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The use of next generation sequencing to study biotic stress on sugar beet

Abdelnaser Elashry
Strube Research GmbH, Germany

Sugar beet is one of the important crops worldwide for sugar production. Several biotic and biotic-stresses can affect negatively the yield of the sugar beet. Due to the increasing demand on sugar plant breeding programs aim, on one side, to maximize the productivity and, on the other side, to minimize the loss of yield. Sugar-beet genome sequencing allows efficient and fast breeding programs. Here we used next generation sequencing combined with genetic mapping to curate and have a better understanding of the sugar beet genome. This approach has resulted in better structural annotation of sugar beet genome (9 Chromosomes has nearly 500 MB of sequences).

We performed RNAseq on plants that were exposed to biotic stresses (i.e. Rhizomania or cyst nematodes). We compared the results of the infected- and the non-infected plants after mapping the resulted reads to the curated sugar beet genome. Our results helped us to determine the differentially regulated genes as a reaction to the infection. The determination of such subsets can help understanding sugar beet biology and help designing plant breeding programs aim to have resistant sugar beet. Also, accurate reference genome helps designing efficient molecular markers that would, in turn, help plant selection within the breeding programs.

Biography

Abdelnaser Elashry has accomplished his PhD in 2004 from University of Gottingen, Germany. He has achieved his post-doctoral studies in BOKU University and in IAEA (UN) in Austria studying plant nematode interaction. He was an assistant professor in Bonn university making research on the nematode effectors, nematode-genome and -transcriptome. His recent position is researcher in Strube Research, sugar beet breeding department, Germany. His recent research is focused on the sugar beet genome studies for plant breeding.

a.elashry@strube-research.net