

Materials and Methods Summary

Experimental Material:

41 genotypes, including 5 check varieties. Genotypes listed with codes.

Experimental Design:

Randomized Block Design (RBD) with three replications per year (three environments).

Standard NPK fertilizer applied (50:30:30 kg/ha).

Plant spacing: 10 cm × 30 cm, thinning at 25 days after sowing.

Standard agronomic practices followed.

Traits Measured:

Days to maturity, Plant height (cm), Main raceme length (cm), Number of siliquae on main raceme, Siliqua density, Number of primary branches per plant, Siliqua length (cm), Number of seeds per siliqua, Oil content (%), 1000-seed weight (g), Seed yield (kg/ha)

Statistical Analyses:

Performed using R Studio (Variability 0.1.0 and Stability packages).

Procedures included:

Analysis of Variance (ANOVA) for genotype effects under RBD.

Estimation of variability parameters: PCV, GCV, ECV, heritability (broad sense), genetic advance.

Correlation coefficients: phenotypic, genotypic, environmental.

Path coefficient analysis to partition direct and indirect effects on seed yield.

Genetic divergence using Mahalanobis D^2 and Tocher's clustering method with estimation of inter- and intra-cluster distances and contribution of traits to divergence.

Stability analysis through:

Eberhart and Russell model (mean, regression coefficient, deviation from regression).

AMMI (Additive Main Effects and Multiplicative Interaction) model combining ANOVA and PCA, with biplot visualization and classification of genotypes by mean and interaction principal components.

GGE biplot analysis focusing on genotype and G×E interaction effects, enabling visualization of "which won where," mean vs stability, and environment discriminativeness/representativeness.

Multi-Trait Stability Index (MTSI) using weighted absolute scores from singular value decomposition of BLUPs for overall stability across multiple traits.

This methodical approach combines classical and multivariate statistical tools to robustly measure genetic variability, divergence, and stability in yellow sarson genotypes across diverse environments.