 g (Arka Aloak) to 1095.00 g/plant (BL1174). It was evident that under high temperature conditions fruit set and yield were drastically reduced in several of the cultivars. The per cent reduction in yield under high temperature regime ranged from as high as 93.59% (Arka Aloak) to as low as 15.28% (LP-1). Considering the performance for all the

characters, it appeared that LP-1 had the highest thermo tolerance among the genotypes followed by CLN2001A, BL1174, CLN2366A and CLN2413R as their yield reduction under high temperature was comparatively less, whereas, Arka Aloak was the most heat sensitive cultivar among the test entries.

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SHORT COMMUNICATION

Diversity in Custard Apple Germplasm Collections from Maharashtra, India**N Dikshit, SG Bharad¹ and MP Badge**

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Twenty one accessions of custard apple germplasm were collected during an exploration programme from six districts of Maharashtra. The physico-chemical characterization of the fruits revealed variation in average fruit weight (90.8-375 g), total soluble sugar (19-26 %), number of seeds per fruit (21.2-73), weight of pulp per fruit (44.4-188 g) and fruit/pulp ratio (37-54.2). Pockets of custard apple areas and physico-chemical traits are discussed in the paper.

Key Words: Custard apple, Maharashtra, Exploration

Custard apple (*Annona squamosa* L.) belongs to the family *Annonaceae* and is commonly known as *Sitaphal* in India. The centre of origin of custard apple is tropical America from where it has spread to different parts of the world (Rathore, 1990). In India, custard apple is grown in an area of 53,000 ha (Shanmughavelu, 1987) in Andhra Pradesh, Tamil Nadu, Maharashtra, Orissa and other states. Andhra Pradesh tops in area and production in the country. In Maharashtra, it is grown in an area of 3,896 ha with the production of 20,047 tonnes (Anon., 1996) and the predominant regions are Marathwada, western Maharashtra and Vidarbha. Custard apple trees are usually propagated by grafting a selected scion variety on to a rootstock and planted mostly in rainy season. In forest, it grows naturally through seeds. The species thrives well under dry conditions in marginal soil, wastelands and can tolerate light to gravelly soils. The fruit is mostly used as a dessert for its delicious taste and nutritive values. The pulp is creamy, custard like, granular with a good blend of sweetness and acidity. The pleasant flavour and mild aroma of the fruit have a universal liking. It is an excellent source of carbohydrates (23.5 %), protein (1.6 %), minerals (0.9 %), and vitamin C (37mg/100gm) (Gopalan, *et al*, 1987). The unripe fruits, seed, leaf and root are used to destroy insect and lice. The oven dried kernels of seeds are found to contain 30% of oil.

Five districts of Vidarbha and one district of Marathwada region of Maharashtra were explored for collection of custard apple germplasm during October 2003. The districts included Akola, Buldana, Amravati, Yavatmal, Washim (Vidarbha) and Nanded (Marathawada). The region is located between 19° 50.850' - 21° 06.808' latitude and 76° 42.785' - 78° 08.105' longitude. The topography of the area is mostly plain with some sporadic hillocks and undulating type areas. The

soil characteristic varies from loam, sandy loam to silt with various colours from black, medium black, yellow and red. The cropping pattern of the region is cotton based and major crops are sorghum, pigeon pea, pearl millet, niger, soybean, minor millets and sugar cane during *kharif* season and wheat, chick pea, safflower, linseed during *rabi*. The major horticultural crops of the area include orange, sapota, papaya, banana, custard apple, citrus, guava and pomegranate. Recently the progressive farmers are planting elite types of custard apple in large areas including deforested and barren land to boost the economic conditions. The local custard apple varieties are facing a danger and may be wiped out in long run. Thus it is essential to collect and conserve the local types prevalent in the region for their effective utilization in crop improvement programmes.

During the exploration, six districts of Maharashtra covering Amravati, Buldana, Yavatmal, Nanded, Akola and Washim were surveyed for collecting maximum diversity of the crop. The fruit samples were collected from the orchards, forests and gardens after making an assessment of the fruit and important traits like growth habit and fruit bearing pattern of the morphotypes. The plants were labeled for future scion wood collection. Data were recorded on 21 accessions of custard apple. Ten fruits were collected from each accession in which observations on fruit and seed characteristics were recorded. Laboratory estimates were made on analysis of fruit weight, fruit length, fruit width, fruit girth, number of seeds per fruit, weight of seeds per fruit, weight of 100 seeds, weight of rind per fruit, weight of pulp/fruit, fruit pulp ratio and total soluble sugar A.O.A.C.(1965). The physico-chemical characteristics and IC number information is presented in Table 1.

Table 1. Physico-chemical characterization of custard apple germplasm from Maharashtra

S.No.	IC No.	Dist.	FR_WT	FR_LT	FR_BT	FR_GR	SED_FR	FR_SED_WT	SED_WT	RD_WT	PL_WT	FR_PL_RT	TSS
1	IC415724	Bul	246.2	8.26	7.46	25.3	48.3	18.62	38.55	94.9	103	41.83	24
2	IC415725	Bul	270.81	7.72	8.52	27.2	35.75	13.72	38.35	118.24	138.84	51.26	24.2
3	IC415726	Bul	150.69	6.12	6.1	21	62.7	12.23	34.03	60.16	78.3	51.96	23
4	IC415727	Bul	211.32	7.06	7.92	24.14	53	18.04	39.69	108.36	81.92	38.76	25
5	IC415728	Bul	189.61	7.16	7.16	23.8	52	16.7	32.11	67.33	70.28	37.06	21.3
6	IC415729	Bul	151.06	6.2	8.4	22.9	21.2	8.36	39.43	74.67	68.03	45.03	26
7	IC415730	Bul	229.76	6.27	6.22	25.8	52	20.54	39.5	74.76	103	44.82	21
8	IC415731	Bul	375	8.85	8.25	29	33	18.32	55.51	187.35	165.33	44.08	23.1
9	IC415732	Bul	346.6	8.8	8.5	27.7	56	30.9	37.32	137.7	188	54.24	24
10	IC415733	Akl	156	7	7	22	63.2	21.1	33.8	58.9	76	48.71	25
11	IC415734	Akl	230	8.1	7.1	23	45.12	17.5	38.78	112.5	101	43.91	24
12	IC415736	Amt	131.2	5.5	6.5	20	44	11.3	25.68	65.3	54.6	41.61	19
13	IC415740	Amt	154.26	6.24	6.4	22.5	73	22.2	30.4	64.33	68	44.08	22
14	IC415743	Amt	204	6.9	7.8	24	33	18.2	54.55	80.79	99.9	48.97	24
15	IC415744	Amt	123.38	5.4	6.2	20	54	16.04	31.85	50.51	56.23	45.57	21
16	IC415745	Amt	134	5.3	6.3	20.5	53.66	12.33	22.97	51.43	70.24	52.41	21
17	IC415747	Amt	90.82	6	6.3	18.3	22	11.25	51.13	30.68	48.89	53.83	24
18	IC415752	Yal	193.26	7.6	7	22.5	36	19.4	53.88	76.75	93.11	48.17	22.5
19	IC415753	Nad	138.7	5	4.5	17	23	10.5	45.62	69.2	59	42.53	22.5
20	IC415754	Nad	142.28	6.1	6.4	22.6	57	16.3	28.59	54.66	71.82	50.3	22
21	IC415760	Yal	90.98	5.1	6	19	26	12.55	48.26	34	44.43	48.83	20
Range			90.8-375	5-8.8	4.5-8.5	17-29	21.2-73	8.3-30.9	22.9-55.5	30.6-187.3	44.4-188	37-54.2	19.026.0
+Mean SE			+188.5 16.4	6.6+0.2	6.9+0.2	22.70.6	44.9+3.2	16.4+1.1	30+2	79.6+8	87.6+8.1	46.5+1	22.7+0.3
CV %			39.9	17.7	14.7	13.7	33.0	30.8	24.1	46.0	42.4	10.4	7.9

FR_WT - Average fruit weight (g), FR_LT - Fruit length (cm), FR_BT - Fruit breadth (cm), FR_GR - Fruit girth (cm), SED_FR - No. of seeds/fruit, FR_SED_WT - Weight of seeds/fruit (g), SED_WT - 100 seed wt. (g), RD_WT - Rind weight (g), PL_WT - Pulp weight (g), FR_PL_RT - Fruit pulp ratio, TSS - ° B Bul - Buldana, Akl - Akola, Amt - Amravati, Yal - Yavatmal, Nad - Nanded

The predominant custard apple growing areas like Wadgaon, Aasegaon, Bhairam, Chandur, Shirasgaon, Chikhaldara and Wara areas of Amravati; Varud and Digras areas of Yavatmal; Manora area of Washim; Dongaon and Janephal areas of Buldana; Patur and Chani areas of Akola and Mahur area of Nanded district of Maharashtra were surveyed. In the Wadgaon forest areas of Paratwada, one accession having different plant type locally called as *Nar* was collected. The leaves are dark green in colour, small in size and fruits were green even after maturity.

The spectrum of variability was assessed by considering the parameters like range of variation, mean, standard error and coefficient of variation in eleven economic traits. Moderate to high variability was observed among all the traits. High coefficient of variation was observed in weight of rind (46.0%) followed by weight of pulp (42.4%) and average weight of fruit (39.9%). Considering the desirable traits, the highest fruit weight (375.0 g) was observed in IC415731, fruit length (8.85 cm) in IC415731, girth of fruit (29.0 cm) in IC415731, weight of pulp (188.0 g) in IC415732, fruit pulp ratio (54.24) in IC415732 and TSS ° B (26.0) in IC415729.

The results when compared with the entire collections, it was observed that the IC415724, IC415725, IC415731 and IC415732 were found to be superior over

the other collections. The accession-wise details are IC415731 for fruit weight (375.0 g), fruit girth (29.0 cm), pulp weight (165.33 g), average fruit pulp ratio (44.08) and TSS ° B (23.1); IC415732 for fruit weight (346.6g), fruit length (8.8 cm), weight of pulp (188.0 g), fruit pulp ratio (54.24) and TSS ° B (24.0); IC415725 for fruit weight (270.81g), pulp weight (138.84g), fruit pulp ratio (51.26) and TSS ° B (24.2) and IC415724 fruit weight (246.2 g), pulp weight (103.0 g), fruit pulp ratio (41.83) and TSS ° B (24.0). It can be inferred that significant variability exists among the local types for various physico-chemical traits and these accessions have been identified as promising for future crop improvement programmes.

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