

22nd Euro-Global Summit on

Food and Beverages

February 28-March 01, 2019 | London, UK

Genetic diversity analysis among Yellow Mosaic Virus (YMV) resistant and susceptible varieties in mung bean (*Vigna radiata* L.) using SSR markers

K. Balakrishna, Y. Hari and V. Thirumala Rao

Professor JayaShankar Telangana State Agricultural University (PJTSAU), India

Mung bean (*Vigna radiata*, L. Wilczek), is a self-pollinated diploid ($2n = 22$) pulse crop, with a genome size of 515 Mb/1C, popularly known as green gram and is native to the Indian subcontinent. Mung bean is an excellent source of proteins (19-28%), mineral (0.18-0.21%) and vitamins which complements the staple rice diet in Asia and particularly in India. Among the various diseases limiting the mung bean productivity, Yellow Mosaic Virus YMV or Yellow Mosaic Disease (YMD) transmitted through the white fly, *Bemisia Tabaci Genn*, is wide spread. In the present investigation, an attempt was made to study the genetic diversity analysis among 17 varieties of mung bean, collected from different geographical regions of India using Simple Sequence Repeat (SSR) markers. Molecular polymorphism was 58.8% with 29 SSR primers indicating the low level of genetic variation among the varieties. The polymorphic bands were scored visually as present (1) or absent (0) on a binary matrix. Genetic similarity between the varieties was estimated using Jaccards Coefficient of similarity. Dendrogram was performed using the Unweighted Pair Group Method with an Arithmetic mean (UPGMA) algorithm and the NTSYS software. The mung bean variety WGG-2 is appeared to be more divergent with 42.1% similarity, while high similarity of 81.7% was recorded between two susceptible varieties KM 14-34 and KM 14-61 and sin between one resistant variety (ESM 14-1413) one susceptible variety (KM 14-57). In one cluster all the resistant varieties (ESM 14-1312, KM14-43 and KM 14-62) and all the susceptible varieties (KM 14-34, Km-14-61 and MGG-295) were grouped together based on their phenotypic disease reaction for YMV resistance, except one resistant variety WGG-42 is grouped with all these susceptible varieties. The study clearly indicates that SSR marker profiles were best-suitable for assessing genetic relationships among Yellow Mosaic Virus (YMV) resistant and susceptible varieties.

Balakrishnakurakula7@gmail.com