Comprehensive profiling and characterization of Arachis stenosperma (peanut) and Meloidogyne arenaria (plant-root nematode) small-RNAs identified during the course of the infection

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1 EMBRAPA RECURSOS GENÉTICOS E BIOTECNOLOGIA

Abstract

Plant-parasitic nematodes have a worldwide distribution. They are virtually able to infest any human-cultivated plant. Annual losses caused by nematodes on life-sustaining crops are estimated to exceed 14% of the production (approximately 65 billion €of loss worldwide). Previously studies were responsible for major advances in the identification of genes and mechanisms responsible for plants response to the Meloidogyne, the root-knot nematode. Meloidogyne spp. are obligate endoparasites that maintain a biotrophic relationship with their hosts. During the infection root cells are differentiated into specialized giant feeding cells through the releasing of effector proteins. However, despite the continuing efforts to identify new effectors and plant resistance mechanisms, studies have shown that the repertoire of both systems is limited. Recently, researchers published strong evidence that small RNAs from a phytopathogenic fungus act as effectors. These small RNAs hijack the host RNA interference (RNAi) machinery by binding to Arabidopsis Argonaute 1 (AGO1) and selectively silencing host immunity genes. These findings gave new insights on nematode-plant interaction as well as for the development of new control strategies through biotechnological methods. The goal of this work is to verify the possible role of Meloidogyne arenaria small RNAs (sRNA) as effectors by identifying, in Arachis stenosperma (peanut), downregulated target genes during the infection. A. stenosperma plants were infected with approximately 5,000 M. arenaria larvae in triplicate. Control and infected A. stenosperma roots were collected 3, 6 and 9 days post-infection. The infected samples were pooled. Six samples (3 controls, 3 infected) and two M. arenaria J2 small-RNA libraries were sequenced with technical replicates using Illumina HiSeq 2500 system. After adaptor and contaminats removal, reads were mapped against miRbase V21.0. One hundred and 151 different conserved miRNAs were counted for M. arenaria and A. stenosperma respectively. The unmapped reads were used as input for miRDeep-P, a plant microRNA prediction tool. The predicted miRNAs were confirmed by using miRDup softare . A total of 625 and 1271 new candidates were predicted for M. arenaria and A. stenosperma respectively. Next steps include the target prediction and validation by qRT-PCR.

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