

## Prebreeding and Use of Genetic Resources for Tomato Quality Improvement

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There is a wealth of genetic variability within modern and heirloom tomato cultivars, land races, and related wild species for product improvement. Many of the genes that condition these traits are not well characterized, are associated with undesirable traits, or may be difficult to effectively transfer to adapted cultivars or breeding lines due to low heritability and/or the presence of numerous genes, all of which are important to achieve the intensity of expression exhibited in the unadapted plant materials. Genetic variation present in wild tomato species for fruit quality is often transgressive in nature but may be exploited to improve fruit quality. This report updates progress on characterization of tomato fruit firmness and color attributes derived from wild accessions.

We characterized inheritance of firmness in adapted processing tomato germplasm developed from interspecific *S. lycopersicum* x *S. galapagense* crosses. We demonstrated that firmness measured via fruit compression force was independent of firmness assayed via fruit puncture resistance. Additive effects accounted for the genetic variance explained by both firmness attributes. Despite the inferior phenotype of the *S. galapagense* accession utilized as a donor parent, *S. galapagense* derived lines exhibited superior fruit firmness and puncture resistance and positive general combining ability for these attributes in crosses with other adapted breeding lines. We have developed an inbred backcross line population using an inbred processing type breeding line derived from intraspecific *S. lycopersicum* crosses and a second inbred parent line descended from an interspecific *S. lycopersicum* x *S. galapagense* cross. Parent lines were selected to discriminate between QTL that contribute to fruit firmness due to compression or puncture resistance. The population consists of 142 BC2F4 lines. Using the IBL population, SNP markers that discriminate parental lines will be utilized to identify and map firmness QTL attributes.

Enhanced fruit pigmentation has long been a goal in tomato cultivar development programs due to the positive association between the intensity of pigmentation and perceived product quality. Recognition of the health benefits associated with carotenoid consumption provides added justification for improving fruit pigmentation. Despite extensive genetic and molecular characterization of simply inherited tomato pigment mutants, definitive information is lacking on the genetics and regulation of tissue-specific carotenoid accumulation in tomato fruit. A molecular genetic basis for quantitatively inherited variation in fruit pigmentation has not been established. Unique genetic stocks exhibiting tissue-specific pigmentation (e.g. lines with dark red locule tissue/lightly pigmented pericarp; light red locule/dark red pericarp; green locule/light pigmented pericarp; dark red pericarp and locule/white columella) have been developed. These lines were identified as segregants from crosses between adapted breeding lines and diverse high-color germplasm descended from initial crosses between *S. galapagense* and *S. habrochaites*. Segregating F2, F3 and backcross populations have been developed to study the inheritance of tissue pigmentation and identify QTL associated with pigmentation traits. The

genetic stocks will be useful in basic studies on carotenoid accumulation and for use in development of cultivars with enhanced fruit pigmentation.