

The mapping population consists of recombinant inbred lines (F₇ to F₉ generation) from the cross between IS3620C and BTx623. A subset of this population (129 RILs) was used as the basis for development of definitive and landmark high-density map of sorghum with 2,926 DNA markers which include AFLP, SSRs and RFLP. Detailed information on marker data for this subset population is accessible at www.gramene.org and <http://sorgblast3.tamu.edu>. The population has been instrumental in the establishment of a physical map of sorghum using BAC clones as scaffold for the whole genome sequence of sorghum. The population has been used in the identification and standardization of sorghum chromosomes. Seven linkage maps have been published using the IS3620C x BTx623 RI population. The subset of the population has been used to identify a total of 110 QTL including those underlying physiological responses associated with tolerance to seedling abiotic stresses. The QTL correspond to 39 important agronomic and morphological traits.

The two parents, IS3620C and BTx623, and their recombinant inbred lines (F₇ to F₉ generation) exhibited continuous variation for numerous important agronomic traits and the population had been very useful for QTL including maturity, plant height, tillering attributes and for a number of panicle traits. QTL has been identified in the population for other important agronomic traits related to yield such as head exertion, head weight, grain weight and kernel weight. Distinct differences between the parents and among the RILs include compact head and larger seeds for BTx623 while IS3620C has an open head with small seeds. Laboratory studies have also shown distinct differences/continuous variation as to the responses of the parents and the RILs at the seedling stage to abiotic stresses. IS3620C accumulates leaf anthocyanin accumulation and are deep purple while BTx623 does not accumulate anthocyanin during chilling stress.