



Research Article

Genetic analysis of some morphological traits of *Brassica napus* (Canola)

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(Received: 29 Jul 2010; Accepted: 05 Aug 2010)

Abstract:

A 4 x 4 diallel cross experiment on *Brassica napus* L. (Canola) was conducted to estimate the genetic control of some important agronomic and quality parameters. The data obtained from the experiment were subjected to analysis of variance. The analysis of variance indicated highly significant differences among the parents and their hybrids for all the characters studied in this experiment. The traits i.e. days taken to flowering, days taken to maturity, primary branches per plant, secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, and seed yield per plant under study showed to be controlled by partial-dominance type of gene action but plant height and 100-seed weight reflected nearly complete dominance type of gene action as compared to other traits. From the estimation of genetic components of variation, it is clear that additive properties were more important in effecting the variation for all the traits.

Key words:

Brassica napus, genetic variability, heritability, diallel, maturity Characters, Pakistan

Introduction

Edible oil is an important constituent of our daily diet. Brassica seed oil has been important source of edible oil in Indo-Pak subcontinent especially Pakistan. Although Pakistan has made progress in agriculture, still our country suffers from acute shortage of edible oil, major portion i.e. 71 % of total requirement, is imported by the cost of 108 billion rupees annually (Anonymous, 2007-08). The total annual domestic demand of edible oil in the country is around 2.9 million tons (including 0.2 million tons export to Afghanistan). However the local production of edible oil is around 1.3 million tons per annum. The rest of the demand is being met through imports. According to official sources, it is proposed that production of Canola should be at least 1/3 of the production of total oilseeds and should include technology for harvesting of Canola crop. The

current area under Canola is 60,000 acres with a production of 18,000 canola oil. There is growing awareness among the consumers for use of Canola oil as it is health friendly. Pakistan Oilseeds Development Board (PODB) has developed new varieties of Canola with indigenous resources. These varieties include synthetic as well as hybrid variety. Local Canola varieties have performed better than the imported varieties at multiplications in the country under difference agro ecological condition and these local varieties are fully acclimatized to local environment. Local Canola seed production has resulted in self-sufficiency in canola seed requirements of the county and now no Canola seed is being imported in Pakistan by public or private sectors. Local Canola seed production has resulted in reduced cost of the seed benefiting the formers.

Material and Methods

The present study was conducted in the experimental area of The Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year 2007-

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08. Four genotypes were sown namely Range, Dunkald, Venguard and RAS-3589 and were crossed in 4×4 diallel fashion. The data of all the characters were recorded and subjected to analysis of variance techniques (Steel *et al.* 1997) to see whether the genotypic effects among the hybrids and their parents were significant. Significantly varying genotypes were subjected to the analysis of simple additive-dominance model. The characters, which showed significant genotypic differences were analyzed using diallel cross technique (Hayman, 1954a, b and Jinks, 1954). Adequacy of the genetic model to the data set was determined using a scaling test, known as regression coefficient (b) analysis. According to (Hayman 1954a, b), regression coefficient (b) must deviate significantly from zero, but not from unity if all the assumptions under the model were fulfilled. To carry out the genetic analysis, the data of each character was presented in the form of diallel table taking the mean of direct and reciprocal crosses, assuming that reciprocal differences are not significant. From the diallel table, variance (Vr) of each array and covariance (Wr) of parents with the non-recurrent parental means were calculated.

Results and Discussion

The combined ANOVA (Table 1) indicated that all of the characters had significant mean sum of squares. The significant genotypic mean sum of squares allowed the use of simple additive dominance model for analyzing the data according to Hayman (1954 a, b) and Jinks (1954). Adequacy of the simple additive dominance model to the data sets was determined using one of the scaling tests i.e. joint regression analysis and regression coefficients (b) of each of the character (Table 2). According to Table 2 significant mean squares due to differences between the arrays (Wr+Vr) signified the presence of dominance for days taken to flowering, days taken to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, 100-seed weight, seed yield per plant, oil contents and non significant differences within the array (Wr-Vr) showed the absence of epistasis in primary branches per plant, secondary branches per plant, number of siliqua per plant and 100-seed weight while significant for other traits. It means that additive dominance model was adequate by both the tests. Whereas, the significant differences between the arrays (Wr+Vr) and within the arrays (Wr-Vr) revealed the inter allelic interaction in the inheritance of number of primary branches per plant, number of

secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, 100-seed weight, seed yield per plant and oil contents. Similar results were also found by Tukamuhabwa *et al.* (2002). Additive dominance model was adequate by both the tests. It is partially adequate for the other traits. The non significant differences between the arrays (Wr+Vr) suggested the presence of dominant and absence of epistasis. It means that model is fully adequate for genetic analysis. According to Hayman (1954a, b), regression coefficient (b) must deviate significantly from zero but not from unity. Scaling test showed that regression coefficient of days taken to flowering ($b=1.067 \pm 0.082$), days taken to maturity ($b=1.025 \pm 0.109$), plant height ($b=0.965 \pm 0.209$), number of primary branches per plant ($b=1.03 \pm 0.122$), number of secondary branches per plant ($b=1.247 \pm 0.143$), number of siliqua per plant ($b=0.872 \pm 0.131$), number of seeds per siliqua ($b=1.038 \pm 0.138$), 100-seed weight ($b=0.861 \pm 0.303$), seed yield per plant ($b=1.152 \pm 0.096$) and oil contents ($b=1.01 \pm 0.0117$) deviated significantly from zero and not from unity, suggesting that the data on these characters were fit for genetic analysis. Additive dominance model was shown inadequate by both the tests. It was partially adequate for the other traits. The non significant differences between the arrays (Wr+Vr) suggested the presence of dominant and absence of epistasis in the inheritance of 100-seed weight. It suggested that the model was fully adequate for genetic analysis. Similar results were found by Zhang and Zhou (2006). The distribution of genotypic values in Fig.1 revealed that Vanguard being farthest from the origin carried maximum number of recessive genes for days taken to flowering, while Range and RAS-3589 were nearer to the origin and so they had maximum number of dominant genes. Dunkled had moderate number of dominant and recessive genes. Additive effects were found by Kant and Gulati (2001). The Fig.2 revealed that RAS-3589 being farthest from the origin carried maximum number of recessive genes for days taken to maturity, while Range and Dunkled were nearer to the origin and so they had maximum number of dominant genes. Vanguard had moderate number of dominant and recessive genes. Fig.3 revealed that Range being farthest from the origin carried maximum number of recessive genes for days taken to flowering, while Vanguard, Dunkled and RAS-3589 were nearer to the origin and so they had maximum number of dominant genes. More additive effects were also found by Kant and Gulati (2001). The Fig.4 revealed that Range being farthest from the

origin carried maximum number of recessive genes for number of primary branches per plant, while Vanguard were nearer to the origin had maximum number of dominant genes. Dunkled and RAS-3589 had moderate number of dominant and recessive genes. Fig.5 revealed that RAS-3589 being farthest from the origin carried maximum number of recessive genes for number of secondary branches per plant while Vanguard, Dunkled and Range had moderate number of dominant and recessive genes. Additive effects were also found by Kant and Gulati (2001). The Fig.6 revealed RAS-3589 and Vanguard being farthest from the origin carried maximum number of recessive genes for number of siliqua per plant, while Range and Dunkled had moderate number of dominant and recessive genes. Similar results were found by Ghosh and Gulati (2001). Fig.7 revealed Vanguard being farthest from the origin carried maximum number of recessive genes for number of secondary branches per plant, while RAS-3589, Dunkled and Range had moderate number of dominant and recessive genes. Fig.8 revealed that Vanguard being farthest from the origin carried maximum number of recessive genes for 100-seeds weight, while Dunkled and Range were nearer to the origin had more number of dominant genes but Range had more as compared to Dunkled and RAS-3589 had moderate number of dominant and recessive genes. Similar results were found by Tanaka and Niikura (2006) for physiological traits and head formation in cabbage. The Fig.9 revealed that RAS-3589 that being farthest from the origin carried maximum number of recessive genes for seeds yield per plant while leading Dunkled with less number of recessive genes, while Range and Vanguard were nearer to the origin and had more number of dominant genes but Vanguard had more as compared with Range. Fig.10 revealed that RAS-3589 being farthest from the origin carried maximum number of recessive genes for oil contents, while Range and Vanguard have moderate type of gene action with recessive and dominant gene proportions and Dunkled has more number of dominant genes as nearer to the origin and similar results were found by Oghan, *et al.* (2007). The relative magnitude of components of variation as mentioned in Table 3 revealed that the value for D was higher for NSP (953.445), OC (15.646), DTF (11.841), DTM (9.835), PH (9.512) and SYP (7.136), while low for other parameters but higher than that of the values of H_1 and H_2 indicating that traits are controlled by the genes which have maximum number with additive effects and the maternal effects were low conformed

from the values of $H_2/4 H_1$ which are less than 0.25 but the value of $H_2/4 H_1$ for number of seeds per siliqua was 0.315 which indicated that there are maternal effects also, so the selection on the basis of number of seeds per siliqua can mislead in future breeding programs. Average degree of dominance was achieved by $\sqrt{H_1/D}$ which was less than 1 indicating partial dominance type of gene action controlling variation in all traits but it was 1.226 for number of primary branches and indicated that it was controlled by over dominance type of gene action. Direction of dominance h^2 for DTF (1.276), DTM (2.194) and for PH (0.727) is positive that which indicated the direction of dominance is more frequent towards the better parent for these traits but negative for the other traits indicated that the direction of dominance is less frequent towards the better parents. The value of F for all the traits indicated that the number of dominant genes is greater as compared to the number of recessive genes in the parents, and this was verified by $\sqrt{4H_1D+F}\sqrt{4H_1D-F}$ which was less than F. The estimation of narrow sense heritability was higher for the traits DTF (78.32%), OC (77.40%), SYP (76.60%), NSS (75.80%) and for NSP it was 75.10% for F_1 but broad sense heritability for DTF (83.53%), SYP (79.50%), OC (72.00%) and for PH was 71.80%. The higher value of heritability indicated that the selection on the basis of following traits in phenotypes can be effective and be helpful in selection of high yielding genotypes. Similar results were obtained by Sharma (1987), Sheikh and Singh (1998) and Khan *et al.* (2006).

All of the above results showed that for the plant traits involving more additive type of gene action in their inheritance pattern, simple selection procedure would be useful for their improvement, whereas the traits having partial dominance type of gene action might be considered when heterosis is to be exploited in appropriate improvement programme.

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Table 1. Combined ANOVA

| <i>SOURCE</i> | <i>D.F</i> | <i>DTF</i> | <i>DTM</i> | <i>PH</i> | <i>NPB</i> | <i>NSB</i> | <i>NSP</i> | <i>NSS</i> | <i>HSW</i> | <i>SYP</i> | <i>OC</i> |
|--------------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|-----------|
| Rep. M.S.S | 2 | 1.39 | 11.4 1* | 6.39* | 0.15 | 2.58* | 361.5* | 0.06 | 0.81 | 2.77* | 3.96* |
| Gen. M.S.S | 15 | 16.66* | 21.3 7* | 14.56* | 0.73* | 2.60* | 4279.3* | 4.91* | 1.06* | 6.20* | 21.06* |
| Error M.S.S | 30 | 2.44 | 8.79 | 3.22 | 0.35 | 0.78 | 630.3* | 1.22 | 0.26 | 1.17 | 5.09 |
| Total | 47 | | | | | | | | | | |

* = Significant, Rep. = Replication, Gen. = Genotypes.

DTF = Days taken to flowering DTM = Days taken to maturity, PH = Plant height, NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliqua per plant, NSS = Number of seeds per siliqua, HSW = 100-seed weight, SYP = Seed yield per plant and OC = Oil contents.

Table 2. Scaling Test (Joint regression analysis) of 10 plant characters of *Brassica napus* (Canola)

| Characters | b | b=0 | b=1 | Wr+Vr | Wr-Vr |
|-------------------|-------------|------------|----------------------|---------------------|---------------------|
| DTF | 1.067±0.082 | 13.029* | -0.814 ^{NS} | 8.705** | 2.238* |
| DTM | 1.025±0.109 | 9.324* | -0.229 ^{NS} | 10.674** | 2.501* |
| PH | 0.965±0.209 | 4.619* | 0.166 ^{NS} | 6.865* | 1.079* |
| NPB | 1.03±0.122 | 8.403* | -0.239 ^{NS} | 0.212 ^{NS} | 0.066 ^{NS} |
| NSB | 1.247±0.143 | 8.717* | -1.732 ^{NS} | 1.205* | 0.406 ^{NS} |
| NSP | 0.872±0.131 | 6.664* | 0.979 ^{NS} | 976.586** | 230.528** |
| NSS | 1.038±0.138 | 7.507* | -0.272 ^{NS} | 2.434* | 0.709 ^{NS} |
| HSW | 0.861±0.303 | 2.843* | 0.459 ^{NS} | 0.228 ^{NS} | 0.022 ^{NS} |
| SYP | 1.152±0.096 | 11.945* | -1.574 ^{NS} | 4.166* | 1.418* |
| OC | 1.01±0.0117 | 8.563* | -4.071 ^{NS} | 11.123** | 3.643* |

DTF = Days taken to flowering DTM = Days taken to maturity, PH = Plant height, NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliqua per plant, NSS = Number of seeds per siliqua, HSW = 100-seed weight, SYP = Seed yield per plant and OC = Oil contents.



Table 3. Genetic components for different quantitative parameters in *Brassica napus* (Canola)

| Components | DTF | DTM | PH | NBP | NSB | NSP | NSS | HSW | SYP | OC |
|---|------------|------------|-----------|------------|------------|------------|------------|------------|------------|-----------|
| D | 11.841 | 9.835 | 9.512 | 0.187 | 1.660 | 953.445 | 3.335 | 0.204 | 7.136 | 15.646 |
| F | 2.768 | -3.006 | 4.538 | -4.416 | 0.466 | -255.748 | 0.854 | 2.849 | 3.626 | 3.824 |
| H₁ | 1.426 | -5.683 | 3.095 | -0.282 | -0.516 | -346.00 | -0.208 | -6.304 | 0.683 | -2.018 |
| H₂ | 1.231 | -4.139 | 2.389 | -0.227 | -0.447 | -261.462 | -0.262 | -5.414 | 0.299 | -1.591 |
| h² | 1.276 | 2.194 | 0.727 | -0.103 | -0.276 | -175.825 | -0.309 | -0.083 | -0.391 | -0.322 |
| E | 0.974 | 3.675 | 1.402 | 0.137 | 0.368 | 251.556 | 0.470 | 0.119 | 0.521 | 2.063 |
| √H₁/D | 0.347 | 0.760 | 0.750 | 1.226 | 0.557 | 0.602 | 0.249 | 0.556 | 0.309 | 0.359 |
| H₂/4 H₁ | 0.216 | 0.182 | 0.192 | 0.202 | 0.217 | 0.189 | 0.315 | 0.215 | 0.109 | 0.197 |
| √4H₁D+F√4H₁D-F | 2.016 | 0.665 | 2.438 | 0.825 | 1.672 | 0.636 | 3.107 | 1.287 | 10.193 | 2.031 |
| Narrow sense heritability | 0.783 | 0.681 | 0.587 | 0.525 | 0.688 | 0.751 | 0.758 | 0.440 | 0.766 | 0.774 |
| F₁ | | | | | | | | | | |
| Broad sense heritability | 0.835 | 0.557 | 0.710 | 0.188 | 0.551 | 0.664 | 0.718 | 0.369 | 0.795 | 0.720 |

* If the value divided by its standard error exceeds 1.96 then it is significant

D = Additive gene effects, H₁ and H₂ = dominance effects of genes, F = Frequency of dominant alleles h² = Direction of dominance, E = Environmental components, DTF = Days taken to flowering DTM = Days taken to maturity, PH = Plant height, NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, NSP = Number of siliqua per plant, NSS = Number of seeds per siliqua, HSW = 100-seed weight, SYP = Seed yield per plant and OC = Oil content

Fig-1: Vr/Wr graph for days taken to flowering

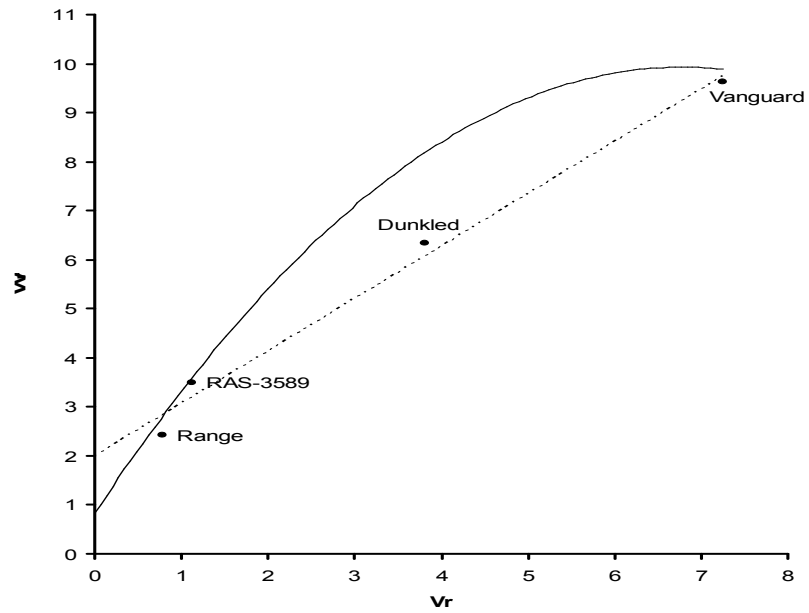


Fig-2: Vr/Wr graph for days taken to maturity

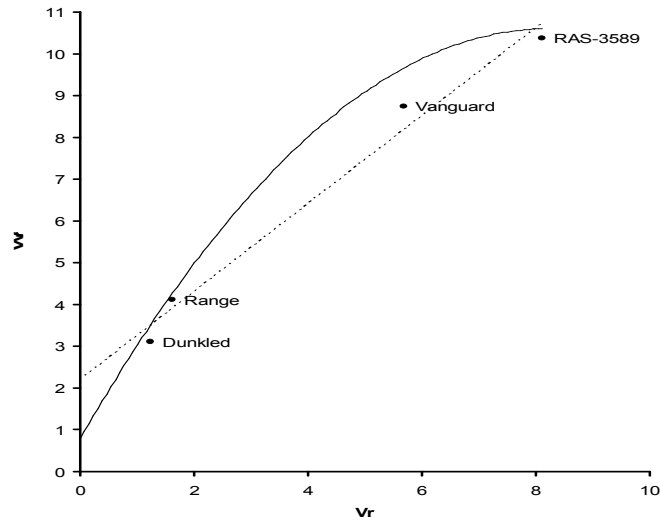


Fig-3: Vr/Wr graph for plant height

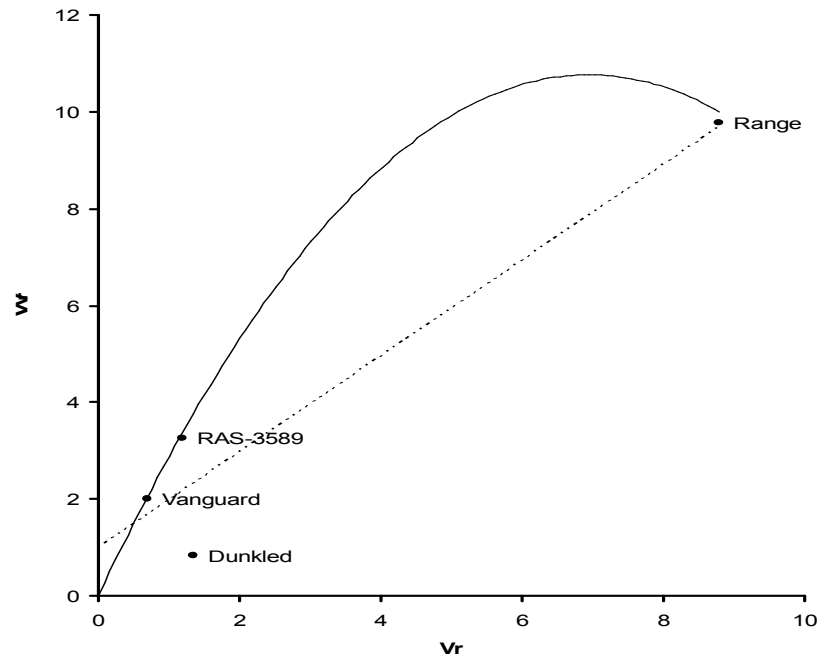


Fig-4: Vr / Wr graph for number of primary branches per plant

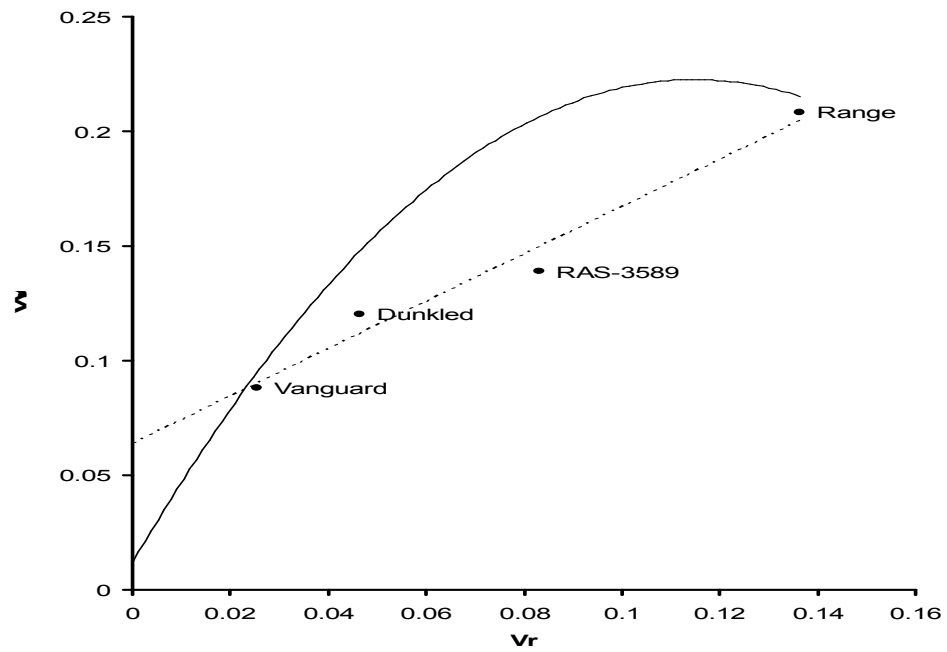


Fig.5 Vr/Wr graph for number secondary branches per plant

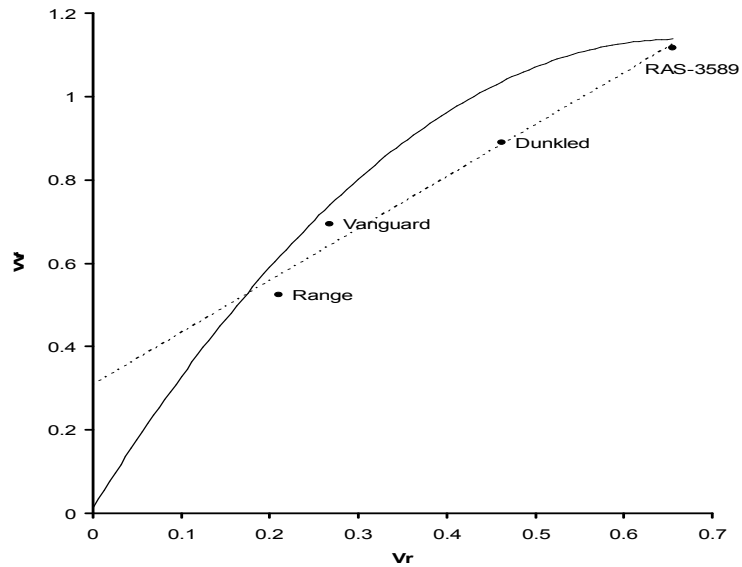


Fig. 6 Vr/Wr graph for Number of siliqua per plant

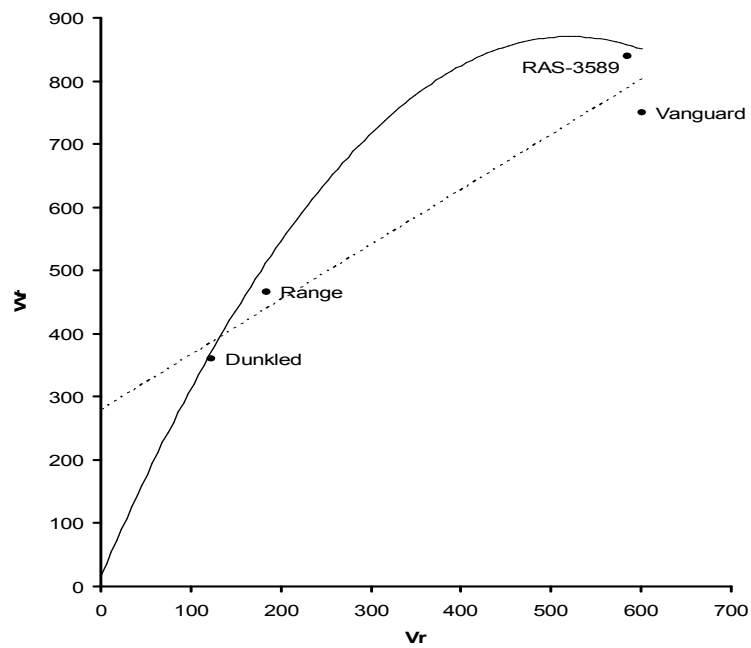


Fig. 7 Vr/Wr graph for Number of seeds per siliqua

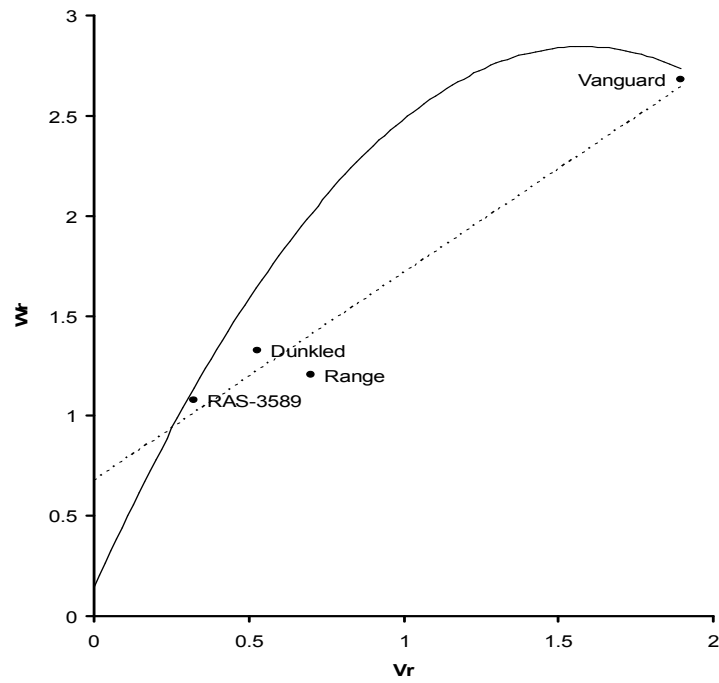


Fig. 8 Vr/Wr graph for 100-seed weight

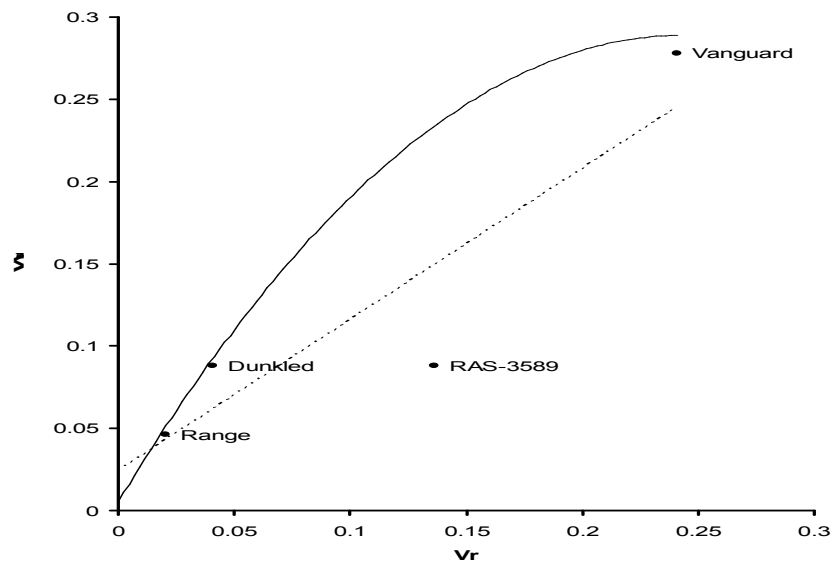


Fig.9: Vr/Wr graph for seed yield per plant

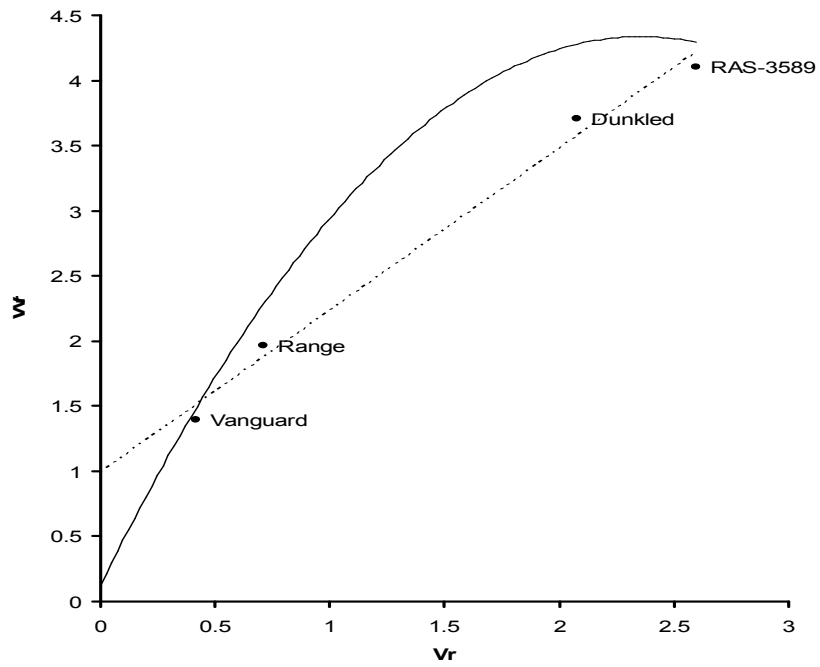


Fig. 10 Vr/Wr graph for oil contents

