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# Relative efficiency of various single plant selection criteria and $F_3$ generation yield testing in wheat (*Triticum aestivum* L.)

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## Abstract

**The relative efficiency of the various single $F_2$ plant selection criteria was evaluated in three $F_2$ populations of wheat (*Triticum aestivum* L.). The criteria considered were: (i) selection for high as well as low values of seven individual plant traits (grain yield *per se*, plant height, grains per spike, 100 grain weight, tiller number, biological yield and harvest index), (ii) selection of single plants based on an index involving greater values of the above seven traits than their means of the population, and (iii) random selection, in association with and without yield testing in the $F_3$ generation. The selection pattern of the parent $F_2$ plant(s) of each of the ten highest yielding $F_3$ selected $F_4$ bulk progenies and $F_4$ bulk progenies revealed that (i) selection of plants in $F_2$ populations on the basis of a single trait was relatively more effective than selection at random while selection based on the index was ineffective, (ii) selection of plants with higher expression of trait(s) resulted into 75% of the highest yielding $F_4$ bulk progenies, (iii) selection of individual plants in $F_2$ generation based on biological yield followed by grain yield *per se* proved most effective, and (iv) the yield testing in $F_3$ generation was only moderately efficient in identification of high yielding $F_4$ bulk progenies.**

**Key words:** Wheat, selection criteria, biological yield, grain yield *per se*, $F_3$ yield testing

## Introduction

One of the major problems in breeding of a self-pollinated crops like wheat (*Triticum* sp.) is the identification of superior genotype(s) from segregating populations that may eventually give rise to high yielding pure lines. In this connection, it has been recognised for a long time now that visual selection and selection based on grain yield *per se* of single plants in early segregating generations is ineffective as a means of developing high yielding pure lines (for a review, see 2). This is attributed to the uncertain meaning of the visual selection and to the low heritability of grain yield *per se* and the confounding effects of non-additive gene action. As a result, due to high heritability of the yield component traits and their significant genetic correlation with grain yield, the attention of plant breeders shifted to these component traits as an indirect selection criteria for developing high yielding pure lines of wheat [1]. Subsequently, biological yield and harvest index were also proposed as indirect selection criteria for the same purpose [2-5].

The success of phenotypic selection of genetically superior plants from a segregating population depends on (i) their frequency, (ii) relative phenotypic advantage, and (iii) the extent to which this advantage is genetically determined and is fixable. It has been suggested that utilisation of the grain yield data of the single $F_2$ plant derived $F_3$ progenies may augment the success of phenotypic selection in $F_2$. In spring wheat, the advantage of testing the progenies in early segregating generation like $F_3$ over testing in later generations was, however, found to be only moderate [6] to small or absent [7-8]. This has been attributed to (i) greater chance of over dominance, (ii) high degree of heterozygosity, and (iii) the evaluation of progenies in small plots in early segregating populations [9].

In the present study on common wheat (*Triticum aestivum* L.), we evaluated the relative effectiveness of selection of individual $F_2$ plants based on (i) grain yield *per se*, (ii) plant height and three individual yield component traits, (iii) biological yield, (iv) harvest index, and (v) random selection, with and without evaluation of grain yield of derived progenies in $F_3$ generation.

## Materials and methods

Two thousand $F_2$ plants derived from each of the three different crosses including CPAN1866/HD2009, CPAN 1866/DL153-2 and CPAN1959/DL153-2 were raised in unreplicated plots in rows of 5 m with plant-to-plant and row-to-row distances of 15 cm and 30 cm, respectively, at the Research Farm of the Department of Agricultural Botany, Ch. Charan Singh University, Meerut. Out of the 2000 plants in each of the three $F_2$ populations, data on 300 disease free plants were

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recorded on the following seven characters including grain yield (g), plant height (cm), grains per spike, 100 grain weight (g), tiller number, biological yield (g), and harvest index. Utilizing these data, selection of individual $F_2$ plants of each of the three crosses was carried out as follows. (i) The 20% plants each with high and low values for each of the grain yield (g), plant height (cm), grains per spike, 100 grain weight (g), tiller number, biological yield (g) and harvest index were separately selected. (ii) The 20% plants were selected on the basis of an index involving greater values of each of the seven traits than their means in the respective populations. (iii) The 20% plants were randomly selected. Since, several plants were selected based on more than one criterion, a total of 272, 274 and 275 plants out of the 300 disease free plants were retained in each of three $F_2$ populations of CPAN1866/HD2009, CPAN1866/DL153-2 and CPAN1959/DL153-2, respectively.

$F_3$ progenies of the above selected $F_2$ plants were evaluated along with their parents and two national check cultivars (WL 711 and Sonalika) in 1.5 m rows in three separate simple lattice design experiments at two diverse locations i.e. Department of Agricultural Botany Research Farm, Ch. Charan Singh University, Meerut and Crop Research Centre, G.B.P.U.A.&T., Pantnagar. Data on grain yield per plot were recorded on the 1 m row of each progeny after slashing 0.25 m on both ends. In each of the three sets of $F_3$ progenies, using the grain yield data of each of the two locations, 10% highest yielding progenies were separately selected. This resulted in the retention of a total of 40, 36 and 37 $F_3$ progenies of CPAN1866/HD2009, CPAN1866/DL153-2 and CPAN1959/DL153-2, respectively.

The above selected three sets of $F_3$ progenies were evaluated as $F_4$ bulk progenies along with their parents and two national check cultivars in three separate randomized block design experiments with three replications at the Department of Agricultural Botany Research Farm, Ch. Charan Singh University, Meerut. Each progeny was evaluated in a plot of 5 rows of 4 m length using a seed rate of 100 kg/ha. The row-to-row distance in a plot was 23 cm. Data on grain yield per plot was recorded on 3 central rows of 3 m in each plot.

The three sets of $F_4$ bulk progenies derived from three sets of 272, 274 and 275 selected $F_2$ plants of respectively CAPN1866/HD2009, CAPN1866/DL153-2 and CPAN1959/D153-2 were also evaluated along with their parents and two national check cultivars in three separate randomized block design experiments with two replications. Each progeny was evaluated in a single row plot of 2m with a row-to-row distance of 23 cm. A seed rate of 100 kg/ha was used. The data on grain yield in each progeny was recorded on a plot of 1.5 m after trimming 25 cm plot from both ends of a plot.

The mean grain yields of the $F_3$/$F_4$ progenies were tested using t-test against the mean grain yield of the parents and the two national check cultivars. Each of the $F_3$ and $F_4$ selected 10% highest yielding $F_4$ bulk progenies were traced back to the selected individual parent $F_2$ plants and the selection criterion of $F_2$ plants were compared to determine the effectiveness of various selection criteria.

## Results and discussion

Selection of promising plants/progenies in early segregating generations that may eventually give rise to high yielding pure line has been a major challenge to the breeders of the self-pollinated crops. With an emphasis on visual selection based on intuition, the selection of promising plants/progenies in the hands of plant breeders has largely become an art rather than science. In the present study, we determined empirically the single $F_2$ plant selection criterion and also the usefulness of $F_3$ yield testing for grain yield improvement in wheat. For this purpose, three $F_2$ populations were derived from two parents each, which differed significantly for several of the seven traits studied. In each of the three $F_2$ populations, moderate to high estimates of heritability and coefficient of variability were observed for the different traits (Table 1). Together with this, the significant differences (expressed as % of mean of plants with high values) between mean values of each of the 20% $F_2$ plants selected for high and low values for each of the seven traits as well as 20% randomly selected $F_2$ plants suggested adequate variability in the three segregating populations (Table 2). All the seven traits except the harvest index (positive and significant in only CPAN1866/DLI53-2) were significantly and positively associated with grain yield in all the populations, although the magnitude of correlation coefficients of grains per spike (r = 0.54**, 0.54** and 0.52**), tiller number (r = 0.79**, 0.83** and 0.55**) and biological yield (r = 0.88**, 0.92** and

**Table 1.** Estimates of coefficient of variability (CV) and heritability for seven traits in $F_2$ populations derived from three crosses

| Trait | CPAN 1866/HD2009 | | CPAN1866/ DL153-2 | | CPAN1959/ DL153-2 | |
|---|---|---|---|---|---|---|
| | CV (%) | Heritability | CV (%) | Heritability | CV (%) | Heritability |
| Grain yield (g) | 34.19 | 0.28 | 40.12 | 0.88 | 38.55 | 0.70 |
| Plant ht. (cm) | 14.26 | 0.95 | 6.61 | 0.86 | 13.26 | 0.93 |
| Grains per spike | 22.18 | 0.81 | 20.34 | 0.19 | 22.56 | 0.43 |
| 100 grain wt. (g) | 11.64 | 0.90 | 14.17 | 0.96 | 13.44 | 0.92 |
| Tiller number | 33.14 | 0.10 | 34.34 | 0.75 | 59.62 | 0.93 |
| Biological yield(g) | 36.22 | 0.77 | 37.69 | 0.91 | 38.94 | 0.76 |
| Harvest index | 19.38 | 0.72 | 17.44 | 0.42 | 16.83 | 0.60 |

**Table 2.** Mean values of plants selected for high (H) and Low (L) expression of each of the seven traits and mean values of seven traits of randomly selected plants (R) in the three $F_2$ populations

| F2 population and trait | Mean value of selected $F_2$ plants | | | | |
|---|---|---|---|---|---|
| | High expression (H) | Low expression (L) | Random (R) | $\frac{H-L}{H}\times 100$*a | $\frac{H-R}{H}\times 100$ **a |
| **CPAN1866/HD2009** | | | | | |
| Grain yield (g) | 27.45 | 11.37 | 18.55 | 58.58 | 32.42 |
| Plant height (cm) | 120.20 | 85.67 | 98.78 | 28.73 | 17.82 |
| Grains per spike | 72.55 | 34.65 | 61.72 | 52.23 | 14.93 |
| 100 grain weight (g) | 4.45 | 2.89 | 3.95 | 35.06 | 11.24 |
| Tiller number | 21.15 | 8.77 | 11.85 | 58.53 | 43.97 |
| Biological yield (g) | 68.20 | 35.50 | 55.20 | 47.95 | 19.06 |
| Harvest index | 0.38 | 0.33 | 0.35 | 13.16 | 7.89 |
| **CPAN1866/DL153-2** | | | | | |
| Grain yield (g) | 38.53 | 18.65 | 32.25 | 51.59 | 16.04 |
| Plant height (cm) | 127.25 | 79.68 | 105.21 | 37.38 | 17.32 |
| Grains per spike | 78.28 | 42.25 | 65.77 | 46.03 | 15.98 |
| 100 grain weight (g) | 4.34 | 3.14 | 3.90 | 27.65 | 10.14 |
| Tiller number | 23.75 | 13.55 | 18.57 | 42.95 | 21.81 |
| Biological yield (g) | 102.58 | 67.60 | 95.45 | 34.10 | 6.95 |
| Harvest index | 0.39 | 0.28 | 0.36 | 28.21 | 7.69 |
| **CPAN1959/DL153-2** | | | | | |
| Grain yield (g) | 41.18 | 17.58 | 26.65 | 57.30 | 35.28 |
| Plant height (cm) | 118.65 | 88.55 | 95.40 | 25.37 | 19.60 |
| Grains per spike | 85.20 | 37.38 | 68.55 | 56.13 | 19.54 |
| 100 grain weight (g) | 4.38 | 3.12 | 4.05 | 28.77 | 7.53 |
| Tiller number | 21.72 | 9.75 | 14.70 | 55.11 | 32.32 |
| Biological yield (g) | 100.16 | 60.45 | 75.75 | 39.65 | 24.37 |
| Harvest index | 0.40 | 0.28 | 0.36 | 30.00 | 10.00 |

*The differences (as % mean of plants with high expression) between mean values of each of the 20% plants selected for high expression and 20% plants selected for low expression; **The differences (as % mean of plants with high expression) between mean values of 20% plants selected for high expression and mean values of 20% plants selected at random; a: Mean differences significant at P = 0.01 for all traits in three populations.

0.90**) with grain yield was highest. This led us to infer that in all the three $F_2$ populations, the selection of plants based on different traits shall result in a positive correlated response of grain yield.

**Table 3.** Analysis of variance for grain yield and the mean grain yield of $F_3$ progenies of three crosses at two locations

| Source of variation and mean grain yield | df | Mean square | |
|---|---|---|---|
| | | Meerut | Pantnagar |
| **CPAN1866/HD2009** | | | |
| Replications | 1 | 589.25 | 24.17 |
| Progenies | 271 | 2826.56** | 3631.66** |
| Error | 271 | 183.01 | 132.61 |
| Mean grain yield (g) | | 93.80 | 94.40 |
| **CPAN1866/DL153-2** | | | |
| Replications | 1 | 57.23 | 52.35 |
| Progenies | 273 | 1690.59** | 3068.91** |
| Error | 273 | 106.18 | 143.07 |
| Mean grain yield (g) | | 86.10 | 84.90 |
| **CPAN1959/DL153-2** | | | |
| Replications | 1 | 86.4 | 1298.13 |
| Progenies | 274 | 2202.39** | 3315.28** |
| Error | 274 | 112.79 | 110.88 |
| Mean grain yield (g) | | 89.90 | 86.30 |

**Significant at P = 0.01

Testing of $F_3$ progenies derived from selected $F_2$ plants revealed significant differences for grain yield, suggesting that the selected parent $F_2$ plants were genetically diverse (Table 3). The mean grain yields of the $F_3$ progenies were significantly lower than the grain yields of their respective parents and two national check cultivars. Nevertheless, a substantial number of $F_3$ progenies (7.64% to 10.55%) had significantly higher grain yield than their better parent and a relatively lower number of $F_3$ progenies (2.19% to 4.01%) had significantly higher grain yield than the check cultivars (Table 4). Although the rank orders of the progenies based on their grain yield at the two locations were different yet a few of the higher yielding progenies (3.65% to 6.25% than the better parent and 1.09% to 2.18% than the check cultivars) were common at the two locations. This suggested that despite the involvement of genotype x environment interaction, the selection of higher yielding genetically superior $F_3$ progenies was eventually likely to give rise to higher yielding lines. Following independent selection of highest yielding 10% progenies, a total 40 (CPAN1866/HD2009), 36 (CPAN1866/DL153-2) and 37 (CPAN1959/DL153-2) $F_3$ progenies were finally selected and evaluated as $F_3$ selected-$F_4$ bulks. The grain yield of

**Table 4.** $F_3$ progenies showing significantly higher mean grain yield than the better parent and two national check cultivars in the three crosses at two locations

| Cross | Meerut location | | | | Pantnagar location | | | | Common progenies from two locations with mean higher than better parent | | Common progenies from two locations with mean higher than checks | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Progenies with mean higher than better parent | | Progenies with mean higher than checks | | Progenies with mean higher than better parent | | Progenies with mean higher than checks | | | | | |
| | No. | % | No. | % | No. | % | No. | % | No. | % | No. | % |
| CPAN1866/HD2009 | 27 | 9.93 | 10 | 3.68 | 28 | 10.29 | 8 | 2.94 | 17 | 6.25 | 4 | 1.47 |
| CPAN1866/DL153-2 | 21 | 7.66 | 11 | 4.01 | 24 | 8.76 | 6 | 2.19 | 10 | 3.65 | 3 | 1.09 |
| CPAN1959/DL153-2 | 21 | 7.64 | 9 | 3.27 | 29 | 10.55 | 10 | 3.64 | 14 | 5.09 | 6 | 2.18 |

$F_4$ bulks differed significantly and a number of progenies from each of the three crosses showed significantly higher grain yield than their parents (Table 5). It is interesting to note that these progenies were derived either from $F_2$ plants selected on the basis of a solitary trait or the plants that were selected at random rather than from plants that were selected on the basis of the selection index (Table 6). Also a majority (75%) of the $F_3$ selected-F4 bulk progenies were derived from $F_2$ plants which were selected for higher values of the traits(s), suggesting that most of the superior $F_2$ plants, in general, had high genetic potential which eventually gave rise to high yielding progenies.

**Table 5.** Analysis of variance for grain yield in $F_3$ selected $F_4$ bulk progenies and number of progenies showing superior performance than the parents in three crosses

| Source of variation and number of superior progenies | df | MS |
|---|---|---|
| **CPAN1866/HD2009** | | |
| Replications | 2 | 1105.50 |
| Progenies | 39 | 21984.15** |
| Error | 78 | 619.77 |
| Number of superior progenies | 5 | |
| **CPAN1866/DL153-2** | | |
| Replications | 2 | 1314.00 |
| Progenies | 35 | 32980.26** |
| Error | 70 | 408.66 |
| Number of superior progenies | 14 | |
| **CPAN1959/DL153-2** | | |
| Replications | 2 | 60.50 |
| Progenies | 36 | 30645.33** |
| Error | 72 | 406.33 |
| Number of superior progenies | 1 | |

**Significant at P = 0.01

The selection pattern of the individual parent $F_2$ plants of the 10 highest yielding $F_3$ selected $F_4$ bulk progenies could give an idea of the relative effectiveness of the different selection criterion used in the present study. At least 50% of each of the 10 highest yielding $F_3$ selected $F_4$ bulk progenies belonging to three different crosses were derived from $F_2$ plants selected for high biological yield (Table 6) The high grain yield *per se* of the $F_2$ plants was the second most important selection criterion. Grain yield *per se* was recommended as a selection criterion in earlier studies also [10-11]. Response to selection of $F_2$ plants based on 100 grain weight, harvest index and also the selection at random was poor as reported earlier [1]. The selection pattern of the individual parent $F_2$ plants with respect to each of the 10 highest yielding $F_3$ selected $F_4$ bulk progenies and $F_4$ bulk progenies were similar (Table 7). It may be noted that the success of high biological yield and high grain yield *per se* as selection criterion in $F_2$ generation was remarkable even though (i) measurements on traits were recorded on space planted $F_2$ plants and their $F_3$ and $F_4$ progenies were evaluated under solid seeding conditions, and (ii) selection was carried out in one year with response measured in the subsequent years. This also assumes importance since effects of differing years and sequential selfing are expected to adversely affect the results of selection. However, it may be noted that the importance of high biological yield for future grain yield improvement in wheat was also suggested in several earlier studies [12-13].

The highest yielding $F_3$ selected $F_4$ bulk progeny each of CPAN1866/HD2009 (progeny number 330) and CPAN1959/DL153-2 (progeny number 167) and similarly the highest yielding $F_4$ bulk progeny each of CPAN 1866/DL153-2 (progeny numbering 018) were derived from $F_2$ plants that were selected for high biological yield (Table 6). These parent $F_2$ plants were also almost invariably selected for high tiller number and high grain yield *per se*, suggesting that more number of tillers contributed in equal measure to both the higher biological yield and higher grain yield. This may be attributed to significant and positive correlation of grain yield with tiller number and biological yield as reported both for the parents and derived populations of wheat in earlier studies [3-5]. Further, the highest yielding $F_3$ selected $F_4$ bulk progenies of CPAN1866/DL153-2 (progeny number 275) and similarly the highest yielding $F_4$ bulk progeny of CPAN 1866/HD2009 (progeny number 205) were derived from $F_2$ plants that were selected for low number of grains per spike and high harvest index, respectively (Tables 6 and 7). These plants, however, could not be selected with any other selection criterion. We assume that an optimum balance of 100-grain weight and tiller number and of biological

**Table 6.** Ten highest yielding $F_3$ selected $F_4$ bulk progenies and the pattern of selection criterion of their parent $F_2$ plants in three crosses

| $F_4$ bulk progeny number | $F_4$ bulk progeny yield (g) | Selection criterion of parent $F_2$ plants | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Grain yield (g) | Plant height (cm) | Grains per spike | 100 grain weight (g) | Tiller number | Biological yield (g) | Harvest index | Random selection | Index selection |
| **CPAN1866/HD2009** | | | | | | | | | | |
| 330 | 946.67 | H | NS | NS | NS | H | H | NS | NS | NS |
| 234 | 941.67 | NS | NS | L | NS | NS | NS | NS | NS | NS |
| 144 | 935.00 | NS | NS | NS | NS | H | H | NS | NS | NS |
| 097 | 928.33 | H | NS | H | NS | NS | H | NS | NS | NS |
| 237 | 916.67 | NS | NS | NS | H | NS | NS | NS | NS | NS |
| 015 | 886.67 | H | NS | NS | NS | NS | H | NS | NS | NS |
| 172 | 861.67 | H | NS | H | NS | NS | H | NS | NS | NS |
| 219 | 853.33 | NS | NS | H | NS | NS | NS | NS | R | NS |
| 092 | 853.33 | NS | NS | H | NS | NS | H | NS | R | NS |
| 290 | 848.33 | NS | NS | NS | NS | NS | NS | L | NS | NS |
| Selection group totals | | 4 | - | 5 | 1 | 2 | 6 | 1 | 2 | - |
| **CPAN1866/DL153-2** | | | | | | | | | | |
| 275 | 876.67 | NS | NS | L | NS | NS | NS | NS | NS | NS |
| 304 | 848.33 | H | NS | H | NS | H | H | NS | NS | NS |
| 044 | 835.00 | H | NS | H | H | NS | H | NS | NS | NS |
| 061 | 831.67 | H | NS | H | NS | H | H | NS | R | NS |
| 172 | 818.33 | NS | NS | NS | H | NS | NS | H | NS | NS |
| 085 | 796.67 | H | NS | NS | H | H | H | H | NS | NS |
| 187 | 786.67 | H | NS | H | NS | H | H | NS | NS | NS |
| 111 | 786.67 | NS | NS | NS | NS | NS | NS | NS | R | NS |
| 078 | 785.00 | L | NS | L | L | NS | L | L | NS | NS |
| 114 | 770.00 | H | NS | NS | NS | H | H | NS | R | NS |
| Selection group totals | | 7 | - | 6 | 4 | 5 | 7 | 3 | 3 | - |
| **CPAN1959/DL153-2** | | | | | | | | | | |
| 167 | 951.67 | H | NS | NS | NS | H | H | NS | NS | NS |
| 140 | 870.00 | NS | NS | NS | NS | H | H | NS | NS | NS |
| 161 | 866.67 | NS | NS | NS | H | H | H | NS | NS | NS |
| 182 | 863.33 | H | NS | H | NS | NS | H | H | R | NS |
| 330 | 856.67 | H | NS | H | NS | H | H | NS | NS | NS |
| 081 | 856.67 | NS | NS | NS | NS | NS | NS | NS | R | NS |
| 087 | 853.33 | H | NS | NS | NS | NS | NS | H | NS | NS |
| 219 | 846.67 | NS | NS | NS | NS | NS | NS | NS | R | NS |
| 144 | 841.67 | NS | NS | NS | H | NS | NS | NS | NS | NS |
| 303 | 773.33 | L | NS | L | NS | L | L | NS | NS | NS |
| Selection group totals | | 5 | - | 3 | 2 | 5 | 6 | 2 | 3 | - |

H, L, R and NS indicate that parent $F_2$ plants were selected for high expression, low expression, at random and not-selected, respectively.

yield and grain yield may be the basis of high grain yield of the progenies derived from these plants.

The number of common progenies among the 10 highest yielding $F_3$ selected $F_4$ bulk progenies and 10 highest yielding $F_4$ bulk progenies in each of the three crosses may give an idea of the effectiveness of early generation ($F_3$) yield testing for selection of high yielding progenies. In the present study, the number (3 to 5 progenies) of common high yielding $F_4$ bulk progenies selected on the basis of grain yield data in $F_3$ and $F_4$ generations in the three crosses was rather low (Tables 6 and 7). This suggested only moderate success of selection of high yielding progenies based on $F_3$ yield testing, although this approach was earlier recommended for selecting high yielding genotypes in early generation [14]. This may be attributed to (i) genotype × year interaction, because comparison of the generations was not made in the same year, and (ii) the failure of heterozygous high yielding genotypes to breed true due to segregation in the succeeding generations.

In conclusion, the results of the present study suggested (i) superiority of biological yield followed by grain yield *per se* as the selection criterion for the selection of genetically superior $F_2$ plants, and (iii) moderate efficiency of yield testing in $F_3$ generation for the identification of high yielding progenies.

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**Table 7.** Ten highest yielding $F_4$ bulk progenies and the pattern of selection criterion of their parent $F_2$ plants in three crosses

| $F_4$ bulk Progeny number | $F_4$ Bulk progeny yield (g) | Parent $F_2$ plants selected for | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Grain yield (g) | Plant height (cm) | Grains per spike | 100 grain weight (g) | Tiller number | Biological yield (g) | Harvest index | Random selection | Index selection |
| **CPAN1866/HD2009** | | | | | | | | | | |
| 205 | 335.00 | NS | NS | NS | NS | NS | NS | H | NS | NS |
| 186 | 290.00 | NS | NS | H | NS | NS | NS | NS | R | NS |
| 259 | 282.50 | NS | NS | H | NS | H | H | NS | NS | NS |
| 330 | 277.50 | H | NS | NS | NS | H | H | NS | NS | NS |
| 172 | 265.00 | H | NS | H | NS | NS | H | NS | NS | NS |
| 113 | 252.50 | NS | NS | NS | NS | NS | NS | H | R | NS |
| 097 | 237.50 | H | NS | H | NS | NS | H | NS | NS | NS |
| 202 | 232.50 | NS | NS | NS | H | NS | NS | NS | NS | NS |
| 005 | 232.50 | H | NS | H | H | H | H | NS | NS | NS |
| 077 | 225.00 | NS | NS | NS | NS | H | H | NS | NS | NS |
| Selection group totals | | 4 | - | 5 | 2 | 4 | 6 | 2 | 2 | - |
| **CPAN1866/DL153-2** | | | | | | | | | | |
| 018 | 455.00 | H | NS | H | H | NS | H | NS | NS | NS |
| 304 | 425.00 | H | NS | H | NS | H | H | NS | NS | NS |
| 033 | 405.00 | H | NS | H | H | H | H | NS | NS | NS |
| 044 | 402.50 | H | NS | H | H | NS | H | NS | NS | NS |
| 261 | 395.00 | NS | NS | NS | NS | H | H | NS | NS | NS |
| 085 | 385.00 | H | NS | NS | H | H | H | H | NS | NS |
| 156 | 385.00 | NS | NS | NS | NS | H | NS | NS | R | NS |
| 187 | 365.00 | H | NS | H | NS | H | H | NS | NS | NS |
| 176 | 342.50 | NS | NS | H | NS | NS | NS | NS | R | NS |
| 078 | 337.50 | L | NS | L | L | NS | L | L | NS | NS |
| Selection group totals | | 7 | - | 7 | 5 | 6 | 8 | 2 | 2 | - |
| **CPAN1959/DL153-2** | | | | | | | | | | |
| 167 | 385.00 | H | NS | NS | NS | H | H | NS | NS | NS |
| 001 | 382.50 | NS | NS | H | NS | NS | NS | NS | R | NS |
| 182 | 325.00 | H | NS | H | NS | NS | H | H | R | NS |
| 330 | 320.00 | H | NS | H | NS | H | H | NS | NS | NS |
| 236 | 315.00 | NS | NS | NS | NS | H | H | NS | NS | NS |
| 151 | 302.50 | NS | NS | NS | H | NS | NS | H | NS | NS |
| 257 | 297.50 | NS | NS | NS | L | NS | NS | NS | R | NS |
| 246 | 295.00 | H | NS | H | H | NS | NS | H | NS | NS |
| 221 | 287.50 | NS | NS | NS | NS | H | H | NS | NS | NS |
| 189 | 280.00 | H | NS | NS | NS | H | H | NS | NS | NS |
| Selection group totals | | 5 | - | 4 | 3 | 5 | 6 | 3 | 3 | - |

H, L, R and NS indicate that parent $F_2$ plants were selected for high expression, low expression, at random and not-selected, respectively.

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