

**Selection Signatures in CIMMYT's
International Elite Spring and
Semi-Arid Wheat Yield Trials**

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Abstract

Over the last four decades as part of the International Wheat Improvement Network, the International Maize and Wheat Improvement Center (CIMMYT) annually distributes germplasm to collaborators worldwide. The two most important yield trials distributed are the Elite Spring Wheat Yield Trial (ESWYT) for optimal (irrigated and high production) and the Semi-arid Wheat Yield Trial (SAWYT) for low rainfall conditions. Both trials target 45 million ha of wheat production area globally. The trials started in 1979 (ESWYT) and 1992 (SAWYT) and have almost three decades of shared history. All lines from these trials were genotyped with genotyping-by-sequencing markers to explore the selection footprints associated to improvement and adaptation of ESWYT and SAWYT germplasm. Population structure was uncovered using discriminant analysis of principal components and revealed moderate levels of admixture among sub-populations. The fixation index (F_{ST}) values for both trials increased with the time difference between years, suggesting the occurrence of genetic shifts over time, most likely because of selection. This genetic shift was higher in the SAWYT than in the ESWYT. The F_{ST} values between the two trials maximized between 2004 and 2006. Overall, we identified 9.8% of the genome under signatures of selection over time. A larger percentage (84%) reflected footprints of breeders' selection from early to the most recent trials, while (2%) of the genome could be associated to differences in allele frequency between the most recent ESWYT and SAWYT, which is expected to represent signatures of selection related to environmental adaptation. Some genomic regions showed a large concurrent parallel allele frequency change over time indicating low recombination events within these regions. We also visualized the expected position of key genes and QTL that breeders selected for or against to. The results showed several of the genes falling into the genomic regions with directional selection. Subsequent association studies involving phenotypic and genotypic data combined with detailed functional annotations can provide comprehensive understanding of temporal and environmental selection effects at the genome level. Consequently, such understanding has implications for the design of future breeding experiments.