

Plant Genomics

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Faba bean (*Vicia faba*) seed gene function expression profile study

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Faba bean (*Vicia faba*) is one of the important grain legume crops worldwide, which is commonly consumed as human food and animal feed. The faba bean ($2n=12$) genome is approximately 13.4 Gb, the largest genome in the grain legume family. The faba bean seeds size is the biggest one in all of the grain crops. Our study applying RNA-Seq technology to construct the first faba bean genome de novo assembling. There was a total number of 47621 All-Unigene discovered in faba bean seeds by RNA-Sequence, length 27605508 bp. And then investigated the faba bean seed genes function expression profile on comparison of the following traits: Hydration index, rust resistance, photoperiod response, seed staining and ascochyta blight pathogen resistance.

Biography

Shi Ying Yang has completed her PhD from Charles Stuart University, Australia. She has been an Associate Professor at Guangxi Academy of Agricultural Sciences, China until 2009. Currently she is a Research Officer at School of Agriculture, Food and Wine, The University of Adelaide, Australia. Her major research work on the germplasm evaluation, grain legume crops breeding and molecular marker, herbicide selection and genomic study. She has published two book chapters with colleagues and 30 refereed journal papers.

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