



Genetic Diversity and Breeding Strategies for Tomato Improvement

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ABOUT THE STUDY

In Genetic diversity tomato originated from Latin America, where it was domesticated from wild cherry tomatoes that spread as weeds from the Andean region to Mexico. Italy and Spain are considered secondary centres of diversification for tomato.

Tomato has a high morphological diversity, with different fruit shapes, sizes, colours and flavours. However, it also suffers from genetic erosion and loss of variability due to domestication, breeding and population bottlenecks. This limits the potential of tomato to adapt to changing environmental conditions and consumer preferences, as well as to resist pests and diseases.

Therefore, it is essential to conserve and characterize the genetic diversity of tomato and its wild relatives, which constitute an important source of genes for breeding and genetic research. Tomato belongs to the *Lycopersicon* section of the genus *Solanum*, which comprises 13 species that can be divided into two groups: red-fruited (*S. lycopersicum*, *S. pimpinellifolium*, *S. cheesmaniae* and *S. galapagense*) and green-fruited (*S. chmielewskii*, *S. neorickii*, *S. peruvianum*, *S. corneliomulleri*, *S. arcanum*, *S. huaylasense*, *S. habrochaites* and *S. pennellii*).

These wild species have a wide range of adaptation to different habitats and climates, and possess valuable traits such as drought tolerance, salt tolerance, disease resistance and fruit quality. However, their utilization in breeding programs is hampered by reproductive barriers such as self-incompatibility, hybrid sterility and endosperm imbalance. Therefore, various techniques have been developed to overcome these barriers, such as embryo rescue, ploidy manipulation, interspecific hybridization and genetic transformation.

Another source of genetic diversity for tomato is represented by landraces, which are local varieties that have been cultivated by farmers for generations and have adapted to specific agro-ecological conditions. Landraces are rich in phenotypic variation and can provide useful traits for improving yield stability, stress

tolerance and consumer acceptance. However, their use in breeding programs is limited by the introduction of high-yielding modern cultivars that have replaced them in many regions.

To preserve the genetic diversity of tomato and its wild relatives, both *in situ* and *ex situ* conservation strategies are needed. *In situ* conservation involves maintaining the natural habitats where these species grow or supporting the traditional farming systems where landraces are cultivated. *Ex situ* conservation involves storing seeds or other plant materials in gene banks or cryopreservation facilities.

Gene banks are repositories where seeds are kept at low or freezing temperatures under controlled conditions to ensure their viability and genetic integrity over time. Cryopreservation is a technique that involves freezing plant tissues or cells in liquid nitrogen at -196°C to stop all metabolic processes and prevent deterioration. Both methods require proper documentation and characterization of the conserved germplasm to facilitate its access and utilization.

One way to characterize the genetic diversity of tomato germplasm is by using molecular markers, which are DNA sequences that can be detected by laboratory techniques and can reveal the genetic variation among individuals or populations. Molecular markers can be used for various purposes such as assessing genetic relationships among accessions or species; identifying genes or Quantitative Trait Loci (QTLs) associated with desirable traits; selecting parents or progeny for crossing or backcrossing; evaluating genetic diversity within or among populations; estimating gene flow or genetic drift; tracing pedigrees or origins; verifying cultivar identity or purity; etc.

Molecular markers can be classified into different types based on their features such as abundance; polymorphism; co-dominance; reproducibility etc. Some examples of molecular markers used for tomato are Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNAs (RAPDs), Amplified Fragment Length Polymorphisms (AFLPs).

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