

## Dissection of Genomic Loci for Yellow Vein Mosaic Virus Resistance in Okra (*Abelmoschus esculentus*)

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**Abstract :** Okra (*Abelmoschus esculentus* L. Moench) or lady's finger is an important vegetable crop belonging to the Malvaceae family. Unfortunately, production and productivity of Okra are majorly affected by Yellow Vein mosaic virus (YVMV). The AO: 189 (resistant parent) X AO: 191(susceptible parent) used for the development of mapping population. The mapping population has 143 individuals (F<sub>2</sub>:F<sub>3</sub>). Population was characterized by physiological and pathological observations. Screening of 360 DNA markers was performed to survey for parental polymorphism between the contrasting parents', i.e., AO: 189 and AO: 191. Out of 360; 84 polymorphic markers were used for genotyping of the mapping population. Total markers were distributed into four linkage groups (LG1, LG2, LG3, and LG4). LG3 covered the longest span (106.8cM) with maximum number of markers (27) while LG1 represented the smallest linkage group in terms of length (71.2cM). QTL identification using the composite interval mapping approach detected two prominent QTLs, QTL1 and QTL2 for resistance against YVMV disease. These QTLs were placed between the marker intervals of NBS-LRR72-Path02 and NBS-LRR06- NBS-LRR65 on linkage group 02 and linkage group 04 respectively. The LOD values of QTL1 and QTL2 were 5.7 and 6.8 which accounted for 19% and 27% of the total phenotypic variation, respectively. The findings of this study provide two linked markers which can be used as efficient diagnostic tools to distinguish between YVMV resistant and susceptible Okra cultivars/genotypes. Lines identified as highly resistant against YVMV infection can be used as donor lines for this trait. This will be instrumental in accelerating the trait improvement program in Okra and will substantially reduce the yield losses due to this viral disease.

**Keywords :** Okra, yellow vein mosaic virus, resistant, linkage map, QTLs

**Conference Title :** ICABBBE 2018 : International Conference on Agricultural, Biotechnology, Biological and Biosystems Engineering

**Conference Location :** Montreal, Canada

**Conference Dates :** May 24-25, 2018