

Quantifying the Drivers of Genetic Change in Plant Breeding

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It has long been recognized that efficient use of genetic diversity is required within a breeding programme. A possible practice to maximize the diversity is by exchanging germplasm between programmes. However, there has been little research into how exchanging germplasm contributes to genetic mean and variance over time. This research aims to partition the genetic mean and variance according to germplasm origin over 60 years of maize-breeding. A single trait representing grain yield controlled by 3,000 QTLs uniformly distributed over ten chromosomes was simulated. Each QTL was assigned an additive and dominance genetic effect. Two germplasm exchange scenarios were defined as i) 0% and ii) 40% of the elite germplasm annually imported into the breeding programme (BP2) from an external source (BP1). We also simulated multiple locations and years to investigate genotype by environment interaction (GEI). Three scenarios of GEI were considered: i) no GEI within and across programmes (i.e. correlation of one), ii) low GEI within and across programmes and iii) high GEI within and across programmes. The results show that importing the external germplasm into BP2 most improved the genetic mean under no GEI, while it most improved genetic variance under high GEI. The partitioning methodology enabled quantifying the contribution of each origin to these trends. This research represents a significant step forward in quantifying the impact of germplasm exchange between breeding programmes on their genetic diversity.