Article
Morphological characterization of NERICA mutant lines and their parents

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Abstract: A total of 10 NERICA lines (7 mutants along with 3 parents) of advanced generations were used for morphological and molecular characterization. The experiments were conducted in both Aus and Aman season, 2014 under different field conditions at the field of Biotechnology division, BINA, BAU Campus, Mymensingh-2202 following Randomized Complete Block Design (RCBD) with three replications. The genotypes differed significantly for all the traits. The seasonal differences on all the traits except 100-seed weight were also highly significant. The season's × genotypes interactions were highly significant. The mean value of days to maturity was the lowest in Aman season than Aus season and the mean yield of rice lines was the highest in Aman season than Aus season. The phenotypic co-efficient of variations (PCV) were higher than genotypic co-efficient of variations (GCV) for all the traits studied indicating that they all interacted with the environment to some extent. All the traits studied expressed moderate to high heritability estimates ranging from 53.70 to 99.54%. High heritability along with high genetic advance was noticed for the traits, number of filled grain panicle[-1], number of unfilled grain panicle[-1] and plant height. Significant positive correlations were recorded for yield plot[-1] with effective tillers hill[-1] and panicle length and significant negative correlations were recorded for yield plot[-1] with days to maturity and unfilled grains panicle[-1]. Plant height, total tillers hill[-1], effective tillers hill[-1], panicle length, filled grains panicle[-1] and 100-seed weight showed direct positive effect on yield plot[-1] at both genotypic and phenotypic level. Therefore, these characters would be reliable criteria for improving yield.

Keywords: NERICA; mutant; genotype; yield; heritability

1. Introduction
Rice (*Oryza sativa* L.) is a staple food for over 60% of the world's population (Sellamuthu *et al*., 2011). In the coming 30 years, the world will require 70% more rice than it requires today. In respect of area and production of rice, Bangladesh ranks fourth following China, India and Indonesia (FAO, 2008). Rice plays an important role in the Agro-economy and national health of Bangladesh. Bangladesh earns about 21.10% of her gross domestic product (GDP) from agriculture (Annonymous, 2008). It provides about 75% of the calorie and 66% of the protein in the average daily diet of the people in Bangladesh (Bhuiyan *et al*., 2002). In Bangladesh, rice is grown in three seasons (Aus, Aman and Boro) of the year.In three distinct seasons namely Aus, Aman and Boro (AIS, 2011) reported with the production of 2.63, 12.74 and 18.53 million tons, respectively. However, both area (1.41 million ha) and yield (2.05 thac[-1]) of Aus rice were very low compared with other two seasons (BBS,

Asian J. Med. Biol. Res. **2018**, 4 (2)

208

2011). The total cropped area of Bangladesh is 33422 thousand acres of which 26130 thousand acres are used for rice cultivation and the production of rice is 28931 thousand metric tons (BBS, 2012). NERICA has been introduced recently in Bangladesh for growing in drought prone areas. The term NERICA stands for New Rice for Africa, an extended family of some 3000 siblings. NERICA is the product of interspecific hybridization between the cultivated rice species of Africa (*O. glaberrima*) and Asia (*Oryza sativa*). Development of improved rice varieties, with stress tolerance traits from NERICA could significantly increase productivity (Mzengeza, 2010). Drought is the most devastating among abiotic stresses and it depresses yield by 15-50% depending on the vigour and period of stress in rice (Srividya *et al.*, 2011). Severe drought during flowering and ripening stages reduces the grain yield up to 70%. Drought affects rice crops in three different cropping seasons namely pre-Kharif, Kharif, and Rabi seasons, where rice is the main staple food in Bangladesh accounting for more than 80% of the total cultivable land of the country. Developing high yielding and drought resistant varieties for rain fed area is priority for improving rain fed rice production. NERICA varieties have high yield potential and short growth cycle. Several of them possess early vigor during the vegetative growth phase and this is a potentially useful trait for weed competitiveness. Likewise, a number of them are resistant to African pests and diseases, such as the devastating blast, to rice stem borers and termites. They also have higher protein content and amino acid balance than most of the imported rice varieties (WARDA, 2008). Induced rice mutants are useful research tools for genetic and physiological assessments of yield contributing factors in rice. Since 1960s, several collections of mutant lines from different species have been isolated and successfully used in many different areas of plant biology and crop breeding (Fu *et al.*, 2008). More than 2700 mutant varieties, that have been released worldwide, 64 per cent were created through exposure to gamma-rays, 22% through exposure to X-rays and the rest by other mutagenic treatments (Shu and Lagoda, 2007). Gamma (γ) rays are physical mutagens; gamma irradiation has proven to be useful method for introducing new trait variations that may result in crop improvement and can be used as a complementary tool in plant breeding (Babaei *et al.*, 2010).

2. Materials and Methods
2.1. Plant materials and experimental design
In this experiment, a total of ten NERICA lines (seven mutant lines along with three parents) of advanced generations were used which were obtained from Bangladesh Institute of Nuclear Agriculture (Table 1). Field experiments were conducted following randomized complete block design (RCBD) with three replications. Unit plot size was 1.8 m × 1 m.

Table 1. List of the genotypes used in the experiment.

Sl. No	Genotypes	Source
1.	$N_4/350/P-4(5)$	
2.	$N_{10}/350/P-5-4$	
3.	$N_4/250/P-1(2)$	
4.	$N_1/250/P-6-2$	
5.	$N_4/250/P-2(6)-26$	
6.	$N_{10}/300/P-7-1$	Bangladesh Institute of Nuclear Agriculture (BINA)
7.	$N_{10}/300/P-2(1)-4$	
8.	N_1 Parent	
9.	N_4 Parent	
10.	N_{10} Parent	

Here, N_1= NERICA-1, N_4= NERICA-4, N_{10}= NERICA-10

2.2. Data collection
Data for the following morphological traits were recorded from all genotypes at each of the replication: Days to flowering, Days to maturity, Plant height, Total tillers $hill^{-1}$, Effective tillers $hill^{-1}$, Non effective tillers $hill^{-1}$, Panicle length (cm), Filled grains $panicle^{-1}$, Unfilled grains $panicle^{-1}$, 100-seed weight (g) and Yield $plot^{-1}$ (kg).

2.3. Statistical analysis
Analysis of variance was performed using the plant breeding statistical program (Utzzal, MSTATc and PLABSTAT, Version 2N, 2007). Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1995). Heritability in broad sense (h^2_b) was estimated according to the formula

Asian J. Med. Biol. Res. **2018**, 4 (2)

209

suggested by Johnson *et al*. (1955) and Hanson *et al*. (1956). Genotypic and phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Choudhury (1985). Estimation of genetic advance was done following formula given by Johnson *et al*. (1955) and Allard (1960). Genetic advance in per cent of mean was calculated by the formula of Comstock and Robinson (1952). The phenotypic and genotypic correlations were estimated by the formula suggested by Miller *et al*. (1991). Direct and indirect path co-efficient were calculated as described by Lynch and Walsh (1998).The Mahalanobis distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury (1985). The D^2 values were estimated for all possible pairs of combinations among genotypes. The D^2 value obtain for a pair of population was taken as the calculated value of χ^2 and was tested against the tabulated value of χ^2 for 'p' degrees of freedom, where 'p' is the number of characters considered. Average intra-cluster distances were calculated by the following formula as suggested by Rao (1952). Average inter-cluster distances were calculated by the following formula as suggested by Rao (1952).

3. Results
3.1. Analysis of variance
The analysis of variance of different NERICA mutant lines based on seasons and genotypes for quantitative traits are shown in Table 2. Analysis of variance indicated that the difference among genotypes for all the traits under study viz., days to flowering (1st, 50%, 80%), days to maturity, plant height, total tillers and effective tillers hill[-1], filled and unfilled grains panicle[-1], 100-seed weight (g) and yield plot[-1] (kg) were highly significant. The seasonal differences on the traits viz., days to flowering (1st, 50%, 80%), days to maturity, total tillers hill[-1], filled and unfilled grains panicle[-1] and yield plot[-1] (kg) were also highly significant. Considering season × genotypes, the traits under study viz., days to flowering (1st, 50%, 80%), plant height, total tillers and effective tillers hill[-1], filled and unfilled grains panicle[-1], 100-seed weight (g) and yield plot[-1] (kg) were highly significant.

3.2. Season wise mean performance of 10 rice genotypes
Season wise mean performances of 10 rice lines are shown in Table 3. From the results, it was observed that rice lines took the lowest days to 1st flowering (68.59 days) in Aman season and rice lines took the highest days to 1st flowering (73.14 days) in Aus season. Rice lines took the lowest mean value of days to 50% flowering (73.61 days) in Aman season and rice lines took the highest mean value of days to 50% flowering (78.58 days) in Aus season. Rice lines took the lowest mean value of days to 80% flowering (81.84 days) in Aman season and rice lines took the highest mean value of days to 80% flowering (85.53 days) in Aus season. The mean value of days to maturity was the lowest (107.6 days) in Aman season than Aus season (112.5 days). The lowest mean value of plant height (102.8 cm) was observed in Aus season and the highest mean of plant height (104.2 cm) was observed in Aman season. The mean value of total tillers hill[-1] was the highest (11.78) in Aus season than Aman season (9.483). The mean number of effective tillers hill[-1] was the highest (8.190) in Aus season than Aman season (7.840). The highest mean of panicle length (23.99 cm) was observed in Aman season and the lowest mean of panicle length (23.30 cm) was observed in Aus season. The mean number of filled grains panicle[-1] was high in Aman season (98.67) and low in Aus season (93.82). The mean number of unfilled grains panicle[-1] was high in Aman season (54.87) and low in Aus season (33.15). The mean yield of rice lines was the highest in Aman season (1.035 kg plot[-1]) than Aus season (0.9953 kg plot[-1]).

3.3. Mean performance of 10 rice genotypes on different morphological traits related to yield
The mean performances of 10 genotypes on different morphological traits related to yield of 10 rice genotypes are shown in Table 4.Days to 1st flowering among the genotypes ranged from 64.18 to 76.90 days with a mean value of 70.86 days.N_4/250/P-2(6)-26 took the lowest days to 1st flowering (64.18 days) and N_{10} parent took the highest days to 1st flowering (76.90 days). Days to50% flowering among the genotypes ranged from 69.68 to 82.37 days with a mean value of 76.09 days.N_4/250/P-2(6)-26 took the lowest days to 50% flowering (69.68 days) and N_1 parent took the highest days to 50% flowering (82.37days). Days to80% flowering among the genotypes ranged from 77.39 to 90.73 days with a mean value of 83.69 days.N_4/250/P-2(6)-26 took the lowest days to 80% flowering (77.39 days) and N_1 parent took the highest days to 80% flowering (90.73 days). Days to maturity among the genotypes ranged from 103.33 to 117.66 days with a mean value of 110.02 days.N_4/250/P-2(6)-26 took the lowest days to maturity (103.33 days) which was followed by N_4/250/P-1(2) and N_{10}/350/P-5-4 and N_1 Parent took the highest days to maturity (117.66 days) which was followed by N_1/250/P-6-2, N_4 parent and N_{10} parent. Plant height among the genotypes ranged from 88.62 to 120.99 cm with a mean value of 103.50 cm. N_1 parent had the lowest plant height (88.62 cm) and N_{10}/300/P-2(1)-4 had the highest plant height (120.99 cm). The number of total tillers hill[-1] ranged from 6.44 to 14.97 with a mean value of 10.63.N_{10}/350/P-5-4 had

Asian J. Med. Biol. Res. **2018**, 4 (2)

210

the maximum number of total tillers hill^{-1} (14.97) and N_{10} Parent had the minimum number of total tillers hill^{-1} (6.44) which was followed by N_4 parent and N_{10} parent. The number of effective tillers hill^{-1} ranged from 4.07 to 12.63 with a mean value of 8.02.N_{10}/350/P-5-4 had maximum number of effective tillers hill^{-1}(12.63) which and N_1 parent had minimum number of effective tillers hill^{-1}(4.07). Panicle length among the genotypes ranged from 22.10 to 25.10 cm with a mean value of 23.64 cm. N_4/250/P-2(6)-26 had the longest panicle (25.10 cm) and N_4 parent had the lowest panicle length (22.10 cm). The number filled grains panicle^{-1} ranged from 61.30 to 112.88 with a mean value of 96.99.N_4/250/P-1(2) had the highest number filled grains panicle^{-1} (112.88) and N_1/250/P-6-2 had the lowest number filled grains panicle^{-1}(61.30). The number unfilled grains panicle^{-1} ranged from 30.12 to 90.10 with a mean value of 44.01.N_1/250/P-6-2 had the highest number unfilled grains panicle^{-1} (90.10) and N_4/250/P-2(6)-26 had the lowest number unfilled grains panicle^{-1}(30.12). 100-seed weight ranged from 2.61 to 1.73 g with a mean value of 2.20 g. N_1/250/P-6-2 had maximum 100-seed weight (2.61 g) andN_{10}/300/P-2(1)-4 had minimum 100-seed weight (1.73 g). Yield plot^{-1} (kg) ranged from 0.53 to 1.64 kg plot^{-1} with a mean value of 1.02 kg plot^{-1}. N_{10}/350/P-5-4 had maximum yield plot^{-1} (1.64 kg) andN_1 parent and N_4 parent had minimum yield plot^{-1} (0.53 kg).

3.4. Estimation of genetic parameters of 10 rice genotypes
3.4.1. Variability parameters
Phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits. Coefficient of variation studied indicated that phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits (Table 5) indicating that they all interacted with the environment to some extent. Among the all traits number of unfilled grains panicle^{-1} (34.90 and 37.94%) exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by effective tillers hill^{-1} (34.29 and 35.91%) and total tillers hill^{-1} (17.65 and 20.38%). On the other hand, 100-seed weight showed very close GCV and PCV (13.13 and 13.16%). 100-seed weight (13.13 and 13.16%) and filled grains panicle^{-1} (13.95 and 16.06%) showed moderate value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Days to 1st flowering (6.34 and 6.45%), days to 50% flowering (5.83 and 6.00%), days to 80% flowering (5.71 and 5.85%), days to maturity (5.04 and 5.15%), plant height (9.19 and 9.43%), panicle length (2.63 and 3.59%) exhibited low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

3.4.2. Heritability
The traits studied in the present investigation expressed moderate to high heritability estimates ranging from 53.70 to 99.54%. Among the traits, high heritability was recorded by 100-seed weight (99.54%), days to 1st flowering (96.60%), days to maturity (96.07%), days to 80% flowering (95.40%), plant height (94.99), days to 50% flowering (94.25%), effective tillers hill^{-1} (91.15%), unfilled grains panicle^{-1} (84.60%), filled grains panicle^{-1} (75.51%) and total tillers hill^{-1} (75.03%) and moderate heritability value was recorded by panicle length (53.70%) (Table 5).

3.4.3. Genetic advance
In the present study genetic advance was highest for number of unfilled grains panicle^{-1} (29.10) followed by filled grains panicle^{-1} (24.22) and lowest for 100-seed weight (0.59) among yield contributing traits (Table 5). The genetic advance as per cent of mean was highest in case of number of effective tillers hill^{-1} (67.43%), while lowest recorded by panicle length (3.97%) among the yield contributing traits.

3.5. Relationship among yield and yield contributing traits
3.5.1. Estimation of correlation coefficient
Phenotypic and genotypic correlation co-efficient among different traits of 10 rice genotypes are presented in Table 6. In the present study out of 66 associations, 38 associations were significant both at genotypic and phenotypic level. Among the 38 associations, 15 associations were positively significant and the rest 23 were negatively significant. Besides, 11 associations were positive and non-significant both at genotypic and phenotypic level. On the other hand 11 relationships were found negative and non-significant both at genotypic and phenotypic level. Again 5 associations were significant at genotypic level only. Among these 5 associations, 2 associations were negatively significant and 3 associations were positively significant. Significant positive correlations at both genotypic and phenotypic level were recorded for days to 1st flowering with days to 50% flowering, days to 80% flowering, days to maturity and 100-seed weight and significant negative correlations with total tillers hill^{-1}, effective tillers hill^{-1}, panicle length, filled grains panicle^{-1} and yield plot^{-1}. Significant

Asian J. Med. Biol. Res. **2018**, 4 (2)

211

positive correlations at both genotypic and phenotypic level were recorded for days to 50% flowering with days to 80% flowering, days to maturity and 100-seed weight and significant negative correlations with total tillers hill^{-1}, effective tillers hill^{-1}, panicle length, filled grains panicle^{-1} and yield plot^{-1}. Significant positive correlations at both genotypic and phenotypic level were recorded for days to 80% flowering with days to maturity and 100-seed weight and significant negative correlations with effective tillers hill^{-1}, panicle length, filled grains panicle^{-1} and yield plot^{-1}. Days to 80% flowering was negatively significant with total tillers hill^{-1} at genotypic level. Significant positive correlations at both genotypic and phenotypic level were recorded for days to maturity with 100-seed weight and significant negative correlations with total tillers hill^{-1}, effective tillers hill^{-1}, panicle length, filled grains panicle^{-1} and yield plot^{-1}. Significant positive correlations at both genotypic and phenotypic level were recorded for total tillers hill^{-1} with effective tillers hill^{-1} and significant positive correlations with yield plot^{-1} at genotypic level. Significant positive correlations at both genotypic and phenotypic level were recorded for effective tillers hill^{-1} with panicle length and yield plot^{-1} and significant negative correlations with 100-seed weight at genotypic level. Significant positive correlations at both genotypic and phenotypic level were recorded for panicle length with filled grains panicle^{-1} and yield plot^{-1} and significant negative correlations with 100-seed weight. Significant positive correlations were for filled grains panicle^{-1} with yield plot^{-1} at genotypic level and significant negative correlations with unfilled grains panicle^{-1} and 100-seed weight at both levels. The results of correlation coefficients implied that significant positive correlations at both the levels were recorded for yield plot^{-1} with effective tillers hill^{-1}, panicle length. The results of correlation coefficients implied that significant negative correlations at both the levels were recorded for yield plot^{-1} with days to 1st flowering, days to 50% flowering, days to 80% flowering, days to maturity.

3.5.2. Estimation of path co-efficient
In the present study, all the 11 traits were considered as causal variables of yield plot^{-1}. Phenotypic and genotypic correlation coefficients of these traits with yield plot^{-1} were partitioned into the direct and indirect effects through path coefficient analysis.

3.5.3. Path coefficient analysis for phenotypic correlation
Partitioning of phenotypic correlation coefficients into direct and indirect effects of 11 important traits of 10 rice genotypes by path analysis is shown in Table 7. Path coefficient analysis for phenotypic correlation revealed that plant height (0.082), total tillers hill^{-1} (0.560), effective tillers hill^{-1} (1.05), panicle length (0.747), filled grains panicle^{-1} (0.199) and 100-seed weight (0.915) had direct positive effect on yield plot^{-1}. However days to 1st flowering (-0.526), days to 50% flowering (-0.55), days to 80% flowering (-0.106), days to maturity (0.568) and unfilled grains panicle^{-1} (-0.588) had direct negative effect on yield plot^{-1}. Effective tillers hill^{-1} (1.05) and unfilled grains panicle^{-1} (-0.588) had highest direct positive and negative effect on yield plot^{-1}, respectively. The residual effect was 0.2353 at phenotypic level.

3.5.4. Path coefficient analysis for genotypic correlation
Partitioning of genotypic correlation coefficients into direct and indirect effects of 11 important traits of 10 rice genotypes by path analysis is shown in Table 8. Path coefficient at genotypic level revealed that plant height (0.056), total tillers hill^{-1} (0.075), effective tillers hill^{-1} (0.255), panicle length (0.171), filled grains panicle^{-1} (0.487) and 100-seed weight (0.057) had direct positive effect on yield plot^{-1}. However days to 1st flowering (-0.833), days to 50% flowering (-0.578) days to 80%flowering (-0.099), days to maturity (-0.821) and unfilled grains panicle^{-1} (-0.243) had direct negative effect on yield plot^{-1}. Effective tillers hill^{-1} (0.255) and days to 1st flowering (-0.833) had highest direct positive and negative effect on yield plot^{-1}, respectively. The residual effect was 0.1976 at genotypic level.

3.5.5. Nature and magnitude of diversity
Depending upon the range of diversity, 10 genotypes were grouped into four clusters (Table 9, Figure 2). The distribution pattern revealed maximum number of genotypes (4 genotypes) in cluster I while cluster II included minimum number of genotypes (1genotype). Cluster III and IV included 2 and 3 genotypes, respectively. The inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider diversity among the genotypes of the distant groups (Table 10). Maximum intra-cluster degree of diversity was observed in cluster III (22.59) and minimum in cluster II (0.00). Maximum inter-cluster distance (37.49) was showed from cluster I and II followed by the distance between cluster I and IV (35.41), cluster II and III (33.53) and cluster III and IV (30.37), I and III (26.81), II and IV (15.31). Minimum distance was found between the genotypes of the cluster I and VI (12.40) followed by the genetic distance between clusters II and IV (15.31).

Asian J. Med. Biol. Res. **2018**, 4 (2)

212

Mean performance of different clusters for the traits studied (Table 11) reflected that all the short duration (104.66 days) genotypes were grouped into cluster I whereas cluster IV included long (116.69 days) duration genotypes indicating maximum contribution of this character towards the divergence between cluster I and IV.
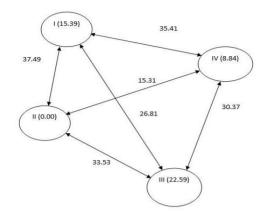

Figure 1. Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$ values).
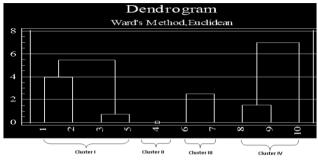
Again all the high yielding genotypes with high number of total tillers hill[-1], high number of effective tillers hill[-1], maximum panicle length, high number of filled grains panicle[-1] were grouped into cluster I whereas cluster IV included low yielding genotypes with less number of total tillers hill[-1], less number of effective tillers hill[-1], less panicle length, less number of filled grains panicle[-1] indicating maximum contribution of these traits towards the divergence between cluster I and IV. The cluster I was divergent from cluster III mainly due to days to maturity, plant height, effective tillers hill[-1] and 100-seed weight indicating maximum contribution of these traits towards the divergence. The cluster III was divergent from cluster IV mainly due to days to maturity, plant height, total tiller hill[-1], effective tillers hill[-1], panicle length, filled grains panicle[-1], 100-seed weight and yield plot[-1] indicating maximum contribution of these traits towards the divergence.

4. Discussion
All of the morphological traits studied among genotypes viz., days to flowering (1st, 50% and 80%), days to maturity, plant height, total tillers and effective tillers hill[-1], filled and unfilled grains panicle[-1], 100-seed weight (g) and yield plot[-1] (kg) were highly significant. The seasonal variations among the genotypes for days to flowering (1st, 50%, 80%), days to maturity, total tillers hill[-1], filled and unfilled grains panicle[-1] and yield plot[-1] (kg) were also highly significant. Considering season × genotypes, the traits under study viz., days to flowering (1st, 50% and 80%), plant height, total tillers and effective tillers hill[-1], filled and unfilled grains panicle[-1], 100-seed weight (g) and yield plot[-1] (kg) were highly significant. Yaqoob *et al.* (2012) observed significant variations among genotypes for days to maturity, tillers plant[-1], effective tillers plant[-1], plant height, panicle length, 100-grains weight and yield plant[-1]. Tiwari *et al.* (2011) also observed significant variations among genotypes for days to 50% flowering, effective tillers plant[-1], panicle length, number of spikelets panicle[-1], number of fertile spikelets and grains yield plant[-1]. These results suggest that all the genotypes under study had significant variation with each other. Seasonal variation was also highly significant. In the present study, 10 diverse genotypes of NERICA were studied to assess their genetic potential. All the genotypes displayed considerable amount of differences in their mean performances with respect to all the characters studied. This had also been exemplified by highly significant mean sum of squares for these characters, which indicated that, the lines under study were genetically diverse. Univariate statistical analysis gave an excellent opportunity to identify and group the genotypes into different categories with respect to various traits individually. Mean performance of plant materials helps to determinate the diversity of the rice genotypes. Seasonal variations were determined by the season wise mean performances. Plant height in rice is a complex character and is the end product of several genetically controlled factors (Cheema *et al.*, 1987). Reduction in plant height may improve their resistance to lodging and reduce substantial yield losses associated with this trait (Abbasi *et al.*, 1995). The semi dwarf plant type has been extensively utilized in the improvement of rice throughout the world. Plant height and flowering duration in rice plants may be influenced by genetical inheritance and availability of nutrient content in soil (Rajendran and Namboodiri, 1971). Since, greater number of filled grains per panicle is one of the major criteria which contribute to higher grains yield could be utilized in further program. The genotypes showed a wide range of variation which provides ample scope for selection of superior and desired genotypes by the plant breeder for

Asian J. Med. Biol. Res. **2018**, 4 (2)

213

further improvement. The perusal of data revealed that variance due to treatment was highly significant for all the traits (Table 2). This suggested that there were inherent genetic differences among the genotypes. Significant genetic variation in various component traits exhibited by the genotypes indicated these traits might be effective. Phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits. Prajapati *et al*. (2011) also mentioned the same result. Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits (Table 5) indicating that they all interacted with the environment to some extent. Similar findings were earlier reported by Bhadru *et al*. (2012). The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for these traits suggested the possibility of yield improvement through selection of these traits. Tiwari *et al*. (2011) also observed the higher magnitude of PCV and GCV for grains yield plant[-1], number of fertile spikelets, effective tillers hill[-1], panicle length and number of spikelets panicle[-1]. The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait. Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al*. (1955). All the traits studied in the present investigation expressed moderate to high heritability estimates ranging from 53.70 to 99.54%. High heritability values indicate that the traits under study are less influenced by environment in their expression and have greater possibility of genetic improvement through selection methods. Patel *et al*. (2012) observed the highest heritability for days to 50% flowering, plant height, total tillers, panicle length, total number of spikelets panicle[-1], number of filled spikelets panicle[-1], number of unfilled spikelets panicle[-1] and grains yield meter square[-1].The plant breeder, therefore, may make his selection safely on the basis of phenotypic expression of these traits in the individual plant by adopting simple selection methods. The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population and heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al*. 1955). Babu *et al*. (2012) also found highest genetic advance for number of filled grains panicle[-1] and highest genetic advance as per cent of mean in case of number of unfilled grains panicle[-1].The information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. In general, the traits that show high heritability with high genetic advance are controlled by additive gene action (Panse and Sukhatme, 1957) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability coupled with high genetic advance is likely to accumulate more additive genes leading to further improvement of their performance. In the present study, high heritability along with high genetic advance was noticed for the traits, number of filled grains panicle[-1], number of unfilled grains panicle[-1] and plant height. Other traits showed high heritability along with moderate or low genetic advance which can be improved by inter-mating superior genotypes of segregating population developed from combination breeding as suggested by Samadia (2005). Correlation studies provide information on the nature and extent of association between any two pairs of metric characters. From this, it would be possible to bring about genetic up-gradation in one character by selection of the other of a pair. Relationship between yield and yield contributing characters was studied through analysis of correlation between them at both phenotypic and genotypic level. The significant and positive association between the traits suggested additive genetic model thereby less affected by the environmental fluctuation. The positive and non-significant association referred information of inherent relation among the pairs of combinations. The negative and non-significant association referred a complex linked of relation among the pair of combinations. Genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients which might be due to masking or modifying effect of environment (Singh, 1980). These findings were corroborating the observations of Meenakshi *et al*. (1999) and Bhattacharyya *et al*. (2007). Very close values of genotypic and phenotypic correlations were also observed between some traits combinations 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 traits would be reliable. Thus selection for higher yield on the basis of above traits would be reliable. Similar findings were also reported by Prasad *et al*. (2001) and Yogamenakshi *et al*. (2004). When traits having direct bearing on yield are selected, their associations with other traits are to be considered simultaneously as this will indirectly affect yield. Any of these morphological traits can be discarded to reduce the number of traits to characterize. This correlation can be used as basis for character discard if similar research is conducted in the future using additional morphological traits. Elimination of redundant traits will reduce the workload of researcher and will render characterization less cumbersome and more efficient. This outcome was supported by the findings of Lasalita-Zapico *et al*. (2010). The correlation value denotes only the nature and extent of association existing between

Asian J. Med. Biol. Res. **2018**, 4 (2)

214

pairs of characters. The yield is dependent on several contributing characters that are mutually associated which will in turn impair the true association existing between a yield contributing characters and economic characters and change in any one component is likely to disturb the whole network of cause and effect. Each contributing character has two parts of action viz., the direct effect and the indirect effects through yield contributing characters on economic characters which are not revealed from the correlation studies.

1= N4/350/P-4(5); 2= N10/350/P-5-4; 3= N4/250/P-1(2); 4= N1/250/P-6-2; 5= N4/250/P-2(6)-26; 6= N10/300/P-7-1; 7= N10/300/P-2(1)-4; 8= N1 Parent; 9= N4 Parent; 10= N10 Parent

Figure 2. Dendrogram based on summarized data on differentiation among 10 rice genotypes according to Ward's method.

Table 2. Analysis of variance for different morphological plant traits of 10 rice genotypes.

Sources of variation	d.f	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height	Total tillers hill^{-1}	Effective tillers hill^{-1}	Panicle Length	Filled grains panicle^{-1}	Unfilled grains panicle^{-1}	100-seed weight	Yield plot^{-1}
Replication	2	2.600	5.576	10.908	9.935	22.909	0.719	0.007	0.300	0.862	0.126	0.000	0.005
Season(A)	1	311.26**	370.21**	204.64**	358.09**	27.93*	79.36**	1.84*	7.11**	169.34**	7072.03**	0.001NS	0.024**
Genotype (B)	9	126.70**	127.70**	145.97**	194.36**	583.66**	31.00**	51.75**	5.20**	1627.18**	1797.78**	0.505**	1.038**
AxB	9	5.46**	9.77**	8.75**	9.52*	40.70**	9.869**	6.44**	2.88**	528.51**	382.55**	0.003**	0.203**
Error	38	1.871	2.038	2.334	3.638	4.559	1.365	0.321	0.235	12.243	7.865	0.001	0.003

Here, d.f = Degree of freedom, * and ** indicate significant at 5% and 1% level of probability, respectively, NS indicates non-significant.

Table 3. Season wise mean performance on different morphological traits related to yield of 10 rice genotypes.

Season	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height (cm)	Total tillers hill^{-1}	Effective tillers hill^{-1}	Panicle length (cm)	Filled grains panicle^{-1}	Unfilled grains panicle^{-1}	100-seed weight (g)	Yield plot^{-1} (kg)
Aus	73.14 a	78.58 a	85.53 a	112.5 a	102.8 b	11.78a	8.190 a	23.30 b	93.82 b	33.15 b	2.19	0.9953b
Aman	68.59 b	73.61 b	81.84 b	107.6 b	104.2 a	9.483b	7.840 b	23.99 a	98.67 a	54.87 a	2.20	1.035 a
LSD$_{0.05}$	0.741	0.746	0.797	0.997	1.12	0.612	0.296	0.253	1.83	1.47	0.017	0.029
Level of sign.	**	**	**	**	*	**	*	**	**	**	NS	**
CV%	1.93	1.88	1.83	1.73	2.06	10.99	7.07	2.05	3.61	6.37	1.05	5.43

Notes: Different letter(s) are significantly different.

Table 4. Mean performance of 10 rice genotypes on different morphological traits related to yield.

Genotypes	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height (cm)	Total tillers hill⁻¹	Effective tillers hill⁻¹	Panicle length (cm)	Filled grains panicle⁻¹	Unfilled grains panicle⁻¹	100-seed weight (g)	Yield plot⁻¹ (kg)
$N_4/350/P-4(5)$	68.33ef	73.15de	80.51e	105.8cd	100.8d	10.17de	8.73cd	23.77cd	111.8a	47.53b	2.37c	1.39bc
$N_{10}/350/P-5-4$	66.71f	71.96e	79.23e	105.2cde	91.99f	14.97a	12.63a	23.54cd	106.9bc	41.63c	2.13d	1.63a
$N_4/250/P-1(2)$	66.84f	72.26de	79.73e	104.3de	102.1cd	11.93bc	10.37b	24.57ab	112.9a	36.23d	1.89g	1.33c
$N_1/250/P-6-2$	74.36c	79.88b	88.62bc	115.3a	112.6b	10.62cde	7.23e	23.20d	61.30g	90.10a	2.60a	0.703f
$N_4/250/P-2(6)-26$	64.18g	69.68f	77.39f	103.33e	103.8c	12.53b	10.90b	25.10a	105.8c	30.12e	2.03e	1.43b
$N_{10}/300/P-7-1$	68.71e	73.82d	80.76e	107.0c	112.5b	9.371e	8.21d	24.03bc	110.6ab	38.17d	1.97f	1.06d
$N_{10}/300/P-2(1)-4$	70.75d	75.70c	82.79d	109.3b	120.99a	11.27bcd	9.01c	24.12bc	98.10d	45.27b	1.72h	0.923e
N_1 Parent	76.67ab	82.38a	90.73a	117.66a	88.62g	9.737e	4.07f	22.29e	86.47f	45.90b	2.51b	0.530h
N_4 Parent	75.18bc	80.19b	87.27c	115.5a	97.00e	9.301e	4.53f	22.10e	82.47f	32.67e	2.37c	0.528h
N_{10} Parent	76.90a	81.93a	89.82ab	116.9a	104.7c	6.435f	4.47f	23.71cd	93.57e	32.48e	2.39c	0.605g
$LSD_{0.05}$	1.59	1.67	1.78	2.23	2.50	1.37	0.662	0.567	4.09	3.28	0.037	0.064
Maximum	76.90	82.37	90.73	117.66	120.99	14.97	12.63	25.10	112.88	90.10	2.61	1.64
Minimum	64.18	69.68	77.39	103.33	88.62	6.44	4.07	22.10	61.30	30.12	1.73	0.53
Mean	70.86	76.09	83.69	110.02	103.50	10.63	8.02	23.64	96.99	44.01	2.20	1.02
Level of sign.	**	**	**	**	**	**	**	**	**	**	**	**
CV%	1.93	1.88	1.83	1.73	2.06	10.99	7.07	2.05	3.61	6.37	1.05	5.43

Notes: Genotypes with different letter(s) are significantly different.

Table 5. Estimation of genetic parameters for morphological traits related to yield.

SL. No.	Traits	Phenotypic variance (σ^2_p)	Genotypic variance (σ^2_g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
1	Days to 1st flowering	20.92	20.21	6.45	6.34	96.60	9.10	12.84
2	Days to 50% flowering	20.85	19.66	6.00	5.83	94.25	8.87	11.65
3	Days to 80% flowering	23.97	22.87	5.85	5.71	95.40	9.62	11.50
4	Days to maturity	32.07	30.81	5.15	5.04	96.07	11.21	10.19
5	Plant height (cm)	95.27	90.49	9.43	9.19	94.99	19.10	18.45
6	Total tillers hill⁻¹	4.69	3.52	20.38	17.65	75.03	3.35	31.49
7	Effective tillers hill⁻¹	8.29	7.55	35.91	34.29	91.15	5.40	67.43
8	Panicle length (cm)	0.720	0.387	3.59	2.63	53.70	0.94	3.97
9	Filled grains panicle⁻¹	242.52	183.11	16.06	13.95	75.51	24.22	24.97
10	Unfilled grains panicle⁻¹	278.82	235.87	37.94	34.90	84.60	29.10	66.12
11	100-seed weight(g)	0.084	0.084	13.16	13.13	99.54	0.59	26.98

Note: PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, GA= Genetic advance, GA (%) = Genetic advance as percent of mean.

Table 6. Coefficients of phenotypic and genotypic correlation among different yield components.

Traits	correlation	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height	Total tillers hill^{-1}	Effective tillers hill^{-1}	Panicle length	Filled grains panicle^{-1}	Unfilled grains panicle^{-1}	100-seed weight	Yield plot^{-1}
Days to 1st flowering	r_p	0.957**	0.958**	0.960**	-0.083	-0.694*	-0.898**	-0.806**	-0.783**	0.296	0.644*	-0.938**
	r_g	0.986**	0.997**	0.996**	-0.079	-0.781**	-0.931**	-0.956**	-0.914**	0.339	0.650*	-0.947**
Days to 50% flowering	r_p		0.949**	0.959**	-0.093	-0.652*	-0.877**	-0.766**	-0.817**	0.321	0.656*	-0.933**
	r_g		0.994**	0.998**	-0.086	-0.723*	-0.907**	-0.974**	-0.976**	0.372	0.669*	-0.950**
Days to 80% flowering	r_p			0.970**	-0.945**	-0.620	-0.866**	-0.739*	-0.848**	0.374	0.698*	-0.922**
	r_g			0.989**	-0.984**	-0.687*	-0.893**	-0.963**	-0.976**	0.425	0.709*	-0.993**
Days to maturity	r_p				-0.091	-0.693*	-0.905**	-0.781**	-0.867**	0.371	0.676*	-0.971**
	r_g				-0.081	-0.811**	-0.949**	-0.935**	-0.985**	0.443	0.683*	-0.966**
Plant height	r_p					-0.136	0.139	0.448	-0.016	0.252	-0.440	-0.037
	r_g					-0.140	0.153	0.597	0.025	0.251	-0.446	-0.019
Total tillers hill^{-1}	r_p						0.759*	0.329	0.199	0.150	-0.424	0.612
	r_g						0.838**	0.508	0.179	0.243	-0.484	0.646*
Effective tillers hill^{-1}	r_p							0.650*	0.560	-0.027	-0.621	0.849**
	r_g							0.834**	0.638*	-0.008	-0.649*	0.886**
Panicle length	r_p								0.709*	-0.281	-0.734*	0.676*
	r_g								0.990**	-0.424	-0.991**	0.930**
Filled grains panicle^{-1}	r_p									-0.737*	-0.712*	0.610
	r_g									-0.915**	-0.824**	0.644*
Unfilled grains panicle^{-1}	r_p										0.509	-0.165
	r_g										0.568	-0.158
100 Seed Weight	r_p											-0.376
	r_g											-0.559

Here, * and ** indicate significant at 5% and 1% level of probability, respectively. r_p= Phenotypic Correlation and r_g= Genotypic Correlation

Table 7. Partitioning of phenotypic correlation coefficients into direct and indirect effects of 11 important traits of 10 rice genotypes by path analysis.

Traits	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height	Total tillers hill⁻¹	Effective tillers hill⁻¹	Panicle length	Filled grains panicle⁻¹	Unfilled grains panicle⁻¹	100-seed wt.	Correlation with yield plot⁻¹
Days to 1st flowering	**-0.526**	-0.532	-0.101	0.546	-0.007	-0.388	-0.939	-0.602	-0.156	-0.174	0.589	-0.938**
Days to 50% flowering	0.791	**-0.555**	-0.100	0.545	-0.008	-0.365	-0.918	-0.572	-0.163	-0.189	0.600	-0.933**
Days to 80% flowering	0.792	-0.527	**-0.106**	0.551	-0.077	-0.347	-0.906	-0.552	-0.169	-0.220	0.638	-0.922**
Days to maturity	0.793	-0.533	-0.103	**-0.568**	-0.007	-0.388	-0.946	-0.583	-0.173	-0.218	0.618	-0.971**
Plant height	-0.069	0.052	0.099	-0.052	**0.082**	-0.076	0.145	0.335	-0.003	-0.148	-0.403	-0.037
Total tillers hill⁻¹	-0.574	0.362	0.066	-0.394	-0.011	**0.560**	0.794	0.246	0.040	-0.088	-0.388	0.612
Effective tillers hill⁻¹	-0.742	0.487	0.092	-0.514	0.011	0.425	**1.05**	0.485	0.112	0.016	-0.568	0.849**
Panicle length	-0.666	0.425	0.078	-0.444	0.037	0.184	0.680	**0.747**	0.141	0.165	-0.671	0.676*
Filled Grains panicle⁻¹	-0.647	0.454	0.089	-0.493	-0.001	0.111	0.586	0.529	**0.199**	0.433	-0.651	0.610
Unfilled grains panicle⁻¹	0.2445	-0.178	-0.040	0.211	0.021	0.084	-0.028	-0.210	-0.147	**-0.588**	0.466	-0.165
100 Seed Wt.	0.532	-0.364	-0.074	0.384	-0.036	-0.237	-0.649	-0.548	-.0.142	-0.299	**0.915**	-0.376

Diagonally bold figures indicate the direct effect   Residual effect = 0.2353

Table 8. Partitioning of genotypic correlation coefficients into direct and indirect effects of 11 important traits of 10 rice genotypes by path analysis.

Traits	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height	Total tillers hill⁻¹	Effective tillers hill⁻¹	Panicle length	Filled grains panicle⁻¹	Unfilled grains panicle⁻¹	100 seed Weight	Correlation with yield plot⁻¹
Days to 1st flowering	**-0.833**	-0.569	0.099	0.818	-0.004	-0.058	-0.237	0.164	-0.445	0.083	0.037	-0.947**
Days to 50% flowering	-0.821	**-0.578**	0.099	0.820	-0.005	-0.054	-0.231	0.167	-0.475	0.091	0.038	-0.950**
Days to 80% flowering	-0.830	-0.574	**-0.099**	0.812	-0.055	-0.051	-0.228	0.165	-0.475	0.103	0.040	-0.993**
Days to maturity	-0.830	-0.577	0.098	**-0.821**	-0.005	-0.061	-0.242	0.160	-0.479	0.108	0.039	-0.966**
Plant height	0.066	0.050	-0.098	-0.067	**0.056**	-0.010	0.039	-0.102	0.012	0.061	-0.025	-0.019
Total tillers hill⁻¹	0.650	0.418	-0.068	-0.666	-0.008	**0.075**	0.214	-0.087	0.087	0.059	-0.028	0.646*
Effective tillers hill⁻¹	0.775	0.524	-0.089	-0.779	0.009	0.063	**0.255**	-0.143	0.310	-0.002	-0.037	0.886**
Panicle length	0.796	0.563	-0.096	-0.768	0.033	0.038	0.213	**0.171**	0.482	-0.103	-0.056	0.930**
Filled grains panicle⁻¹	0.761	0.564	-0.098	-0.809	0.002	0.013	0.163	-0.169	**0.487**	-0.223	-0.047	0.644*
Unfilled grains panicle⁻¹	-0.282	-0.215	0.042	0.364	0.014	0.018	-0.002	0.073	-0.445	**-0.243**	0.032	-0.158
100 seed weight	-0.541	-0.386	0.071	0.561	-0.025	-0.036	-0.165	0.170	-0.401	0.138	**0.057**	-0.559

Diagonally bold figures indicate the direct effect   Residual effect = 0.1976

Asian J. Med. Biol. Res. **2018**, 4 (2)

219

Table 9. Number, percent and name of genotypes in different cluster.

Cluster number	Number of genotypes	Percent (%)	Name of genotypes
I	4	40.00	N$_4$/350/P-4(5), N$_{10}$/350/P-5-4, N$_4$/250/P-1(2), N$_4$/250/P-2(6)-26
II	1	10.00	N$_1$/250/P-6-2
III	2	20.00	N$_{10}$/300/P-7-1, N$_{10}$/300/P-2(1)-4
IV	3	30.00	N$_1$ parent, N$_4$ parent, N$_{10}$ parent

Table 10. Intra and inter-cluster average distance in 10 rice lines.

Cluster	I	II	III	IV
I	**15.39**	37.49	26.81	35.41
II		**0.00**	33.53	15.31
III			**22.59**	30.37
IV				**8.84**

Note: Values in bold illustrate the intra-cluster distance and others show inter-cluster distance.

Table 11. Cluster mean for different yield and yield contributing traits of 10 rice genotypes.

Traits	Cluster I	Cluster II	Cluster III	Cluster IV
Days to 1st flowering	66.52	74.36	69.73	76.25
Days to 50% flowering	71.76	79.88	74.75	81.49
Days to 80% flowering	79.22	88.62	81.78	89.27
Days to maturity	104.66	115.26	108.13	116.69
Plant height (cm)	99.68	112.56	116.74	96.75
Total tillers hill^{-1}	12.40	10.62	10.32	8.49
Effective tillers hill^{-1}	10.66	7.23	8.61	4.36
Panicle length (cm)	24.24	23.20	24.08	22.70
Filled grains panicle^{-1}	109.35	61.30	104.33	87.50
Unfilled grains panicle^{-1}	38.88	90.10	41.72	37.02
100-seed weight (g)	2.11	2.61	1.85	2.43
Yield plot^{-1} (kg)	1.45	0.703	0.992	0.554

The relations between yield and yield contributing characters were studied in detail by path co-efficient analysis. Besides, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield. Plant height, total tillers hill^{-1}, effective tillers hill^{-1}, panicle length, filled grains panicle^{-1} and 100-seed weight showed direct positive effect on yield plot^{-1} at both genotypic and phenotypic level. Therefore, these characters would be reliable criteria for improving yield. Similar results had also been reported by Osman *et al*. (2012), Kiani and Nematzadeh (2012). Yolanda and Das (1995) and Zahid *et al*. (2006) reported that number of filled grains panicle^{-1} has highest positive direct effect on yield. So the number of filled grains per panicle could be considered as critical criteria for yield improvement in these genotypes of rice. Similar results had also been reported by Samonte *et al*. (1998) and Mahto *et al*. (2003). The residual effect determines how best the causal factors account for the variability of the dependent factor, the yield per plot in this case. Depending upon the range of diversity, 10 rice genotypes were grouped into four clusters. Huidong and Shiliang, (1987) have reported that based on hierarchical and dynamic clustering, the frequency of the cultivars in a given cluster is increased by increasing the number of traits under study. The inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider diversity among the genotypes of the distant groups. The similar results regarding inter and intra-cluster distances have been described by Zia-Ul- Qamar *et al*. (2012), Islam *et al*. (2003) in rainfed low land rice. The range of intra-cluster values indicated generally heterogeneous nature of the genotypes within the clusters. It indicates that the genotypes in cluster III were more heterogeneous and these in cluster II were comparatively more closely related. Previously, Iftekharudaulla *et al*. (2002) examined the range of intra-cluster distances in irrigated Boro rice and reported homogeneous nature of the genotypes within the clusters. Zia-Ul-Qamar *et al*. (2012) also found divergence among various cluster due to grain yield, panicle fertility percentage, plant height and days to flowering. In this context, Jagadev *et al*. (1991) reported that the traits contributing maximum towards the divergence should be given greater emphasis for deciding the type of cluster for the purpose of further selection and the choice of parents for hybridization.

Asian J. Med. Biol. Res. **2018**, 4 (2)

220

Conflict of interest
None to declare.

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Asian J. Med. Biol. Res. **2018**, 4 (2)

221

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