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Genetic Trait Analysis of RIL Barley Genotypes to Sort-out the Top Ranked Elites for Advanced Yield Breeding Across Multi Environments of Tigray, Ethiopia

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Abstract : Barley (Hordeum vulgare L.) is one of the most important cereal crops in the world, grown for the poor farmers in Tigray with low yield production. The purpose of this research was to estimate the performance of 166 barley genotypes against the quantitative traits with detailed analysis of the variance component, heritability, genetic advance, and genetic usefulness parameters. The finding of ANOVA was highly significant variation (p ≤ 0.01) for all the genotypes. We found significant differences in coefficient of variance (CV of 15%) for 5 traits out of the 12 quantitative traits. The topmost broad sense heritability (H2) was recorded for seeds per spike (98.8%), followed by thousand seed weight (96.5%) with 79.16% and 56.25%, respectively, of GAM. The traits with H2 ≥ 60% and GA/GAM ≥ 20% suggested the least influenced by the environment, governed by the additive genes and direct selection for improvement of such beneficial traits for the studied genotypes. Hence, the 20 outstanding recombinant inbred lines (RIL) barley genotypes performing early maturity, high yield, and 1000 seed weight traits simultaneously were the top ranked group barley genotypes out of the 166 genotypes. These are; G5, G25, G33, G118, G36, G123, G28, G34, G14, G10, G3, G13, G11, G32, G8, G39, G23, G30, G37, and G26. They were early in maturity, high TSW and GYP (TSW ≥ 55 g, GYP ≥ 15.22 g/plant, and DTM below 106 days). In general, the 166 genotypes were classified as high (group 1), medium (group 2), and low yield production (group 3) genotypes in terms of yield and yield component trait analysis by clustering; and genotype parameter analysis such as the heritability, genetic advance, and genetic usefulness traits in this investigation.

Keywords: barley, clustering, genetic advance, heritability, usefulness, variability, yield

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