

Unraveling zucchini transcriptome response to aphids

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Cucurbita pepo belongs to the Cucurbitaceae, the second-most large horticultural family of economic importance after Solanaceae. One major issue related to zucchini cultivation is the damage caused by aphids such as *Aphis gossypii* (Homoptera: Aphididae). The aim of this study is the identification of candidate genes involved in zucchini plant response to *A. gossypii*. In order to monitor the effect of zucchini-aphid interaction at transcriptomic level, zucchini plants (cv "San Pasquale") were grown in controlled conditions in presence or absence of *A. gossypii*. Leaf material was collected at 24, 48 and 96 hours after aphid infestation. RNA extracted was sequenced using the Illumina HiSeq 2500 platform. The sequencing generated ~34 million of paired-end reads of 100 nucleotides in length per sample. High quality reads were *de novo* assembled into 71,648 transcripts. About 94% of the assembled transcripts contain coding sequences that could be translated into proteins. Over 60% of the transcripts were functionally annotated and assigned to one or more InterPro domains and Gene Ontology terms. A subset of 42,517 sequences of the *C. pepo* transcriptome was used for read mapping and differentially expressed genes (DEG) identification. Largest number of DEG were observed after 48 hours from aphid infestation. The transcriptome represents a high-quality reference for read alignment and DEG call. The understanding of the molecular response of infested plants will be essential to develop new tools for *A. gossypii* control.