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## Identification of promising genotypes

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1 Works for me dx.doi.org/10.17504/protocols.io.984h9yw



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- 1 Average the yield data generated for genotypes across locations and years.
- 2 Perform the Welch's variance-weighted analysis of variance for studied genotypes (across years and locations), at each location (across genotypes and years) and for each year (across genotypes and locations) using One-Way ANOVA model of SAS University Edition version 3.8 with Levene test for homogeneity of variance and adopting Tukey comparison method.
- 3 Calculate mean genetic deviation in successive cycles
- 4 Corresponding above mean values facilitate the partitioning of promising genotypes, location and years



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