

Identification of stable oat wild relatives among *Avena* species for seed and forage yield components using joint regression analysis

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ABSTRACT

Crop wild relatives are a good source of useful alleles for climate change adaptation. In present investigation, seven oat wild relatives (OWRs) including different *Avena* species tested against one commercial check of cultivated species *A. sativa* across three consecutive cropping seasons (Rabi 2018-19 to 2020-21) prevalent in North-western Himalayas at CSKHPKV, Palampur. Stability analysis was performed using Eberhart and Russell model for sixteen seed, forage yield and quality attributes. The mean squares for GE interaction were significant for most of the traits indicating differential response of genotypes to different environments. Both linear and non-linear components significantly contributed to genotype \times environment interactions. Higher mean over commercial check, above average responsiveness with wider adaptable or stable genotypes identified were HFO 103 (*A. orientalis*) for seeds per panicle, HFO 498 (*A. longiglumis*) for harvest index and all the genotypes for protein content. Thus, these selected OWRs found stable and well adapted to all the types of climatic conditions of humid sub-temperate climate could be exploited in future breeding programme.

Keywords: *Avena sativa*, oat, regression analysis, stability

INTRODUCTION

Oat is an economically important crop and ranks sixth in world cereal production after wheat, maize, rice, barley and sorghum. It is used as green fodder, straw, hay or silage. In India, oat is cultivated in Himalayan states like Punjab, Haryana, Uttar Pradesh, Madhya Pradesh, Kashmir, Himachal Pradesh, some parts of Maharashtra and Uttarakhand. Oats in these regions have a wider adaptability because of its excellent growing habitat, quick re-growth, better nutritional value with drought and cold tolerance ability. Oat landraces and wild relatives are the good sources of beneficial untapped alleles for favor against climate change (Kumar *et al.* 2022). Wider adaptability is the ultimate goal of plant breeders in crop improvement program usually tested by the degree of genotypes interaction with different environments under which it is planted. Predictable response can be minimized applying better management practices but cannot unpredictable responses such as climate change, biotic, abiotic and excessive effects of nutritional components such as salt, mineral toxicity etc. A variety or genotype is considered to be more adaptive or stable in diverse

environments whereas wild relatives are considered as more adaptive or stable in concerned environment. Regression based model (Eberhart and Russell, 1966) is most commonly used has in various crops based on three parameters such as mean, regression and deviation from linearity. Thus the present investigation was undertaken to identify the stable oat wild relatives (OWRs) for both grain and forage yield attributes.

MATERIALS AND METHODS

The experiment was conducted for three consecutive years from Rabi 2018-19 to 2020-21 at Experimental Farm of the Fodder Section, CSK HPKV, Palampur which is represents the mid-hill zone of Himachal Pradesh (Zone-II) and is characterized by humid sub-temperate climate with high rainfall (2500 mm). The soil is acidic in nature with pH ranging from 5.0 to 5.6 and soil texture is silty clay loam. The experimental material comprised of seven OWRs which contributed three diploid species *viz.*, *Avena orientalis* (HFO-103), *A. longiglumis* (HFO-498) and *A. strigosa* (HFO-505), one tetraploid species *i.e.* *A. barbata* (HFO-58) and three hexaploid *Avena* species namely, *A. byzantina*

(HFO-60), *A. sterilis* (HFO-508 and HFO-878) along with commercial check variety HJ-8 (*A. sativa*) were evaluated in randomized complete block design with three replications. Each genotype was grown in two rows of one meter length with 25 × 10 cm spacing. The data was recorded on five randomly selected competitive plants in each replication on sixteen traits *viz.*, days to 50% flowering, days to 75% maturity, plant height, number of leaves per plant, number of tillers per plant, flag leaf area, spikelets per panicle, harvest index, seed yield per plant, biological yield per plant, protein content (%), dry matter yield per plant, test weight, leaf: stem ratio, seed length and green fodder yield per plant. Data were subjected to stability analysis according to Eberhart and Russell (1966) using OPSTAT software (Sheoran *et al.* 1998) and SPAR 3.0.

RESULTS AND DISCUSSION

Pooled analysis of variance

The pooled analysis of variance (Table 1) showed significant differences among the genotypes for most of the traits studied except number of leaves per plant, leaf: stem ratio, dry

matter yield per plant, seeds per panicle, seed yield per plant, biological yield per plant, test weight and harvest index, Whereas significant differences were observed among the environments for most of the traits except leaf area, harvest index, test weight and seeds per panicle which revealed that there was considerable variation present among both the genotypes and environments. Similar findings for genotypic and environmental variation under different environments were also observed by Devi *et al.* (2019) in oat. The mean squares for Genotype × Environment (GE) interaction were significant for most of the traits except days to 75% maturity and protein content indicating differential response of genotypes to different environments. A non significant GE interaction difference adequately describes potentials of environments and performance of genotype. Variance due to G×E (linear) was significant for the traits *viz.*, plant height, leaf: stem ratio, seeds per panicle, seed length and protein content revealed that the major component for differences in stability was due to linear regression and the performance can be predicted with some reliance under different environments for these traits.

Table 1: Joint regression analysis of variance for seed, fodder and quality traits over environments

| Source of variation | df | PH | LPP | TPP | DTF | GFY | LSR | DMY | LA |
|---------------------|----|-----------|-----------|----------|------------|-----------|---------|----------|---------|
| Genotype | 7 | 119.46* | 39.48 | 5.10* | 120.44* | 482.96 | 0.007 | 55.1 | 155.23* |
| Environment | 2 | 2457.90* | 827.69* | 15.59* | 56.71* | 2744.36* | 0.125* | 138.89* | 6.19 |
| GxE | 14 | 23.64* | 30.19* | 1.77* | 14.85* | 307.57* | 0.004* | 23.23* | 14.60* |
| E+GxE | 16 | 327.93* | 129.88 | 3.5 | 20.08 | 612.17* | 0.019* | 37.69 | 13.55 |
| Env (Linear) | 1 | 4915.79** | 1655.39** | 31.19** | 113.43** | 5488.72** | 0.250** | 277.77** | 12.38 |
| E x G (Linear) | 7 | 37.83* | 17.53 | 2.09 | 19.89 | 389.88 | 0.008* | 30.25 | 14.47 |
| Pooled Deviation | 8 | 8.27 | 37.49 | 1.27 | 8.58 | 197.1 | 0.001 | 14.18 | 12.88* |
| Pooled Error | 42 | 8.45 | 8.12 | 0.74 | 6.82 | 58.18 | 0.001 | 5.17 | 5.42 |
| Source of variation | df | DM | SPP | SYP | BYP | TW | SL | HI | PC |
| Genotype | 7 | 101.39* | 180.41 | 28.7 | 440.66 | 17.69 | 2.82* | 29.18 | 2.20* |
| Environment | 2 | 57.35* | 308.9 | 299.51** | 6709.62** | 32.42 | 1.53* | 31.4 | 6.62** |
| GxE | 14 | 12.69 | 136.97** | 27.65** | 265.43** | 11.91** | 0.37* | 21.95** | 0.38 |
| E+GxE | 16 | 18.27** | 158.46 | 61.63* | 1070.95 | 14.47** | 0.51 | 23.13 | 1.16** |
| Env (Linear) | 1 | 114.70** | 617.79** | 599.02** | 13419.23** | 64.84** | 3.06** | 62.80* | 13.24** |
| E x G (Linear) | 7 | 18.03 | 260.86** | 29.3 | 181.67 | 15.75 | 0.65** | 28.12 | 0.68** |
| Pooled Deviation | 8 | 6.43 | 11.44 | 22.75* | 305.53* | 7.05* | 0.07 | 13.81* | 0.08 |
| Pooled Error | 42 | 7.86 | 8.52 | 2.73 | 8.39 | 1.24 | 0.17 | 3.4 | 0.28 |

*Significant at $P < 0.05$; **Significant at $P < 0.01$

Note: PH, Plant height; LPP, Leaves per plant; TPP, Tillers per plant; DTF, Days to 50% flowering; GFY, Green fodder yield per plant; LSR, Leaf: stem ratio; DMY, Dry matter yield per plant; LA, Leaf area; DM, Days to 75% maturity; SPP, Spikelets/panicle; SYP, Seed yield/ plant; BYP, Biological yield/ plant; TW, Test weight; SL, Seed length; HI, Harvest index; PC, Protein content (%)

Similarly, significant mean squares due to pooled deviation or non-linear component of G×E interaction suggested that the deviation from linear regression also contributed substantially towards the difference in stability of genotypes for leaf area, seed yield per plant, biological yield per plant, test weight and harvest index. Thus, both linear (predictable) and non-linear (unpredictable) components significantly

contributed to genotype × environment interactions observed for the traits studied but with the predominance of the former component suggesting that the performance of genotype across environments could be predicted with greater precision. The results are in accordance of the findings were reported by Mehraj *et al.* (2017) and Devi *et al.* (2019).

Table 2: Estimates of stability parameters for seed, fodder and quality traits in oat

| Genotypes | PH | | | LPP | | | TPP | | | DTF | | |
|-----------|---------|-------|------------------------------|--------|-------|------------------------------|---------|--------|------------------------------|---------|---------|------------------------------|
| | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | B | S ² _{di} |
| HFO 58 | 132.61 | 1.05 | -6.84 | 37.00 | 0.57 | -7.68 | 9.78 | 0.47 | 1.14* | 132.89 | 1.28 | -6.74 |
| HFO 60 | 129.06 | 1.12 | 21.49 | 40.56 | 0.52 | 131.74* | 10.61 | 1.79 | -0.69 | 137.50 | -0.20 | -6.22 |
| HFO 103 | 128.33 | 0.56 | -7.20 | 38.19 | 1.21 | 37.77* | 9.67 | 1.55 | -0.54 | 126.56* | 0.11 | 33.52* |
| HFO 498 | 119.11 | 0.90 | -5.66 | 42.17 | 1.12 | 30.45* | 12.44* | 1.92 | 2.71* | 126.11* | 0.14 | 18.29 |
| HFO 505 | 135.92 | 0.93 | -6.20 | 40.37 | 1.22 | 3.86 | 11.11 | -0.13 | 2.38* | 120.17* | 0.20 | -6.22 |
| HFO 508 | 118.22* | 1.24 | 7.73 | 47.63 | 1.25 | -4.15 | 11.94* | 0.37 | 0.43* | 136.5 | 3.26* | -6.70 |
| HFO 878 | 131.28 | 1.36 | -0.33 | 38.37 | 1.07 | 49.81* | 8.89 | 0.96 | -0.47 | 136.78 | 2.00* | -6.82 |
| HJ 8 | 124.67 | 0.85 | -4.44 | 36.28 | 1.05 | -6.82 | 9.14 | 1.08 | -0.73 | 134.42 | 1.22 | -5.03 |
| GM | 127.40 | | | 40.07 | | | 10.445 | | | 131.37 | | |
| CD | 5.79 | | | 12.36 | | | 2.28 | | | 5.91 | | |
| Genotypes | DMY | | | LA | | | SPP | | | HI | | |
| | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | B | S ² _{di} |
| HFO 58 | 29.83 | 0.04 | -0.82 | 28.88 | -1.00 | -3.48 | 67.64 | 3.76* | -6.79 | 27.59 | 2.84 | 4.09 |
| HFO 60 | 32.96 | 0.62 | -2.16 | 33.15 | 6.53 | 7.10 | 66.94 | 0.87 | -7.18 | 27.49 | -1.14 | -3.14 |
| HFO 103 | 34.69* | 0.41 | 40.08* | 48.82* | 0.001 | 59.65* | 74.35* | 2.74* | -7.79 | 24.67 | 0.88 | 11.15* |
| HFO 498 | 33.53* | 0.68 | 1.51 | 27.68 | 0.36 | 0.54 | 60.13 | 1.42 | 37.96 | 33.27* | -1.93* | -3.28 |
| HFO 505 | 34.23* | 2.65 | -0.18 | 35.70 | -2.05 | -5.28 | 51.32 | -2.32* | -5.78 | 25.59 | 0.72 | -1.65 |
| HFO 508 | 26.00 | 1.75 | 4.63 | 26.80 | 4.97 | 8.15 | 53.29 | 0.29 | -5.57 | 24.75 | 3.82 | 75.59* |
| HFO 878 | 24.34 | 1.73 | 12.28 | 30.11 | -0.85 | -3.76 | 64.62 | 1.34 | -7.56 | 23.33 | 1.71 | 0.70 |
| HJ 8 | 25.58 | 0.13 | 16.75* | 29.25 | 0.04 | -3.27 | 66.67 | -0.09 | 26.10* | 24.83 | 1.09 | -0.18 |
| GM | 30.14 | | | 32.55 | | | 63.12 | | | 26.44 | | |
| CD | 7.59 | | | 7.25 | | | 6.82 | | | 7.5 | | |
| Genotypes | GFY | | | LSR | | | SYP | | | BYP | | |
| | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | b | S ² _{di} |
| HFO 58 | 132.56 | 0.50* | -57.75 | 0.39 | 1.17 | 0.0001 | 25.56 | 1.25 | 5.03 | 118.48 | 1.08 | -8.12 |
| HFO 60 | 131.31 | 1.47 | 331.59* | 0.42 | 0.16* | 0.0001 | 27.59 | 1.55 | -1.92 | 96.02 | 1.06 | 65.03* |
| HFO 103 | 144.00* | 0.03 | 279.41* | 0.33 | 1.02 | 0.0001 | 27.73 | 0.54 | 44.25* | 104.57 | 1.47 | 719.97* |
| HFO 498 | 114.28 | 0.79 | -24.25 | 0.36 | 1.40 | 0.0001 | 27.81 | 1.87* | -2.71 | 82.36 | 0.90 | 109.64* |
| HFO 505 | 126.45 | 2.20 | 90.38 | 0.40 | 1.62* | 0.0001 | 27.88 | 1.34 | 11.81* | 109.88 | 1.23 | 260.23* |
| HFO 508 | 108.85 | 0.78* | -58.09 | 0.32 | 0.65 | 0.0001 | 22.94 | 0.36 | 36.48* | 88.02 | 0.49 | 53.11* |
| HFO 878 | 118.63 | 1.83 | 567.43* | 0.42 | 1.43 | 0.001* | 20.44 | 0.06 | 68.59* | 89.43 | 0.59 | 1169.04* |
| HJ 8 | 108.22 | 0.40 | -17.42 | 0.30 | 0.55* | 0.0001 | 21.60 | 1.03 | -1.38 | 96.20 | 1.19 | 8.25 |
| GM | 123.04 | | | 0.37 | | | 25.19 | | | 98.12 | | |
| CD | 28.34 | | | 1.06 | | | 9.62 | | | 35.27 | | |
| Genotypes | TW | | | SL | | | DM | | | PC | | |
| | Mean | B | S ² _{di} | Mean | b | S ² _{di} | Mean | b | S ² _{di} | Mean | b | S ² _{di} |
| HFO 58 | 35.00 | -0.30 | 8.03* | 14.02* | -0.14 | -0.16 | 170.67 | 1.19 | -7.58 | 10.35* | 0.75** | -0.10 |
| HFO 60 | 38.87 | 1.21 | 9.70* | 14.99* | -0.24 | -0.14 | 175.28 | -0.93 | -7.14 | 9.52* | 1.37** | -0.28 |
| HFO 103 | 36.19 | -0.99 | 10.06* | 15.12* | 2.29 | -0.15 | 164.33* | 1.23 | 10.60 | 9.14* | 0.70** | -0.08 |
| HFO 498 | 37.30 | 2.43 | 0.33 | 14.00* | -0.15 | -0.16 | 166.89* | 1.75 | 12.46 | 10.39* | 0.64** | -0.17 |
| HFO 505 | 36.49 | -0.14 | 2.02 | 13.99* | -0.30 | -0.13 | 159.16* | 2.17 | -6.06 | 10.15* | 1.28** | -0.16 |
| HFO 508 | 40.90 | 2.85 | 9.25* | 13.27 | 1.77 | 0.27 | 172.50 | 2.27* | -7.84 | 9.22* | 2.07** | -0.28 |
| HFO 878 | 41.66 | 0.88 | -1.12 | 12.17 | 2.34* | -0.17 | 174.67 | 0.29 | 1.79 | 9.32* | 1.25** | -0.27 |
| HJ 8 | 40.11 | 2.06 | 8.23* | 13.17 | 2.44* | -0.17 | 174.64 | 0.02 | -7.63 | 7.78 | -0.07** | -0.26 |
| GM | 38.32 | | | 13.84 | | | 169.77 | | | 9.48 | | |
| CD | 5.36 | | | 0.51 | | | 5.11 | | | 0.57 | | |

*Significant at $P < 0.05$; **Significant at $P < 0.01$

Stability analysis

The stability parameters (mean, b_i and S^2_{di}) for all the traits were carried out (Table 2). Characters namely, days to 50 % flowering, seeds per panicle, harvest index, green fodder yield per plant, leaf: stem ratio, seed yield per plant, days to 75 % maturity and protein content % were favorable environment responsiveness ($b_i > 1$) for respective genotypes while, the regression coefficient (b_i) of all genotype was not significantly different from unity ($b_i < 1$) which indicated there is no high responsiveness of any genotype across the environments for the character namely, plant height, number of leaves per plant, number of tillers per plant, dry matter yield per plant, leaf area, biological yield per plant, test weight and seed length under studied. According to regression model of stability proposed by Eberhart and Russell (1966), higher mean, b_i is considered as unit parameter of response and S^2_{di} indicates instability due to the deviation from zero. Higher mean over commercial check, above average responsiveness with wider adaptable or stable genotypes identified were HFO 103 for seeds per panicle, HFO 498 for harvest index and all the genotypes for protein content. For plant height, mean values ranged from 118.22-135.92 g with average value of 127.40 g and only one genotype HFO 498 was found stable and nearly unit regression coefficient (b_i) (1.24) so this trait may suitable across all environmental conditions.

For the major character *i.e.* green fodder yield, mean values ranged from 108.22-144.00 g with average value of 123.04 g and only two genotypes namely HFO 60 (*A. byzantina*) and HFO 508 (*A. sterilis*) were found stable with linearity response and zero deviation from regression (Table 1) while, mean values for seed yield per plant ranged from 20.44-27.88 g with average value of 25.19 g and only one genotype HFO 498 was found stable with linearity response and zero deviation from regression. Genotypes possess less than one, non

significant and negative regression coefficient (b_i) value with zero deviation from regression for these traits so these may be grown only in poor environment. Cultivated species HJ-8 (*A. sativa*) for seed yield per plant showed unit regression coefficient ($b_i = 1$) and non significant deviation from regression value indicating the suitability of the genotype under across all environments of NW Himalayas however, mean value across the environments was statistically at par over population mean. Thus the present results indicated that there was sufficient variation for performance of the genotypes under different environments. This was also in confirmation with the findings of Singh *et al.* (2019), Mehraj *et al.* (2017) and Devi *et al.* (2019) in haploid oat; Naheed and Rahman (2021) in bread wheat; Bouchareb and Guendouz (2022); Hussain *et al.* (2022) in durum wheat where the genotypes showed varied response with the changing environments, accepting existence of genetic variability among the genotypes.

In conclusion, it may be stated that the mean squares for GE interaction were significant for most of the traits except days to 75 % maturity and protein content. A non significant GE interaction difference adequately describes potentials of environments and performance of genotype. Variance due to G x E (linear) was significant for the traits *viz.*, plant height, leaf: stem ratio, seeds per panicle, seed length and protein content. Characters namely days to 50 % flowering, seeds per panicle, harvest index, green fodder yield per plant, leaf: stem ratio, seed yield per plant, days to 75 % maturity and protein content were favorable environment responsiveness ($b_i > 1$) for respective genotypes. Higher mean over commercial check, above average responsiveness with wider adaptable or stable genotypes identified were HFO 103 for seeds per panicle, HFO 498 for harvest index and all the genotypes for protein content. For green fodder and seed yield, genotypes possess less than one, non significant and negative regression coefficient (b_i) value with zero deviation from regression for these traits.

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