DEVELOPMENT OF COTTON NAM POPULATION FOR FINE GENETIC MAPPING

O.S. Turaev
A.Kh. Makamov
M.M. Darmanov
N.N. Husenov
A.A. Tulanov
I.S. Normamatov
F.N. Kushanov
Z.T. Buriev
I. Abdurakhmonov
Center of Genomics and Bioinformatics, Academy of Sciences of Uzbekistan
Tashkent, Uzbekistan

Abstract

In many cases, the large part of molecular markers that being recommended to the practice are non-functional because of their unknown extent of linkage dissiquilibrium (LD), mostly mapped on genetically limited biparental populations. The best way to solve this kind of problems is to perform molecular mapping of QTLs on nested association mapping population (NAM).

The NAM method not only combines the advantages of both QTL-mapping and Association Mapping (ASM), but also, to eliminate the shortcomings and problematic processes encountered in these methods.

The main objectives of this study were the development of NAM population for genetic mapping of complex quantitative trait loci (QTL) with high accuracy in cotton. In order to develop the NAM population in cotton 19 diverse donor lines, previously characterized for economically important traits, rare QTL alleles, and LD parameters, and the Uzbekistan standard Upland genotype “Namangan-77” cultivar (as a common parent) were selected from the Uzbekistan cotton germplasm. Each of 19 donor lines were individually crossed with “Namangan-77” and 3079 recombinant inbred lines of 19 NAM families were developed. NAM RILs were generated by self-pollinating in every generation using single seed descent method.