

FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



Contribution ID: 184

Type: Oral

CREATION AND CHARACTERIZATION OF AN EMS MUTANT POPULATION OF JATROPHA CURCAS

Significant efforts toward the identification, characterization, screening and discovery of mutations in genes of interest have been made successfully in plants and animal by targeting induced local lesions in genomes (TILLING). The combination of induced mutagenesis with high throughput sequencing is a powerful tool for generating allelic series, introducing variation and enables gene function study by reverse genetic approaches in many crop species, especially in plants with a narrow genetic diversity like *Jatropha curcas*, a tropical biofuel crop. *J. curcas* is a semi-wild plant, and an economically important shrub as a useful source of biofuel or in soil reclamation, but it requires genetic improvement, to select the best genotypes for these purposes. A mutant population of *J. curcas* with similar genetic background was generated using three concentrations (0.4, 0.8 and 1.6%) of the chemical mutagen ethyl methanesulphonate (EMS) treated for 3 different durations (0.5, 1.5 and 3 h). 1800 EMS mutation lines (M1V6) was used to identify beneficial mutation in 97 genes related to oil composition, toxin production and stress response in *J. curcas*. Three-dimensional pooling strategy were used to generate 112- and 256- fold pooling, which were PCR-amplified. The equal amount of amplicon pools was used for library preparation and sequencing using Illumina MiSeq. Different software programs were used for data analyses. Among different software, CAMBa showed to be the reliable one to identify the mutation changes with lowest false discovery. This study shows that TILLING by sequencing is a high-throughput, fast and cost effect methods to identify allelic variations and gene functions in mutant populations, which control important traits.

Country or International Organization

PBU, BOKU University, Austria

Author: Prof. MAGHULY, Fatemeh (PBU, BOKU, Vienna)

Co-authors: Dr TILL, Bradley (IAEA/FAO Laboratories, Seibersdorf); Dr JANKOWICZ-CIESLAK, Joana (IAEA/FAO Laboratories, Seibersdorf); Prof. LAIMER, Margit (PBU, DBT, BOKU); Dr GUPTA, Prateek (3Department of Plant Sciences, University of Hyderabad, India)

Presenter: Prof. MAGHULY, Fatemeh (PBU, BOKU, Vienna)

Track Classification: Enhancing agricultural biodiversity through new mutation induction techniques