Abstract ID 136

Development and agronomic and morphological characterization of a large EMS mutant population in Cotton cv. VAGAD

TILLING (Targeting Induced Local Lesions IN Genomes) is classical mutagenesis based, non-transgenic, and effective reverse genetic technology, which is used for functional genomics studies. Gossypium herbaceum (2n=2x=26) have innate capacity to withstand drought, therefore, it maximum cultivation occurs in the rain-fed regions of Asia. Now, the available of cotton genome(s) and transcriptome(s) sequence of Gossypium spp. provide better information of candidate genes that determine different traits. Mutagenesis generates several new alleles (SNPs/ Indel) for targeted gene(s). These new alleles need to functional validation before being used in breeding. In current EMS mutagenized TILLING population for G. herbaceum (cv. VAGAD) used 70 mM EMS and developed 5,473 M3 plants resource. The morphological data for 11 agronomical traits were recorded for 4,453 matured M3 plants. The range of dispersion, mean performance and coefficient of variation (CV) was more variable in the mutants when compared to control plants. The phenotyping of M3 population bared 31.63% plants having the variation than control. The visual inspection of plant morphology showed that 2.29% of plants have visible changes in leaf morphology, leaf colour, sterility, and plant habits. This mutant population provides the opportunity for functional genomics studies of cotton that might potentially be useful in breeding.

Comments

It is recommended to revise the language of this abstract for a better understanding of the experiment. On the other hand, you describe correctly what TILLING is, but you abstract did not mention any application of TILLING technique in this work. Please specify how you know it is saturated? A better title for your abstract would be: “Development and agronomic and morphological characterisation of a large EMS mutant population in Cotton cv. VAGAD.”

Please specify the genes considered ”interesting”, and provide additional information the 5473 independent M3 lines? From how many M2s? probably better to call them M3 families? Please revise the language for a greater impact of the abstract (i.e plant habits???).

Answer:

Thank you very much for giving the patience to read very carefully my abstract.

As per your suggestion, I have changed the title of the abstract as Development and agronomic and morphological characterization of a large EMS mutant population in Cotton cv. VAGAD.

The term “interesting” define as our future target genes that will be resequence and screen novel SNPs in our targeted genes. We have developed 5,473 M3 plants from 2597 M2 plants