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BOOK OF ABSTRACTS



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An RNAseq approach towards deciphering mechanisms involved in bruchid tolerance in faba bean

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Broad bean weevil (*Bruchus rufimanus*) is a major pest of faba bean. Once eggs are laid on the pods, larvae penetrate, develop in the seeds and create damage that affects the quality of the beans. This renders them unsuitable for the human consumption market. Therefore, in the context of reducing pesticide use and in order to develop faba bean varieties resistant to bruchid, the search for tolerant accessions is an important issue.

A germplasm screen has identified two accessions with good levels of tolerance, suggesting that these genotypes are less attractive to the insects and/or that their seeds contain compounds toxic for the larvae. In order to understand the underlying molecular mechanisms, we used an RNAseq transcriptomic approach on different plant tissues (leaf, flower, young pod and developing seed) of these two tolerant accessions and one additional sensitive cultivar.

As the *Vicia faba* genome has not yet been sequenced, a *de-novo* assembly was performed to build a set of genes to be used for differential expression analyses: individual assemblies per tissue and genotype have been done and clustered to eliminate redundancy. A SuperTranscript [1] of 30825 genes (average size of contigs 1945bp) has been obtained with good completeness (97% of BUSCO [2]) representing the transcriptome from the four organs of each of the three genotypes. Differential expression studies using this Unigene have highlighted contrasted response of the three genotypes for specific pathways and will help identifying regulated genes.

References

[1] Hawkins, A. et al, *SuperTranscript: a reference for analysis and visualization of the transcriptome*. *bioRxiv*, 2016, p. 077750.

[2] Simao, F.A. et al, *BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs*. *Bioinformatics*, vol. 31, no. 19, 2015, p. 3210-3212.

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