CHAPTER V

DISCUSSION

The demand for rice is increasing every day with the rise in population. It is therefore, imperative to have continuous and concerted efforts to increase rice production to keep pace with the demand. Among the several approaches, improvement of varieties through development of inherent high yielding potential, resistance to major biotic and abiotic stresses and ability of adaptation to various rice growing environment is of paramount importance. Local land races are naturally adapted to utilize the natural resource-base better than the introduced modern cultivars (Bhattacharya and Ghosh 2004). Moreover, the land races have broad genetic base which provide them wider adaptability and protection from various stresses. According to Chauhan et al., (1991) the traditional varieties present a rich source of gene pool despite of their low yield ability, because they posses high degree of drought tolerance and adaptability to the rain fed upland ecosystems. Selection of biologically superior and physiologically efficient indigenous cultivars with high grain yield potential is thus essentially required.

The success of any plant breeding programme aimed at the evolution of high yielding, better quality and disease resistant varieties depends upon the selection of suitable genotypes to be utilized in breeding programme. The development of superior rice population is mainly depends on the intelligent use of available genetic variability of that particular population. Grain yield is a complex character, which depends on its main components viz; number of panicles per plant, panicle length, number of grains
per panicle, 1000 grains weight etc. In both favourable and unfavourable environments, grain yield is the primary trait targeted for improvement of rice productivity from its present level. These grain yield components are further dependent for their expression on several morphological and developmental traits, which are interrelated with each other. Hence, the parents selected for the breeding programmes aimed at increased seed yield should possess wide range of genetic variation for the above mentioned morphological and developmental characters. Besides, it could be of interest to know the magnitude of variation due to heritable component, which in turn would be a guide for selection for the improvement of a population. In crop improvement programme, genetic variability for agronomic traits as well as quality traits in almost all the crops is important, since this component is transmitted to the next generation (Singh et al., 1996i).

The knowledge of nature and extent of genetic variation and diversity available in the germplasm or breeding material helps the breeder for planning sound breeding programmes. Hence, the present investigation was undertaken to evaluate 68 rice cultivars of different agro ecosystems. Results of the present investigation are discussed in the light of available literature and explanation wherever possible is provided for the trends revealed by these observations under following heads.

5.1 Comparative study of the morpho-physiological diversity and extent of genetic variability of important yield and yield attributing characters

5.2. Range of expression of variation and extent of variability of nutritional aspects.

5.3. Comparative study of morpho-physiological and genetic variability of some additional traits related to yield and abiotic stresses.
5.4. Comparative study of the seasonal groups for genetic parameters

5.5. Screening for drought and pre-harvest sprouting tolerance.

5.6. Character association studies of important yield and yield attributes.

5.7. Genetic diversity analysis and identification of promising lines

5.8. Reason of popularity of some indigenous rice cultivars.

5.1 Comparative study of the morpho-physiological diversity and extent of genetic variability for important yield and yield attributing characters of different rice cultivars:

One of the main objectives of any breeding programme is to produce high yielding and better quality lines for release as cultivar to farmers. The prerequisite to achieve this goal is the presence of sufficient amount of variability, on the basis of which desired lines are to be selected for further manipulation. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Genetic variability may itself be due to additive and non-additive gene action. It is obvious that if the genetic variance observed is due to non additive gene action, it will not be heritable and thus selection may not be effective even though the estimated variability may be high. Hence it is essential to partition the observed variability into its heritable and non heritable components by appropriate genetic analysis. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. The present study was conducted to evaluate the performance of
some indigenous cultivars in order to assess the presence of variability for desired traits.

5.1.1 Height:

Plant height is an important trait contributing yield. Prasad et al., 2001 also reported that plant height has significant correlation with grain yield. The trait varied significantly among the studied entries which is in agreement with the results of Mohammad et al., (2002). The range of this trait in present investigation was from 78.8 cm to 217.8 cm which is close to the findings of Rajesh et al., 2010 (98 cm. to 195cm.) and Chakraborty and Chakraborty, 2010 (100 cm to 175 cm.). The maximum height was shown by a bao seasonal cultivar Dalbao whereas lowest value for this trait among indigenous cultivars was shown by Kolajoha. Most of the indigenous cultivars were tall (which is also a characteristic of traditional varieties), whereas the experimented high yielding check varieties were of semi-dwarf in nature. Bao seasonal cultivars showed more plant height than sali and ahu seasonal cultivars. It is noteworthy that these cultivars have the ability to elongate with the rise of water. This peculiarity of these cultivars might be used in rice breeding programmes for flood prone areas. Since the end of 1950s, high-yielding rice varieties of reduced plant height have been released in almost all rice-growing countries (Ming, 1987). Some indigenous cultivars of present study such as Kolajoha, Rongabora etc. can compete with high yielding varieties regarding this trait showing almost similar results with check varieties.

Plant height in rice is generally considered to be controlled by both qualitative and quantitative genes (Huang et al., 1996). Ashrafuzzaman et al., (2009) also
considered that plant height is mostly governed by genetic makeup of the cultivar, but the environmental factors also influence it. The phenotypic variance for this character was higher than corresponding genotypic variance. The phenotypic coefficient of variation (PCV) was also higher than genotypic coefficient of variation (GCV). It is interesting to note that the differences between GCV and PCV values were minimum implying least influence of environment. Similar result was also found by Okelola et al., (2007) and Prajapati et al., (2011) for this trait. The character showed high phenotypic and genotypic coefficient of variation, high heritability, high genetic advance and high genetic advance as percentage of mean. This indicates that this character is governed by additive genes and phenotypic selection is adequate to bring about desirable improvement of this character. Pal and Sabesan, (2010); Lal and Chauhan, (2011) and Prajapati et al., (2011), also found high GCV and PCV, high heritability and high genetic advance as percentage of mean. These results were also in agreement with the observations of Ahmadikhah (2010). On the other hand Okelola et al., (2007), Ahmed et al., (2010i) and Ullah et al., (2011), reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean for this trait and Chakraborty and Chakraborty, (2010) revealed moderate GCV and PCV, high heritability and moderate genetic advance as percentage of mean for this trait.

5.1.2. Tillers per plant:

Rice tillering is a major determinant for panicle production (Miller et al., 1991; Smith and Dilday, 2003) and as a result, it affects total yield (Gallagher & Biscoe, 1978). The genotypes, which produced higher number of effective tillers per plant showed higher grain yield in rice (Kusutani et al., 2000; Dutta et al., 2002). A wide
range (7.6 to 29.6) of morphological variability was found for tillers per plant. These findings are in conformity with the results of Rajesh et al., 2010 (ranging from 7 to 25 tillers per plant) and Adeyemi et al., 2011 (ranging from 3 to 23 tillers per plant). Analysis of variance showed significant variation among the studied cultivars which is in conformity with the results of Jamal et al., (2009). The highest number tiller per plant among indigenous cultivars was shown by cultivar Kokuwabao which is comparable with check varieties. The indigenous cultivars have low tillering ability as compared to high yielding varieties but they produce heavy panicles and well filled grains. Although most of the cultivars showed moderate tillering ability, some cultivars viz. Amanabao, Kokuwabao and Panikokuwa showed high tillering indicating their importance in rice improvement programmes. It is interesting to note that almost all bao seasonal cultivars had high tillering ability. This variation may be due to the ability of producing nodal tillers by bao seasonal cultivars as flood subside.

The character tillers per plant showed high GCV-PCV, high heritability and high genetic advance as percentage of mean indicating the effect of additive gene on this trait. Thus, this trait may be used directly as selection index in plant improvement programmes. The PCV was higher than corresponding GCV in this trait also. This implies that this trait was also under the influence of environment. Sinha, et al., (2004) and Padmaja et al., (2008) also found similar results. Singh et al., (2010i) found moderate coefficients of variation for this trait. Anbanandan et al., (2009) and Prajapati et al., (2011), reported high heritability and high genetic advance as percentage of mean for this trait. Ahmad et al., (2010i) reported moderate GCV-PCV, high heritability and high genetic advance and Bisne et al., (2009) reported moderate
heritability for this trait. High genetic advance for tillers per plant was also recorded by Kuldeep et al., (2004) and Karthikeyan et al., (2010).

5.1.3. Days to 50% flowering:

Significant variation was observed among the genotypes for days to 50% flowering with a wide range (65.60 days to 226.20 days). Findings of present study were supported by the findings of Rangel et al., 1991 (76.00 days to 229.00 days) for days to 50% flowering. Bao seasonal cultivars took maximum days for flowering, whereas ahu seasonal cultivars took minimum days exhibiting early flowering. Breeding efforts are underway to develop short lived varieties with high yield potential (Ashrafuzzaman et al., 2009). The wide range (65.6 days to 226.2 days) of the trait indicates ample variability among cultivars and a better scope for improvement in terms of this character.

High phenotypic and genotypic variances were exhibited by days to 50% flowering and these results were in agreement with the observations of Sawant et al. (1994); Padmaja et al., (2008) and Prajapati et al., (2011). Genotypic and phenotypic coefficients of variation were high and PCV was higher than corresponding GCV for this trait but is noteworthy that the differences between GCV and PCV values were minimum implying least influence of environment. This result is in accordance with the finding of Shahidullah et al., (2009a). The broad sense heritability, genetic advance and genetic advance as percentage of mean were also high indicating the governance of additive genes for this character. This implies that phenotypic selection on the basis of this character will be adequate to bring about desirable improvement. Moderate GCV-PCV, high heritability and moderate genetic advance for days to 50%
flowering were found by Ahmed et al., (2010i) and Prajapati et al., (2011) and moderate GCV-PCV, high heritability and high genetic advance were reported by Vange, (2009). Bisne et al., (2009) also reported moderate genetic advance for this trait.

5.1.4. Leaf area:

Leaf area is indirectly related but an important trait attributing yield. Analysis of variation showed significant variation among the cultivars for this trait. A wide range (36.89 cm$^2$ to 146.5 cm$^2$) was exhibited by the cultivars for this trait in present study. Adeyemi et al., (2011) also observed wide range (2.86 cm$^2$ to 106 cm$^2$) for this trait when studying 25 upland cultivars. It was observed that all the ahu cultivars had comparatively lower leaf-area than sali and bao cultivars. This might be due to lack of optimum available water which favours the plant growth. The check varieties had not showed any significant differences than indigenous cultivars for this trait. The wide range indicates sufficient variability and scope for improvement for this character.

High phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic advance as percentage of mean were exhibited by leaf area and these results were in agreement with the observations of Ahmed et al., (2010i). Hence substantial improvement of this trait could be achieved through selection. The PCV was quite high than GCV indicating the influence of environment on the trait.
5.1.5. Flag leaf length:

Flag leaf characters differ from cultivars to cultivars and is affected by the temperature, photoperiod and other traits like; plant height and plant population density (Jamal et al. 2009). Bharali et al. (1994) reported higher direct effect of flag leaf area on grain yield. Flag leaf length varied significantly among the studied entries from 27.04 cm to 54.28 cm which is close to the findings of Chakraborty and Chakraborty, 2010 (16 cm. to 45 cm.). Highest flag leaf length was shown by an indigenous cultivar Konjoha. No remarkable differences were observed in the check varieties for this character. Cultivars with high values for flag-leaf length might be considered for further improvement.

In the present study, the phenotypic and genotypic coefficients of variability were moderate for flag leaf length and this is in line with observation of Lal and Chauhan, (2011). This trait showed high heritability and high genetic advance as percentage of mean. Although heritability and genetic advance as percentage of mean were higher for this trait indicating a prominent role of additive genes, moderate genotypic and phenotypic coefficient of variation showed relatively low magnitudinal differences. This indicates that still there is possibility of improvement of cultivars through this character. Chakraborty and Chakraborty, (2010) also reported moderate genotypic and phenotypic coefficients of variation, moderate heritability and moderate genetic advance as percentage of mean for this trait whereas Yadav, et al., (2010ii), observed high GCV-PCV, high heritability and high genetic advance as percentage of mean and Yadav, et al., (2010i) reported moderate GCV PCV, high heritability and high genetic advance as percentage of mean for this trait. According to Muhammad

5.1.6. Flag leaf breadth:

Flag leaf plays an important role in panicle size (Bashar et al., 1990; Rao, 1992) and grain size and weight (Das et al., 1981). Present study had showed significant variation among the cultivars for this trait. The range for flag leaf breadth was 1.12 cm to 2.54 cm and this is close to the results of Chakraborty and Chakraborty, 2010 (0.93 cm to 2.3 cm). Highest flag-leaf breadth was observed in cultivar Titaphuliabora. High yielding varieties showed comparatively higher flag leaf breadth than sali and ahu seasonal cultivars but comparable with bao seasonal cultivars. This variation may be due to genetic makeup of the cultivars.

In the present study the phenotypic and genotypic coefficients of variation were moderate for flag leaf breadth which is in accordance with observation of Chakraborty and Chakraborty (2010); Yadav et al., (2010ii) and Prajapati et al., (2011). On the other hand Yadav et al., (2010i) reported low GCV and PCV for this trait. Differences between PCV and GCV were negligible indicating least influence of environment on the trait and can be considered stable.

Flag leaf breadth showed high heritability and high genetic advance as percentage of mean indicating the major role of additive component of genetic variance. Similar results were also made by Yadav et al., (2010ii) and Prajapati et al., (2011). On the other hand Muhammad Shahid et al., (2002) revealed low genotypic and phenotypic coefficient of variation along with high heritability and Yadav et al.,
(2010i) reported low GCV and PCV, low heritability and low genetic advance as percentage of mean for this trait. Due to high heritability supported with moderately high coefficient of variation and difference between GCV and PCV, flag leaf breadth exhibited the high genetic advance as percentage of mean. Hence substantial improvement of this trait could be achieved through selection. From the present study it appears that effective selection for the character was possible only by progeny testing after phenotypic selection in order to identify the desirable segregants.

5.1.7. Total chlorophyll content:

Leaf chlorophyll content is the best indicator of photosynthetic activity in rice (Ramesh et al., 2002). The correlation between leaf area and yield suggested that chlorophyll and leaf area are important in determining the yield (Raj and Tripathi, 2000). Chlorophyll a and b play vital role in grain filling and are most important elements of photosynthesis (Ashrafuzzaman et al., 2009). A significant difference among the cultivars ranging from 1.51 mg/g to 5.23 mg/g was observed for total chlorophyll content. Similar results were also observed by Ashrafuzzaman et al., (2009). There was no different distinct pattern regarding chlorophyll content among different seasonal cultivars and check varieties.

The variation in chlorophyll a content among the studied cultivars was significant with a range of 0.74 mg/g to 3.19 mg/g. Ashrafuzzaman et al., 2009 reported a range of 2.81 mg/g to 2.85 mg/g for chlorophyll a content. Highest chlorophyll a content was exhibited by cultivar Titaphuliabora. Ahu cultivars showed comparatively low chlorophyll content than sali and bao cultivars. This might be due
to environmental variations. No remarkable differences were observed between check varieties and indigenous cultivars regarding this trait.

Significant variation was also found among the cultivars for the trait chlorophyll b content. The range for this trait was 0.08mg/g to 2.56mg/g for experimented entries whereas Ashrafuzzaman et al., 2009 observed a range of 1.13 mg/g to 1.83 mg/g of chlorophyll b content studying six aromatic rice varieties. There was no predictable variation for this trait between check varieties and indigenous cultivars.

Coefficients of variability observed at phenotypic and genotypic level were high for total chlorophyll content in present study. PCV was slightly higher than GCV indicating little influence of environment on the expression of the trait. As genetic variability remains unaffected by environmental conditions, this type of variability is more useful for genetic improvement through selection or hybridization. The trait showed very high heritability estimates and high genetic advance as percentage of mean. This indicates that phenotypic selection on the basis of this physiological trait along with other yield attributing characters may be rewarding. Ubarhande et al., (2009) also found very high heritability for total chlorophyll content in rice. Wani et al., (2011) observed moderate GCV PCV, high heritability, low genetic advance and moderate genetic advance as percentage of mean for 50 elite wheat genotypes for this trait. On the other hand Ullah et al., (2011) recorded low GCV and PCV, high heritability and low genetic advance as percentage of mean for 10 biroin rice. Sedeek et al., (2009) and Laxuman et al., (2010) reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean.
5.1.8. Grain length:

The prime characters among the various grain quality characters in deciding the overall grain quality in rice are grain length, width, shape, and its weight (Gravois and Helms 1996; Tan et al., 1999). The cultivars were significantly different from each other for the trait grain length with a range 5.62 mm to 11.24 mm. Adeyemi et al., 2011, also found similar results for this trait (4.4 mm to 11.4 mm). This wide range might be a considerable aspect in rice grain improvement programmes.

Grain length registered moderate genotypic and phenotypic coefficient of variations, high heritability and moderate genetic advance as percentage of mean. Hence, grain length may be useful as a criterion for selection only if followed by progeny testing. Bisne et al., (2009), also revealed low genotypic and phenotypic coefficients of variation, high heritability and moderate genetic advance as percentage of mean.

5.1.9. Grain breadth:

Rice grain features such as length, width, and shape have a direct effect on the marketability, and therefore also on the commercial success of modern rice cultivars (Redona and Mackill, 1998). Grain breadth showed polygenic inheritance (Govindaraj et al., 2005). According to Yoshida et al., (2002), 4 to 5 genes are effective on grain length and breadth in rice. Experimented cultivars were significantly different from each other with a range from 2.24 mm to 3.88 mm. The wide range may be due to different genetic makeup of the cultivars. Similar results were also found by Rathi et al., 2010 (2 mm to 3.5 mm).
Co-efficient of variability observed at phenotypic and genotypic level were as moderate. Grain breadth exhibited high heritability and high genetic advance as percentage of mean estimates. Hence substantial improvement of this trait could be achieved through selection. Rathi et al., 2010 also reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean for this trait.

5.1.10. Length-breadth ratio of grain:

Grain length breadth ratio determines grain type and the marketing value of a variety. The existence of great diversity in the seed morphology i.e. length, width and thickness indicates the presence of other related agronomic, physiological, cooking, nutritional traits or cultural aspects for their selection and adoption (Siddiqui et al., 2007). Present study showed wide range of grain length breadth ratio with significant variation among the cultivars. The highest grain length breadth ratio was showed by an ahu cultivar Bejilahi (3.88).

The phenotypic and genotypic coefficients of variability for grain length-breadth ratio were found moderate in the present study. The PCV was higher than their corresponding GCV indicating the influence of environment on this trait. High heritability coupled with high genetic advance as percentage of mean were found which indicated role of additive genes. Vanaja and Babu, (2006) and Devi et al., (2012) also reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean for this trait. This indicates that there is possibility of fruitful phenotypic selection for desirable segregants. Munhot et al., (2000) and Lal and Chauhan (2011) reported high genotypic and phenotypic coefficients of variation and high genetic advance for L/B ratio. Sharma and Sharma (2007) reported high
GCV-PCV, high heritability and high genetic advance as percentage of mean for grain length breadth ratio in forty-four extra early and early maturing rice genotypes. Bharadwaj et al., (2007) also reported high heritability coupled with high genetic advance as percentage of mean in two filial generations of three new plant type based crosses for rice in two environments of normal and high dose of nitrogen.

5.1.11. Harvest index:

Harvest index is a vital character having physiological importance. It reflects translocation on alternatively dry matter partitioning of a given genotype to the economic parts. Kusutani et al., (2000) highlighted the contribution of high harvest index to yields. High yield is determined by physiological process leading to a high net accumulation of photosynthates and their partitioning (Miah et al., 1991). A significant difference between cultivars for this trait was observed in present study which is in the line of the results of Singh et al., (2010ii). Findings of the present study affirm the importance of relative partitioning of dry matter towards grain yield accumulation.

This trait showed high GCV and PCV indicating prominent variation among the cultivars for the trait. PCV was higher than their corresponding GCV which implies that the variation is not only due to genotypes but also due to the influence of environment. Estimates of heritability, genetic advance and genetic advance as percentage of mean for the trait were also high. This feature suggested that the environmental influence on the phenotypic expression of this character was not apparent and the phenotypic expression of this trait was true representation of the genetic makeup. Therefore selection based on this character would be effective. These
results coincide with the findings of Karim et al., (2007) and Bisne et al., (2009). Prajapati et al., (2011) also found high GCV and PCV, heritability and genetic advance for the trait harvest index. Whereas Habib et al., (2005) and Ahmed et al., (2010i) reported moderate genotypic and phenotypic coefficients of variation, high heritability and high genetic advance as percentage of mean for this trait.

5.1.12. Length of Panicle:

A significant difference was observed among the cultivars regarding panicle length and is in accordance with the findings of Rangel et al., (1991); Singh et al., (2010ii) and Rajesh et al., (2010). However Shrirame and Muley (2003) observed that panicle length had no significant difference among the genotypes studied. On the other hand Sharma (2002) worked with fine grain rice and reported that there had been significant variation in panicle length. The range of panicle length in present study was 18.62cm to 34.54cm and is supported by the findings of Chakraborty and Chakraborty, (2010) and Rajesh et al., (2010). They observed a range of 18 cm to 30 cm and 24.66 cm to 37.00 cm respectively. It was interesting to note that indigenous cultivar had showed comparatively higher panicle length than check varieties indicating their importance in crop improvement programmes, although check varieties had showed higher number of panicles per plant than indigenous cultivars.

Panicle length showed moderate genotypic and phenotypic coefficients of variation, high heritability, low genetic advance and high genetic advance as percentage of mean which is in accordance with the findings of Vange et al., (2009). This indicates that although the variation is not so apparent still there is an opportunity to improve this trait through selection. The difference between genotypic and
phenotypic coefficients of variation was negligible indicating little influence of environment. Prajapati et al., (2011) also observed moderate GCV and PCV, high heritability and moderate genetic advance as percentage of mean for this trait. Ahmadikhah (2010) also observed high heritability for this trait. On the other hand, Habib et al., (2005) reported low GCV and PCV and high heritability, Bisne et al., (2009) observed high heritability and moderate genetic advance, Shahidullah et al., (2009a) low GCV and PCV, Chakraborty and Chakraborty, (2010) reported low heritability and low genetic advance as percentage of mean and Singh et al., (2011) reported low GCV PCV and low genetic advance as percentage of mean for this trait.

5.1.13. 1000 seeds weight:

Mondal et al. (2005) studied 17 modern cultivars of transplant aman rice and reported that 1000-grain weight differed significantly among the cultivar studied, which supported the results of present experiment. A wide range (10.45 gm to 40.86 gm) was observed for 1000 seeds weight among cultivars. Results of present study regarding this trait are in conformity with the results of Mustafa and Elsheikh (2007). They found minimum and maximum values for this trait as 28.1 gm and 41.9 gm respectively. Okelora et al., (2007) and Adeyemi et al., (2011) also reported similar results. Maximum 1000 seeds weight was observed in an indigenous cultivar Niokadam and minimum value by Konjoha. High yielding varieties showed comparatively low 1000 seeds weight than indigenous cultivars. Some indigenous cultivars such as Konjoha, Kolapakhi, and Amanabao etc can compete check varieties regarding this trait with similar results.
The genotypic and phenotypic coefficients of variation were high for 1000 seeds weight and the difference was very close indicating apparent variation with negligible environmental influence and possibility of yield improvement through selection of this trait. This trait also exhibited high heritability and high genetic advance as percentage of mean. This feature suggested that the character 1000 seeds weight was mainly controlled by additive genes and thus phenotypic selection based on this trait might be rewarding. Akanda et al., (1997), Choudhury and Das (1997), Karim et al., (2007) and Ullah et al., (2011) have also been reported similar results. Habib et al., (2005) reported moderate GCV and PCV, high heritability and high genetic advance as percentage of mean for this trait. Bisne, et al., 2009 reported high genotypic and phenotypic coefficients of variability, Anbanandan et al., (2009) observed high heritability and high genetic advance and Kumar et al., (2009) revealed high heritability for this trait. On the other hand Lal and Chauhan (2011) reported moderate GCV and PCV and high genetic advance as percentage of mean.

5.1.14. Spikelets per panicle:

Spikelets per panicle is an important character contributing to grain yield. According to Kusutani et al., (2000) and Dutta et al., (2002), genotypes which produced higher number of grains per panicle showed higher grain yield in rice. Present study showed wide range with significant variation among the cultivars for this trait. Check varieties showed comparatively lower number of spikelets per panicle but higher number of panicles per plant.

Coefficients of variability observed at both phenotypic and genotypic level were high for the character spikelets per plant indicating apparent variation among the
cultivars for this trait. The phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation. However a close proximities between GCV and PCV, gave evidence that the variability existing in each cultivar was mainly due to their genetic makeup. Estimates of heritability and genetic advance as percentage of mean were also high for this trait. Thus it can be interpreted that this trait was controlled by additive gene action and hence can be improved through simple selection methods. Similar results were also observed by Vange (2009), Prajapati et al., (2011), Ullah et al., (2011) and Singh et al., (2011). Lal and Chauhan (2011) reported high GCV and PCV and high genetic advance and Mustafa and Elsheikh, (2007) observed high genotypic and phenotypic coefficient of variation for the trait spikelets per panicle.

5.1.15. Percentage of viable seeds:

Percentage of viable seeds showed significant differences for cultivars indicating the existence of prominent variability in study materials. The range was 68.32% to 97.36% and is in conformity with the observations of Rangel et al., (1991) (51.70% to 91.00%). It is noteworthy that cultivars Moubara and Niokadam exhibited higher percentage of viable seeds than check varieties. The better performance of the tested cultivars over the check might be due the genotypic novelty and adaptability to the present environment or the over exploitation of the local cultivars.

The trait percentage of viable seeds showed low GCV-PCV, high heritability, moderate genetic advance and moderate genetic advance as percentage of mean in the present study. It revealed that non-additive gene action was involved for expression of this character. The high heritability was exhibited due to the influence of favourable
environment rather than genotype and selection for such trait might not be rewarding. Hence this trait may not be useful as a criterion for selection for increased grain yield. Karim et al., (2007) reported high GCV and PCV, moderate heritability and high genetic advance as percentage of mean for this trait.

5.1.16. Spikelet density:

Spikelet density recorded highly significant positive correlation with grain yield per plant (Gawai et al., 2006). Present study exhibited highly significant variation with a wide range (4.49 to 18.01) for this trait. On the other hand Ali et al., (2000) reported a range of 3.24g/cm to 5.50 g/cm for this trait. No remarkable variation was observed between check varieties and indigenous cultivars.

This trait showed high GCV PCV, high heritability and high genetic advance as percentage of mean indicating the suitability of the trait as selection index in plant improvement programmes. Although phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation implying the influence of environment on the expression of the trait, the difference of GCV and PCV was negligible. It revealed that the genotypic variation contribute maximum to phenotypic variation and the environmental deviation had minor contribution for the trait. Ali et al., (2000) observed Moderate variability, high heritability and high genetic advance as percentage of mean and Ahmed et al., (2010i) reported low GCV and PCV, moderate heritability and low genetic advance as percentage of mean for spikelet density.
5.1.17. Spikelets per plant:

Although Spikelets per plant mainly depend on panicles per plant and tillers per plant, its suitability as selection index in rice breeding programme is mainly depend on the trait percentage of viable seeds. Hence it might not be a important yield attributing trait in some cases. In the present study a wide range with significant variation was observed. Bao cultivars had showed higher numbers of spikelets per plant comparing to others and check varieties. This might be due to the ability of high tillering and production of nodal tillers by these cultivars.

Genotypic and phenotypic coefficients of variations were high indicating pronounced variation for the character. The phenotypic coefficient of variation was higher than genotypic coefficient of variation but the difference was negligible. This feature suggested that the environmental influence was not considerable and the variation of cultivars regarding this trait was mainly due to genetic makeup. The heritability and genetic advance as percentage of mean were also high. This suggested the feasibility of genetic improvement of this trait under low selection pressure. Lal and Chauhan (2011) reported moderate genotypic and phenotypic coefficients of variation for this trait.

5.1.18. Panicles per plant:

Number of panicles per plant is an important trait contributing grain yield in rice as it is positively correlated to total grain yield. Mirza et al., (1992), reported positive correlation among number of panicles per plant and grain yield. Thus cultivars with higher number of panicles are of great importance in crop improvement programmes. Generally high yielding varieties shows higher number of panicles per
plant which was also obvious in present study. This trait showed significant variation and wide range (7.00 to 28.80) confirming its suitability in future breeding programmes. It is noteworthy that bao seasonal cultivars showed comparatively higher number of panicles in each plant than ahu and sali cultivars. This might be due to the ability of production of nodal tillers by these cultivars.

Panicles per plant registered high genotypic and phenotypic coefficients of variability and this result was in agreement with the earlier observations of Karim et al., (2007) and Singh et al., (2011). This indicated the presence of substantial amount of genetic variability for the trait in the study material and there is scope for selection. The PCV was slightly higher than GCV which implies less influence of environment on the trait. As genetic variability remains unaffected by environmental conditions, this type of variability was more useful for genetic improvisation through selection or hybridization. This character also showed high heritability and high genetic advance as percentage of mean, and this is in compliance with the findings of Prajapati et al., (2011). Thus it can be interpreted that the trait panicles per plant might be controlled by additive gene action, which could be improved through simple selection methods. Karim et al., (2007) and Lal and Chauhan (2011) also reported high genetic advance as percentage of mean. On the other hand, Habib et al., (2005) reported moderate GCV and PCV, moderate heritability and moderate genetic advance as percentage of mean and Ullah et al., (2011) observed moderate genotypic and phenotypic coefficients of variation, high heritability and moderate genetic advance as percentage of mean for this trait.
5.1.19. Grain yield:

Grain yield varies from 16.51% to 149.67% and is close to the observations of Jamal et al., (2009). This variation in the grains yield might be due to the environment (Mahapattra, 1993) or the correlation of grain yield per plant with various yield contributing characteristics like; fertility of soil, flag leaf area, grains per panicle and grain weight. Similarly, Mirza et al., (1992), reported positive correlation among number of panicles per plant, panicle length, number of grains per panicle and 1000-grains weight and grain yield per plant. Varietal differences of grain yield were reported by Biswas et al. (1998) also.

Highest phenotypic and genotypic co-efficient of variability was exhibited by grain yield among studied traits indicating prominently high variations of the cultivars. These findings are in accordance with earlier reports of Habib et al., (2005), Anbanandan et al., (2008), Vange (2009) and Ahmadikhah et al., (2010). The PCV was quite higher than corresponding GCV for this trait. Presence of wide gap between PCV and GCV indicated the predominant role of environment in the expression of the trait which is in consonance with the results obtained by earlier workers (Karim et al., 2007; Vange, 2009 and Ahmadikhah et al., 2010).

The estimates of heritability and genetic advance as percentage of means were also high for this trait suggesting preponderance of additive gene action in expression of this character. The presence of additive genetic variance offers immense opportunity for exploitation of heterosis. These results were in accordance with the findings of Das et al., (1992), Kumar et al., (1998), Habib et al., (2005), Anbanandan et al., (2008), Bisne et al., (2009) and Ullah et al., (2011). Vange, 2009 reported high
genotypic and phenotypic coefficients of variation, moderate heritability and high genetic advance as percentage of mean, while Mustafa and Elsheikh, (2007) and Prajapati et al., (2011) observed high GCV and PCV, high heritability and moderate genetic advance.

The order of genetic variability for different yield attributing characters was as follows, grain yield > spikelets per plant > panicles per plant > spikelets per panicle > tillers per plant > harvest index > spikelet density > days to 50% flowering > total chlorophyll content > leaf area > 1000 seeds weight > height > flag leaf breadth > L/B ratio > flag leaf length > length of panicle > grain breadth > grain length > percentage of viable seeds.

Based on the above results, it is suggested that the characters with high genotypic variability viz., grain yield, spikelets per plant, panicles per plant, spikelets per panicle, tillers per plant, harvest index, spikelet density, days to 50% flowering, total chlorophyll content, leaf area index, 1000 seeds weight and height would be responsive to selection in the positive direction. Estimated heritability value alone is less reliable as these values are prone to alter with change in the environment and experimental material (Swarup and Changale, 1962). Hence, the use of heritability values coupled with genetic advance would be more reliable than heritability alone. In the present investigation, along with high genetic variability high heritability coupled with high genetic advance as percent of mean were observed for traits viz. Height, tillers per plant, days to 50% flowering, leaf area, total chlorophyll content, harvest index, 1000 seeds weight, spikelets per panicle, spikelet density, spikelets per plant, panicles per plant and grain yield. Thus these traits are most probably controlled by
additive gene action and hence these traits can be fixed by selection. High heritability with moderate genetic advance was recorded for percentage of viable seeds and grain length. These traits are most likely controlled by both additive and non additive gene actions.

5.2. Range of expression of variation and extent of variability of nutritional aspects:

5.2.1. Total carbohydrate content:

Carbohydrate is the main component of rice grains. Milled rice has been shown to contain about 78% carbohydrate (Devi et al., 2008). Present investigation showed significant variation between experimented cultivars with a wide range (67.39% to 88.46%). This range was in conformity with the results of Devi et al., 1012 (70% to 89.25%) when studying eighteen indigenous cultivars of North-eastern hill regions of India. Devi et al. (2008) reported 73.77% to 85.33% of carbohydrate content studying fifteen indigenous rice cultivars. No remarkable variation was observed between high yielding and indigenous cultivars for this trait. Total carbohydrate content is appreciable in case of all varieties except Bordhan, Gejepsali, Katibora and Khoiron (>70%) and showed nearly same amount with the high yielding varieties. Many reports on variability of carbohydrate content in rice are available. A range of 73-87% (Juliano et al., 1985 and Pedersen and Eggum 1983) in brown rice has been observed. 79% carbohydrate content is recommended by USDA Nutritional database, U.S. More than half of the experimented cultivars showed more than 79% total carbohydrate content. Thus these cultivars might be considered in plant breeding programmes.
Analysis of genetic parameters revealed that the genotypic and phenotypic coefficients of variations and genetic advance as percentage of mean were low and moderate respectively, whereas heritability was high for the trait total carbohydrate content. Thus this trait was mostly governed by non additive gene action. Hence, total carbohydrate content may not be useful as a criterion for direct selection. Although PCV was higher than GCV, a close agreement between GCV and PCV was observed. This indicates that the genetic variability observed among the cultivars for this trait was more or less remains unaffected by environmental conditions. Thongbam et al., (2010) reported low GCV PCV, moderate heritability and low genetic advance while studying 13 indigenous medicinally used cultivars of Manipur while Devi et al., (2012) observed low GCV-PCV, high heritability, moderate genetic advance as percentage of mean studying eighteen indigenous rice cultivars of Tripura.

5.2.2. Total starch content:

The range of starch content in present study was 28.36% to 82.21%. Experimented cultivars had showed significant variation and this was supported by the findings of Devi et al. (2008) and Rathi et al. (2010).

Present study revealed high genotypic and phenotypic coefficients of variability, high heritability and high genetic advance as percentage of mean for the trait total starch content, indicating the governance of additive gene for this trait. Hence selection for this trait in early segregating generations might be successful. High phenotypic variation was composed of high genotypic variation and less environmental variation implying stability of the trait. Chakraborty et al., (2009) and
Chakraborty et al., (2010ii) reported high heritability with low genetic advance for total starch content.

5.2.3. Amylose content:

Amylose content is considered to be the single most important characteristics for predicting rice cooking and processing behaviours (Juliano, 1979a, 1979b; Webb, 1985). It is commonly used as an objective index for cooked rice texture (Webb 1991). Amylose content of milled rice has been found to be correlated positively with hardness values of cooked rice and negatively with stickiness values (Juliano et al., 1965; Perez and Juliano, 1979). Low amylose levels are associated with cohesive, tender, and glossy cooked rice. Conversely, high levels of amylose cause rice to absorb more water and consequently expand more during cooking, and the grains tend to cook dry, fluffy, and separate (Juliano 1971). Varieties with intermediate amylose content are generally most preferred because they look dry and fluffy retaining their soft texture even after cooling (Rathi et al., 2010). Available reports indicate that amylose content in rice varied from 0 to about 37% (Govindaswami 1985; Nakagahara et al, 1986). Present investigation showed that cultivars were significantly different with a wide range (8.28% to 33.86%) of amylose content. However among the evaluated 68 cultivars, 3 cultivars showed very low amylose content (2% to 12%), 14 cultivars showed low amylose content (12.1% to 20%), 15 cultivars showed intermediate amylose content (20% -25%), 33 showed high amylose (25-33%) content and 3 cultivars showed very high amylose (>33%) content. Grains with very low amylose content are indispensible part of assamese culture. It is mainly used to prepare
Pitha (rice cake) of different kinds and also used in preparation of many other delicacies. All the four check varieties showed high amylose content.

Amylose, in combination with the water-insoluble polymer ethyl-cellulose, which is necessary to control the swelling of amylose, has been exploited as a film coating in colonic drug delivery (Sinha et al., 2000). Rice starch is easily available and can be potentially used in pharmaceutical science. In our present study 36 cultivars have shows more than 25% amylose content and can be used as film former in colon specific drug delivery.

Variability estimates for genotypic and phenotypic levels were high for amylose content which is in consonance with Subbaiah et al., (2011). This indicated prominent variations among the cultivars for this trait and could be exploited in crop improvement programmes. Amylose content exhibited high heritability and high genetic advance as percentage of mean. It seems to be controlled by few genes with additive effects and the high extent of phenotypic variation was mostly due to additive gene effects. Thus effectiveness of the selection of this trait would be high. Subbaiah et al., (2011) also reported high heritability and high genetic advance as percentage of mean for 48 hybrids of rice. Devi et al., (2012) also observed high genotypic and phenotypic coefficients of variability, high heritability and high genetic advance as percentage of mean for amylose content. while Vanaja and Babu, (2006) and Thongbam et al., (2010) reported moderate GCV and PCV, high heritability and high genetic advance and Chakraborty et al., (2010ii) reported high heritability with moderate genetic advance for this trait.
5.2.4. Amylopectin content:

Water soluble polysaccharides such as amylopectin are most effective oncotic agents which are used for treatment of intravascular volume deficiency. Thus amylopectin can be used as basic material for plasma volume expander. Plasma volume expander based on starch has lower tendency to remain in any major organ of body in comparison to other plasma volume expander. Amylopectin isolated from Assam bora rice were characterized for use as plasma volume expander by Ahmed and Bhattacharya in 2010. Five cultivars viz. Pakhoribora, Bora, Gumibora, Johabora and Tilbora had showed more than 60% amylopectin content and thus can be potentially used as plasma volume expander.

The study of genetic parameters for amylopectin content revealed high genotypic and phenotypic coefficients of variability, high heritability and high genetic advance as percentage of mean. This suggested high extent of variability among the cultivars for this trait and the existing variability might be due to effect of additive genes. Thus phenotypic selection on the basis of this trait will be fruitful. Chakraborty et al., (2010ii) reported high heritability with low genetic advance and Rathi et al., 2010 reported high heritability with moderate genetic advance for this trait.

5.2.5. Protein content:

The nutritional quality of rice depends on the protein content and quality of protein depends on the composition of amino acids (FAO, 1970). Rice is the poor sources of protein among the cereals, but rice protein is considered as superior and unique because of its composition of essential amino acids (Eggum, 1979). Protein content and other constituents such as amylose, starch, crude fibre, ash and total fat
can be present in different amounts in different rice varieties (Coffman and Juliano 1987; Juliano and Villereal, 1993). Present study showed significant variation among the cultivars for this trait with a wide range of 2.12 % to 13.19 %. Ahmed et al, (1998) reported 9.17 to 11.77% of protein in rice collected from Assam. However Saikia and Bains (1990) and Singh et al. (1998) reported low protein content (around 6-7% in both brown and milled rice of Assam). In another study on protein content of indigenous and exotic varieties, a range of 5.5 to 14% was obtained (Govindaswami and Ghosh 1973). Seventeen (17) cultivars are classified as high protein cultivars of rice, with 10% or more protein content following the classification of Resurrection et al., (1979). Deficiency of protein in the people of rice consuming countries might be improved by these cultivars. Devi et al., (2008) also reported as high as 12.07% protein studying local cultivars from Manipur.

Protein content showed high genotypic and phenotypic coefficients of variability implying greater extent of variation among the cultivars for the trait. This trait also exhibited high heritability and high genetic advance as percentage of mean indicating preponderance of additive genes on the expression of the trait. Chakraborty et al., (2010ii) observed high heritability and moderate genetic advance whereas Samak et al., (2011) reported low genotypic and moderate phenotypic coefficients of variation, moderate heritability and moderate genetic advance as percentage of mean. Thongbam et al., (2010) reported moderate GCV and PCV, moderate heritability and moderate genetic advance as percentage of mean and Devi et al., 2012 reported moderate GCV and PCV, high heritability, moderate genetic advance as percentage of mean for the trait.
The order of genetic variability for different nutritional traits was as follows, amylopectin content > protein content > total starch content > amylose content > total carbohydrate content. Except total carbohydrate content, all other four traits had showed high GCV and PCV, and high heritability with high genetic advance as percentage of mean. Thus these traits can be used as selection indices in rice breeding programmes.

5.3 Comparative study of morpho-physiological and genetic variability of some additional traits related to yield and abiotic stresses.

5.3.1. Additional characters indirectly related to yield:

5.3.1.1. Germination percentage (*in vitro*):

Germination percentage has indirect effect on grain yield by limiting the number of progenies. Differences among cultivars were not significant for this trait. The range of this trait was 61% to 100%. All high yielding varieties had showed 100% germination. Twelve indigenous cultivars also had showed 100% germination indicating maximum viability. They were *Adoliabao, Ahumsali, Bogisali, Bora, Harmoni, Joha, Konjoha, Nekera, Pakhoribora, Solpuna, Sowagmoni* and *Sunmoni*. Remarkable variation was not found between indigenous and high yielding varieties. Germination percentages were found satisfactory almost in all cultivars except *Maiguni, Kokuwabao* and *Gumibora* (less than 75%).

Co-efficient of variability observed at phenotypic level was moderate for germination percentage, where as coefficient of variability noticed at genotypic level was low. The difference between GCV and PCV was not so prominent indicating less influence of environment on the trait. The trait showed high heritability, moderate
genetic advance and moderate genetic advance as percentage of mean. Although heritability measure was high, the variations among the cultivars were not prominent and the value of expected gain was also low. Hence, germination percentage may not be useful as a criterion for selection for increased grain yield. Okelola et al., (2007) also reported high heritability and moderate genetic advance as percentage of mean.

5.3.1.2. Percentage of pollen viability:

Pollen quality is often equated to pollen viability. No significant differences were found for this trait among cultivars in present study. Although the highest value for this trait was shown by a check variety Ronjit, no remarkable differences were observed between check varieties and indigenous cultivars.

Coefficients of variability observed at genotypic and phenotypic level were moderate for percentage of pollen viability which was in consonance with the findings of Tiwari et al., (2011). PCV was higher than corresponding GCV. However a close proximities between GCV and PCV, gave evidence that the variability existing in each cultivar was mainly due to their genetic makeup. Estimates of heritability showed high value whereas genetic advance as percentage of mean showed moderate value. High heritability along with moderate genetic advance indicated the possibilities of improvement of the character through rigorous selection. Tiwari et al., (2011) reported high heritability and high genetic advance as percentage of mean for this trait. On the other hand Manju and Shreelathakumary, (2002) reported high GCV and PCV, high heritability and high genetic advance as percentage of mean for pollen viability percentage in hot chilli.

5.3.1.3. Length of flag-leaf sheath:
The overlapping character of leaf sheath on internodes might be the basis of resistance to lodging in high yielding varieties (Ashrafuzzaman, et al., 2009).

In the present study, the genotypic and phenotypic coefficients of variability were moderate for length of flag leaf sheath which is in the line with observation of Pal and Sabesan, (2010). GCV was slightly higher than corresponding PCV. This closeness of GCV and PCV indicates little influence of environment on expression of the trait.

Flag leaf sheath length showed high heritability, moderate genetic advance, high GA as percentage of mean indicating the major role of additive component of genetic variance. Hence substantial improvement of this trait could be achieved through selection. Nirmalakumari et al, (2010) reported high variability and heritability with high genetic advance as percentage of mean in little millet germplasms for this trait whereas Pal and Sabesan, (2010) reported moderate heritability and moderate genetic advance as percentage of mean in rice for this trait.

5.3.1.4. Grain type:

Grain type is a commercially important character because it is one of the determinants of grain market value. Grain length breadth ratio determines the grain type. Although the preference for rice grain characteristics varies with consumer groups, long and slender grain is generally preferred for indica rice by the majority of consumers in China, USA and most Asian countries (Unnevehr et al., 1992; Juliano and Villareal 1993). Among the 68 cultivars, 15 (13 sali, 1 bao and 1 ahu) were long slender type, 52 were long bold type (36 sali, 9 bao and 7 ahu) and one was medium slender type (sali). The long slender grain type cultivars of present study might be a
good source of GDP (gross domestic products), and hence should given importance. In the present study one cultivar namely Gorundopakhi had showed long empty glumes which might be useful as marker of linkage group IV (Khush and Librojo, 1984).

5.3.2. Additional characters contributing drought resistance:

5.3.2.1. Length of the root:

Length of root contributes indirectly to grain yield because it determines the total water uptake by a plant and in consequence to the total photosynthetic output. It is also related to drought tolerance in rice. In present study length of root varies from 17.74 cm to 33.04 cm. No significant differences were found between high yielding varieties and indigenous cultivars.

Coefficient of variability observed at genotypic and phenotypic level was moderate for this trait. This suggested that the inherent genetic differences among the cultivars were not so prominent. The estimates of heritability and genetic advance as percentage of mean were high implying additive gene effect. This indicates that this trait would respond to selection owing to its genetic variability and transmissibility. Roy et al., (2009) observed moderate GCV, high PCV, moderate heritability and moderate genetic advance and Mohankumar et al., 2011 reported moderate GCV, high PCV, high heritability and moderate genetic advance as percentage of mean for this trait. On the other hand Sumathi et al., 2010 reported low GCV and PCV, high heritability and low genetic advance as percentage of mean while studying 47 pearl millet genotypes.
5.3.2.2. Number of xylem vessels in root:

Number of xylem vessels determines the capacity for water uptake from soil and hence contributing the tolerance of a plant to drought along with grain yield. Sharma and Reddy, (1991) observed positive correlation between root xylem vessel number per plant and grain yield. It ranged from 3.40 to 8.40 in present study with no significant variation. In this study non significant results might be due to the differences in genetic constitution in breeding materials. Allah et al., (2010a) reported a range of 4.00 to 7.10 xylem vessel number studying five rice varieties in drought condition. No significant variation was observed between high yielding varieties and indigenous cultivars.

Coefficient of variability at phenotypic level was high whereas coefficient of variability noticed at genotypic level was moderate for number of xylem vessels in root. Phenotypic coefficient of variation was much higher than genotypic coefficient of variation. This suggested that the extent of environmental influence was high for this trait. Estimates of heritability and genetic advance as percentage of mean were high for this trait. High heritability coupled with high genetic advance as percentage of mean revealed that this trait was controlled by additive gene action which could be improved through simple selection methods.

5.3.2.3. Number of stomata

Number of stomata merits special attention in projects focused on development of drought resistant rice varieties (Muhammad Shahid et al., 2002). Efforts may, therefore, be made to incorporate this character in the upcoming commercial rice
varieties. Present study revealed that the lower surface of leaf showed more variability than upper surface regarding number of stomata.

5.3.2.3.1 Number of stomata on upper surface of leaf:

Number of stomata on upper surface showed significant variation among experimented cultivars with a range of 24.60 to 57.60. Muhammad Shahid et al., (2002) reported 36.57 to 63.70 numbers of stomata studying eight varieties of rice and their five crosses. Highest number of stomata was shown by the cultivar *Moubora*.

Number of stomata on upper surface of leaf showed moderate genotypic and phenotypic coefficients of variation, high heritability and high genetic advance as percentage of mean. This indicated the role of additive gene on the expression of the trait and suggested suitability of the trait as selection indices in plant improvement programmes. Regarding this trait, phenotypic variations were composed of high genotypic variation and less of environmental variation as PCV was negligibly higher than GCV. Thus this trait was more or less stable regardless of environmental change. Muhammad Shahid et al., (2002) reported moderate to high heritability for number of stomata studying five F2 population and their eight parents of rice.

5.3.2.3.2 Number of stomata on lower surface of leaf:

Number of stomata is negatively correlated to drought tolerance. It showed significant variation among the cultivars and varied from 17.60 to 77.80. Highest number of stomata on lower surface was shown by the cultivar *Amanabao*, whereas lowest by an *ahu* cultivar *Betguti*. *Ahu* cultivars showed comparatively lower number of stomata than others. This might be due to the adaptation of these cultivars to water stress condition because of water shortability at the time of their active growth stage.
Cultivars such as *Betguti, Monlohi* etc. with lower number of stomata might be a good source of germplasm in breeding programmes of drought tolerant rice.

The genotypic and phenotypic coefficients of variation were moderate for number of stomata on lower surface of leaf, while high estimates of heritability and genetic advance as percentage of mean were high. High heritability supported with moderate coefficients of variation and high genetic advance supported the suitability of this trait as selection index. Minimum difference of GCV from PCV indicated negligible influence of environment on the expression of this trait.

All the additional traits related to drought tolerance viz. Length of root, number of xylem vessels, number of stomata on both upper and lower surface had showed moderate genotypic and phenotypic coefficients of variations with high heritability and high genetic advance indicating probability of these traits in breeding programmes by selection.

### 5.4. Seasonal variation of genetic parameters:

Different environment and climate show suitability for different rice varieties. The magnitude of genetic parameters for the traits, such as genotypic and phenotypic coefficient of variation, heritability and genetic advance were almost similar for all three seasonal groups except grain yield, tillers per plant, length of root and grain length in present study. High GCV, PCV, heritability and genetic advance were observed for traits viz. total starch content, amylopectin content, protein content, harvest index, spikelets per panicle, spikelet density, spikelets per plant, panicles per plant, number of stomata on upper surface and grain yield in all the three seasonal groups. Along with these traits, *sali* seasonal cultivars showed high GCV, PCV,
heritability and genetic advance for traits viz. amylose content, leaf area index, total chlorophyll content and 1000 seeds weight. Whereas *bao* seasonal cultivars showed high GCV, PCV, heritability and genetic advance for traits viz. Length of flag leaf sheath, tillers per plant and total chlorophyll content and *ahu* seasonal cultivars showed high GCV, PCV, heritability and genetic advance for traits viz. number of xylem vessels, grain length and L/B ratio of grain. From the present study it is obvious that no substantial variations were found for the traits due to seasonal variation.

### 5.5. Screening for drought and pre-harvest sprouting tolerance:

Drought is one of the major abiotic stresses limiting plant production. It adversely affects rice production in the upland areas where rainfall distribution is uncertain. Early drought is the main environmental problem of rice production in Assam during *ahu* season. On average, the estimated yield loss to drought is 144kg/ha. annually in eastern India (Dey and Upadhyaya, 1996). The only way to overcome this problem is the development of new technology and drought resistant varieties which posses certain desirable characteristics such as high root length, more xylem number, less number of stomata etc.

Allah *et al.*, (2010a) reported that the highest xylem vessel number was observed in drought tolerant genotypes. Haque *et al.*, (1989) also reported that xylem vessel number is positively correlated to drought resistance, hence could be directly involved in increasing drought resistance. They also confirmed that xylem vessel number can be used as selection indices in breeding drought resistance in rice. In the present study it was observed that this trait showed high heritability with high genetic
advance indicating additive gene effect. Thus inclusion of this character as selection index in breeding programmes for drought tolerant rice will be rewarding.

Total root length is strongly related to drought tolerance in rice under drought condition (Ingram et al., 1994). According to Allah et al., (2010a) also drought tolerant rice genotypes had fewer numbers of roots, but a higher proportion of the roots were distributed in the lower soil layers below 20 cm. Haque et al., (1989) and Kanbar et al., (2009) also reported that root length correlated positively with drought resistance. According to Kamoshita, (2000) root size, morphology and root depth and length are important in maintaining leaf water potential against evapotranspirational demand under water stress. Loresto et al., (1983) evaluated 27 rice varieties grown in aeroponic culture and found a positive but insignificant correlation between root length and field drought resistance at the vegetative phase. Fukai and Cooper, (1995) and Kondo et al., (2003), also thought that a deeper root system in rice is a promising way of increasing water uptake, and ultimately grain yield under drought stress conditions. In present study this character had showed high heritability with high genetic advance as percentage of mean. Thus this trait might be included in breeding programmes for drought resistance crop production.

According to Kamoshita et al., (2008) and Allah et al., (2010a), low tillering capacity appears to be one desirable characteristic when rice plant has to depend on soil moisture retained in the deep soil layers during drought stress. Flag leaf with short length is also one of the key weapons against drought (Muhammad Shahid et al., 2002). These two traits also showed high heritability with high genetic advance and hence can be included in breeding programmes.
According to Muhammad Shahid et al., (2002) number of stomata merits special attention in projects focused on development of drought resistant rice varieties. Thus effort may therefore, be made to incorporate this character in the upcoming commercial rice varieties. Liu, (1982) also reported that number of stomata have relationship with moisture availability. Number of stomata on both surfaces showed high heritability along with genetic advance. Thus effective selection for this character might be possible.

All six characters showed high heritability along with high genetic advance. Hence effective selection for these characters is possible in appropriate cross combinations and new drought resistance strains possessing these desirable characters may be synthesized.

An ahu cultivar viz. Betguti had showed highest score regarding these six drought resistance contributing characters indicating its adorability in drought conditions. According to Garris et al., (2005) also aus rices are drought tolerant and early maturing. But Yue et al., (2006) concluded that ahu cultivars actually show drought escape by short life cycle. Other screened drought tolerant cultivars were Adoliabao, Monlohi, Laudubi and Nolsitiiki. Thus these selected cultivars might be included in rice breeding programmes for drought tolerance.

Regarding pre-harvest sprouting, it is interesting to note that all the cultivars showing pre-harvest sprouting were ahu cultivars. This indicates that these varieties have no germination inhibition mechanism and texture of seed coat allows absorbing moisture content and enhances seed germination before harvesting. Sali and bao
5.6. Character association studies of important yield and yield attributes.

Grain yield is a complex trait quantitative in nature and an integrated function of a number of component traits (Sharma and Sharma. 2007). Selection of parents based on yield alone often misleading. A successful selection depends on information about the genetic variability and association of agronomic traits with grain yield. Hence knowledge about relationship between yield and its contributing characters is need for an efficient selection strategy. According to Kishor et al., (2008), development of high yielding varieties through breeding requires a thorough knowledge of the association of the yield components. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. While selecting the suitable plant type, correlation studies would provide reliable information in nature, extent and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality characters.

The estimation of genetic variability revealed that, in general, the genotypic and the phenotypic correlation coefficients showed almost similar trend indicated by the same sign in all the character pairs. This revealed identical direction of correlation at both the planes. It would certainly increase the efficiency of phenotypic selection. Most of the genotypic correlation coefficients were of higher or equal in magnitude than the corresponding phenotypic correlation coefficients except panicles per plant...
and spikelets per plant and harvest index and grain yield. This indicates strong inherent association between maximum numbers of pair of characters. Similar results were also observed by Yadav et al., (2010i); Rathi et al., (2010) and Chakraborty et al., (2010ii). Very close values for genotypic and phenotypic correlations were observed between some character combinations, such as grain yield and tillers per plant, grain yield and spikelets per panicle, spikelets per plant and panicles per plant etc., which might be due to reduction in error (environmental) variance to minor proportions as reported by Dewey and Lu, (1959). Thus selection for higher yield on the basis of above character would be fruitful. Similar results were also reported by Rao and Gomathinayagam (1997), Prasad et al., (2001), Surek and Beser (2003) and Yogamenakshi et al. (2004). On the other hand a wide gap between genotypic and phenotypic correlation coefficients for percentage of viable seeds and grain breadth and percentage of viable seeds and length breadth ratio of grain were observed indicating environmental influence. Panicles per plant and spikelets per plant and harvest index and grain yield had showed higher magnitude of phenotypic correlation coefficients than genotypic correlation coefficients. This might be due to masking or modifying effect of environment.

The correlation coefficients showed spikelets per plant serve as most important selection indices (with highest genotypic (0.9***) and phenotypic (0.9***) correlation coefficient values) of grain yield. This was followed by panicles per plant and spikelets per panicle. In the present study grain yield per plant showed significant positive genotypic and phenotypic correlation coefficient with spikelets per plant (0.9 and 0.9 respectively) panicles per plant (0.75 and 0.75 respectively), spikelets per
panicle (0.42 and 0.41 respectively), tillers per plant (0.39 and 0.38 respectively), spikelet density (0.35 and 0.33 respectively), flag leaf breadth (0.35 and 0.32 respectively), days to 50% flowering (0.32 and 0.31 respectively), length of the panicle (0.28 and 0.26 respectively) and height (0.28 and 0.27 respectively). Thus selection for higher yield on the basis of above characters would be reliable. Like the present study, yield per plant was reported to be positively correlated with plant height and panicles/plant by Singh et al. (1979); with panicle length by Sharma and Dwivedi (1980); with grains/panicle and 100 grain weight by Sharma and Sharma (2007). Meenakshi et al. (1999) and Mustafa and Elsheikh (2007), Janardhananam et al. (2001), Rao and Saxena (1999), Ray and Debi (1999)and Pushpa et al. (1999) emphasized the importance of grains per panicle in determining grain yield in rice. Biswas et al. (2000); Singh et al. (2002); Hossain and Haque (2003) and Chakraborty and Chakraborty (2010), reported positive significant association of panicle length with grain yield per plant. But negative genotypic correlation of yield/plant was reported with panicle length by Saini and Gagneja (1975). Insignificant negative correlation of grain yield was observed with flag leaf length (-0.1) and grain breadth (-0.05) in present study. Highest significant negative correlation in both genotypic and phenotypic plane was observed between grain breadth and L/B ratio of grain (-0.72 and -0.74 respectively). The genetic reason for this type of negative association may be linkage or pleiotropy.

According to NeWall and Eberhart (1961) when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety. Hence, under such
situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters.

Harvest index showed significant positive correlation in both genotypic and phenotypic plane with tillers per plant (0.37 and 0.35 respectively), panicles per plant (0.36 and 0.35 respectively) flag leaf breadth (0.35 and 0.32 respectively) and flag leaf length (0.29 and 0.24 respectively). Similar results were reported by Ganesan et al., (1998) and Chakraborty et al., (2010i) for panicles per plant.

5.7. Genetic diversity analysis and identification of promising lines:

Assessment of genetic divergence is important in plant breeding if there is no improvement by selection. For adoption to different ecological areas, the rice cultivars ought to differ for many characteristics. These landraces plays an important role in the local food security (Tang et al., 2002). Thus documentation is important when cultivars show variation for many characters. In any breeding programme, effective identification of superior parental lines for intercrossing is paramount for the construction of base population. Thus quantification of genetic diversity existing within and between groups of germplasm is important and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. Parental selection based on scientific evidence may prevent the possible early failure of a breeding programme. Several methods have been advocated by various workers to estimate the genetic divergence in crop plants (Murthy and Arunachalam, 1966; Bhatt, 1970; Hussain, 1973, Rahaman et al., 1997). Mahalanobis generalized distance estimated by D2 statistic (Rao, 1952) is a unique tool for discriminating populations considering a set of parameters together rather than inferring from indices based upon
morphological similarities, eco-geographical diversity and phylogenetic relationships. Several researchers performed D2 analysis to identify distinct clusters on the basis of different physio-morphological characters in rice (Wu and Hung, 1998; Soni et al., 1999; Chauhan and Singh, 2003). The cultivars belonging to highly diverged clusters should be used in hybridization programme for obtaining wide spectrum of variations in the segregating population. Selection of genotypes is dependent on the objective of breeding programme.

Nineteen yield and yield attributing characters were selected for genetic divergence analysis on the basis of direct effect on yield. It is important to note that all the nineteen selected characters except percentage of viable seeds show moderate to high phenotypic and genotypic coefficient of variation, high heritability and moderate to high genetic advance as percentage of mean. This implies that these characters are under the influence of additive gene. Thus direct selection on the basis of these characters will be rewarding. The analysis of variance for various morpho-agronomic characters revealed that the cultivars differed significantly for all the characters studied indicating the presence of notable genetic variability among them. This implies that there is ample scope for selection of promising lines from the present gene pool for yield and its components. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. Thus it would be judicious to classify the population on the basis of degree of divergence. These findings are in accordance with the findings of Borbora and Hazarika (1998); Chaudhary and Motiramant (2003), Vivek et al. (2005), Singh et al. (2006), Ishwar et al. (2007) and Saravanan and Sabesan (2010) who also observed
significant variability for yield and its components in rice. Similar results were also found by Majumdar et al. (1971); Kotaiah et al., (1986); Rangel et al. (1991). Bharadwaj et al., (2001); Rasheed et al., (2002); Cheema et al., (2004); Thayumanavan et al., (2009); Akter et al., (2009) and Ahmed et al., (2010ii) also reported that the significant differences among the rice genotypes indicated the necessity to group them into clusters to identify the divergent groups. Mehdi and Asghar (1999) also classified the sorghum genotypes in five distinct groups. Many early workers including Pawar et al. (1988), Sharma et al. (1995) and Kamboj et al. (2000) reported high variability for different traits in wheat also.

Via Tocher’s method, 68 rice cultivars were grouped into eleven clusters, based on relative magnitude of $D^2$ values. Five clusters were monogenotypic. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural and human selection for diverse adaptive complexes. Dingkuhn and Asch (1999) also identified several groups of rice cultivars on phenological responses in West Africa. The clustering pattern revealed that the cultivars from different sources were grouped together showing that geographical distributions not necessarily determine genetic divergence. The possible reason for grouping of genotypes of different regions in one cluster could be due to the free exchange of germplasms among the breeders of different regions, or unidirectional selection practiced by breeder in tailoring the promising genotypes for different regions (Verma and Mehta, 1976). Other researchers have also emphasized this (Singh, 1983; Ratho, 1984; De et al., (1988); Sinha et al., (1991); Sarawgi and Srivastava, 1996; Ushakumari and Rangaswamy. 1997; Rathore et al., (2001); Chaturvedi and Maurya, 2005 and Joshi et
Similar results were also observed by Walia and Garg (1996), Dotlacil et al. (2000) and Bergale et al. (2001) and in which they reported non-parallelism between geographic and genetic diversity in case of wheat. This indicated that, in general, selections have been towards the same goal in the different centres of origin of these genotypes and yet, there is sufficient genetic variability that distinctly differentiates them into eleven clusters. Hence, the chosen genotypes used in the present study could be considered as a valid material.

Genetic drift and selection in different environments may cause greater diversity than geographical diversity (Murty and Arunachalam, 1966; Singh et al., 1988). During the past 30 years, the genetic diversity among the improved indica rices has narrowed down due to massive international exchange of germplasm (Khush and Aquino, 1994). The genotypes from the same centre of origin were also distributed in different clusters. This kind of genetic diversity may be due to differential adaptation to varied agro-ecosystems (Senapati and Sarkar, 2005).

The relative divergence of each cluster from other cluster (inter-cluster distance), indicated greater divergence between cluster X and cluster XI followed by cluster IX and XI and cluster III and cluster XI. Such high degree of divergence was found in local collections by Rahaman et al., 1997; Sardana et al., 1997 and Sarawagi et al., 1998 as well as in international collections by Usha Kumari and Rangaswamy., 1997. Here it should be mentioned that cultivars belonging to the clusters with maximum inter cluster distance are genetically more diverged and vice versa. There will be a possibility of obtaining greater variation among segregates by crossing between the genotypes belonging to a divergent cluster which is in agreement with the
study of Jagadev et al. (1991). According to Anand and Murthy (1968) also, hybridization programme involving genetically diverse parents belonging to different distant clusters would provide opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents. Bhatt (1970) also emphasized that Genotypes belonging to clusters separated by high genetic distance may be used in hybridization programme to obtain a wide spectrum of variation among the segregants.

Maximum intra-cluster distance was observed in cluster VI followed by cluster V. Cluster VI comprised of only three high-yielding cultivars and hence we can exclude this cluster from selection process. Thus cluster V had showed maximum intra-cluster distance among the experimented indigenous cultivars. The cultivars included in this cluster had maximum variability among them. Minimum intra-cluster distances were observed in clusters VII (0.00), VIII (0.00), IX (0.00), X (0.00) and XI (0.00), since these clusters consisted with one cultivar. It is important to note that no single cluster having two or more cultivars were observed with minimum genetic distance (0.00) for indicating the duplicates (same cultivar with different name by people of different region), since lower intra-cluster distances indicating lower variability within the cluster. The inter-cluster distances were greater than intra-cluster distances suggesting wider diversity among the cultivars of different clusters. Thus genetic diversity among the cultivars of different clusters was wider than those in the same cluster. Similar results were also observed by Akter et al., (2009) in 44 restorers of rice hybrids. It is noteworthy that cluster VII, VIII, IX, X and XI were monogenotypic. The formation of solitary cluster may be due to total isolation
preventing the gene flow or intensive natural or human selection for diverse adaptive characters. Similar results were also reported by Bose and Pradhan (2005) and Thayumanavan et al., (2009). Parental lines selected from these five clusters may be used in a hybridization programme, since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Rama, 1992). The hybrids developed from the selected cultivars within the limit of compatibility of these clusters may produce high magnitude of heterosis or desirable segregant. Such recommendations were also made by Murty and Arunachalam (1966), Pradhan and Ray (1990), Qian and He (1991), and Rao and Gomanthinayagam (1997) and Rahman et al., (1997) have also reported that selection of parents for hybridisation should be from two clusters having wider inter-cluster distance to get maximum variability in the segregating generations. Iftekharuddaula et al., (2002) also reported that the crosses involving the parents belonging to distinct clusters would offer prime scope in the development of high yielding irrigated rice. To realize much variability and high heterotic effect, Chaturvedi and Maury (2005) recommended that parents should be selected from two clusters having wider inter-cluster distance. The relatively closer clusters were cluster VII and cluster VIII and hence were more or less homogenous. For attaining fruitful results, such homogenous clusters should be avoided. Heterosis is generally due to genetic divergence among the parental lines involved in the crosses. Nevertheless, the genetic divergence for the maximum expression of the heterosis effect has a limit (Moll, et al., 1965; Arunachalam and Bandyopadhyay, 1984). Thus the genotypes included in these clusters were relatively more diverse than those in the other clusters and thus can help
for achieving maximum genetic advance. The hybrids developed from the selected cultivars within the limit of compatibility of these clusters may produce high magnitude of heterosis or desirable segregants which would be rewarding in a rice breeding programme.

Cluster mean value for days to 50% flowering was lowest in cluster III. Thus when observed for early flowering habit cultivars in the cluster III (with lowest mean value for days to 50% flowering) had showed characteristic early flowering habit, indicating its significance in future breeding programme.

After scoring the cluster mean of the characters in desired direction (the character with the higher magnitude in the desired direction was given the highest score), it was observed that cluster VII was the most suitable cluster with maximum number of desirable characters with highest mean values. This cluster had shows highest value for four economically important characters viz. grain length, harvest index, spikelets per plant and grain yield and moderate values for other important yield attributing characters such as tillers per plant, L/B ratio of grain, length of the panicle, spikelet density etc., indicating its importance in future breeding programme. Grain length is an important desirable character in international market. It is noteworthy that this cluster was a solitary cluster comprising the cultivar *Ahumsali*. Cluster VIII comprising only one cultivar viz. *Bogisali* following cluster VII showing second highest scores. This cluster exhibited highest cluster mean for traits viz. spikelets per panicle, length of the panicle and flag-leaf length and moderate mean values for percentage of viable seeds, 1000 seeds weight, spikelet density, harvest index, spikelets per plant, L/B ratio of grain, total chlorophyll content and leaf area index and
hence might also be included in future breeding programme for rice crop improvement. Members of cluster VI showed third highest score, but all the three members of this cluster were high yielding cultivars and hence it is noteworthy that we may exclude this cluster from selection process. Cluster IV and cluster V showed next highest scores respectively. Members of these clusters might be included in crop improvement programmes. Cluster IV comprised of 9 deepwater rice cultivars viz. *Panidhan, Panikokuwa, Happybao, Kokuwabao, Dalbao, Negheribao, Maguribao, Miabao* and *Bhubao*.

Higher cluster values for all characters were not observed within any cluster. This implies that none of the clusters contained genotypes with all the desirable characters which could be directly select for future cultivation. In such context recombination breeding between genotypes of different clusters may be employed as suggested by Singh *et al.* (1996ii).

In all the combinations of inter-cluster distances each character is ranked on the basis of inter-cluster distances. Rank one is given to the character having highest mean difference and rank p is given to the character having lowest mean difference, where p is the numbers of characters. Percentage contribution of each character is calculated on the basis of occurrence of these ranks. Among the 19 characters studied, the most important character contributing to the divergence was total chlorophyll content with 41.44% contribution and was the major force of discrimination among the cultivars. Ullah *et al.*, (2011) reported chlorophyll content as the main contributor to grain yield. This was followed by days to 50% flowering (33.41%) spikelets per panicle (12.16%) and 1000 seeds weight (4.92%). Banumathy
et al., (2010) also reported days to 50% flowering as second important character contributing genetic divergence with 15.02% contribution analysing fifty-three rice genotypes. Similar results were also observed by Bose and Pradhan (2005) with 27.06% contribution analysing thirty-five deep-water rice genotypes, Ubarhande et al., (2009) analysing 44 indica rice cultivars under rainfed condition, Ahmed et al., (2010ii) analysing thirty-six traditional Boro rice germplasms and Rajesh et al., (2010) with 25.61% contribution analysing 29 landraces of rice. Present investigation showed that spikelets per panicle is also an important character contributing 12.16% towards genetic divergence. Bisht et al., (2007) observed 9.19% for thirteen paddy landraces, Banumathy et al., (2010) observed 10.52% for 53 rice genotypes and Saravanan and Sabesan (2010) observed 20.36% for 46 rice genotypes contribution towards divergence by the character spikelets per panicle. These characters should be given importance during hybridization and the selection in the segregating population. Among the 19 experimented characters, two characters viz. Flag leaf length and length and breadth ratio of seeds had not showed any contribution towards divergence.

High amount of genetic diversity in population alone may not be adequate to affect improvement over best existing cultivars (Singh et al., 1988). The yield potential of the genotypes should not be ignored at the time of selection of the parental lines. It is necessary to carefully analyse the selection of a particular cluster from which genotypes are to be chosen in a crossing programme as well as selection of a particular genotype from the selected cluster. While selecting genotypes from distant clusters, their mean values for different traits should also be given importance to generate promising breeding material (Pradhan and Mani, 2005).
5.8. Reasons of popularity of some indigenous rice cultivars:

There are some indigenous rice cultivars which are widely cultivated and very much popular among the farmers of Dhemaji district. These cultivars are still in practice inspite of availability of high yielding varieties. This indicates that these indigenous varieties must have possessed some desirable traits which are suitable for the environment of this region. Some popular indigenous rice cultivars were Nolsitiki, Nekera, Bora, Sowagmoni, Joha, Malbhug, Sokuwa, Monuharsali, Torawali, Konjoha, Memlahi, Amana Kokuwabao and Adoliabao. Bora is a glutinous rice which is used by the people for the preparation of Pitha (rice cake), an indispensible part of traditional cuisines. It is also used for preparation of traditional liquor by different ethnic groups. Experimental findings also showed that it was the waxiest type among all experimented cultivars with lowest amylose content. Joha is an aromatic fine grain rice. Yield of this cultivar is not appreciable, but is popular among the farmers due to its pleasant aroma. Sokuwa is a unique type of rice which can be used either as jalpan (instant breakfast), or as rice. It is preferred by the farmers for the preparation of perboiled rice, an instant food. Amanabao and Kokuwabao are popular among the farmers of riparian belt because these cultivars can withstand flood. They have the ability to elongate with the rise of water during flood. Amanabao shows high grain production and experimental findings also support this view. People cultivating these bao s cultivars believe that consuming bao rice gives feeling of satiety for long time. Most of these cultivars show red kernel colour. Available literature shows that pigmented rice is high in dietary fiber and the minerals viz. iron and zinc, rich in B vitamins and the trace elements viz. manganese and calcium. It has antioxidant
properties also (Lila, 2004). It is noteworthy that maximum number of popular indigenous cultivars are members of cluster one which had intermediate values for almost all yield attributing characters, intermediate amylose content and long slender type grain. Indigenous cultivars show average production without the application of fertilizers and pesticides which is also a cause of popularity of these cultivars.

From the above overall findings of the work it is observed that cultivars Ahumsali and Bogisali are the best performers considering economically important traits. Pakhoribora, Titaphuliabora and Amanabao are the most divergent cultivars and hence can be included in future breeding programmes. It is suggested to test the superior progenies in multi-location trials to confirm their potentiality and to know their stability over different agro-climatic situations in future improvement programmes. Cultivars identified for drought tolerance and pre-harvest sprouting tolerance can be tested further to confirm their superiority in large scale trials.

The present investigation also revealed that genetic diversity is largely contributed by total chlorophyll content, days to 50% flowering, spikelets per plant and test weight. Hence due weightage may be given for these traits in future breeding programmes to improve the yield in rice.