



SWEET gene: Paving the way towards re-emergence of Bacterial Blight of Cotton

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Bacterial blight of cotton (BBC) caused by *Xanthomonas citri* subsp. *malvacearum* (*Xcm*) was first time reported in India from Rajapalayan, Tamil Nadu in 1918. It affects the cotton plant during all growth stages but yield losses are more pronounced when stem lesions are formed along with leaf infection as it reduces photosynthetic activity by destroying the chlorophyll content in leaves and stem. Though it is known to occur in major cotton producing countries, development of resistant varieties since 1990's has led to decline in the disease intensity and hence, its importance. However, it remains a potentially important disease because of the variability of the pathogen and the appearance of new races. There is pressing need to understand the biochemical and molecular mechanisms of susceptibility and resistance to bacterial blight in cotton.

Recently, a team of scientists from Texas A & M University (USA) studied on the underlying mechanisms of sudden re-emergence of the pathogen which created significant yield losses in the United States. They found that transcription activator like (TAL) effectors from the pathogen are essential for the disease development. Even though number of TAL effectors being cloned from *Xcm*, none of the Resistant (R) or Susceptible (S) genes has been deciphered. This could be due to large, complex allopolyploid cotton genome and limited availability of genomic resources. To establish themselves in host, bacteria may target some host genes which facilitates the infection and make the host plant susceptible. The *SWEET* family members are key susceptible (S) genes common to several diseases caused by different *Xanthomonas spp.* After control of 1970's epidemics of BBC in US, it has now claimed its re-emergence with a significant yield constraint in past few years, which raised the concern among scientists to identify the responsible factors for its virulence. Such an effort has been made by a group of scientists (Cox *et al.*, 2017) who sequenced the whole genome of different *Xcm* field strains and deployed this information coupled with TAL effector DNA binding EBE (effector binding element) prediction.

It has been reported that *GhSWEET10D* that encodes a sucrose transporter found as one of the main target for *Avrb6*, a TAL effector mimicking the role of eukaryotic transcription factors. *GhSWEET10* is reported to be a major 'S' gene for BBC and silencing of *GhSWEET10* was found to reduce the infection by *Xcm*. Further, they found that expression of *Avrb6* in two contrasting cotton lines namely, Ac44E (BBC susceptible) and Ac66 (BBC resistant) showed induction of *GhSWEET10*. However, its expression was significantly lower in BBC resistant cotton line, Ac66. Molecular characterization of BBC contrasting lines for BBC resistance revealed that the difference was found in the promoter sequences of *GhSWEET10* gene but not in the EBE. This SNP polymorphism in the promoter region of *GhSWEET10D* gene could be the reason behind its differential expression responsible for impaired activation by *Avrb6* in resistant genotypes of cotton leading to re-emergence of *Xanthomonas citri* subsp. *malvacearum*.

Suggested Readings:

Cox, K. L., Meng, F., Wilkins, K. E., Li, F. *et al.*, (2017). TAL effectors driven induction of a SWEET gene confers susceptibility to bacterial blight of cotton. *Nature Communications*, DOI: 10.1038/ncomms15588.

Talbot, N. J. (2010). Cell biology: raiding the sweet shop. *Nature*, 510-511.

Meetings attended

Dr D. Monga Head, CICR, Regional Station, Sirsa and Dr Rishi Kumar, Principal Scientist (Entomology) attended the 6th Interstate Consultative Committee meeting on whitefly management held in Mini Secretariat, Bathinda on 12.08.2017 under the chairmanship of Sh M. P. Singh, Additional Chief Secretary, Govt. of Punjab; Special Agriculture Secretary Shri Garg Dr B. S. Dhillon; Vice Chancellor, PAU, Ludhiana, Dr B. S. Sidhu; Commissioner of Agriculture, Punjab; Director of Agriculture, Punjab Dr. Bains; Director of Research & Director of Extension Education, PAU, Ludhiana; JDA Cotton Punjab; Dr Sukhdev Singh, Director of Research, CCSHAU Hisar; Dr. Sethi, Dr. S. S. Siwach, Principal Scientist Cotton,,CCSHAU Hisar; Dr K. K. Dahiya, Principal Scientist Entomology; Dr. Omender Sangwan, Cotton Breeder attended the meeting. Chief Agriculture Officers of all 8 cotton growing Districts of Punjab presented information regarding survey and surveillance and other activities conducted in Punjab. Dr Rishi Kumar presented the survey and surveillance report of entire zone with respect to whitefly.



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