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Participation of the mediator complex in the soybean - *Phytophthora sojae* interaction
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Phytophthora root and stem rot, caused by *Phytophthora sojae*, is a kind of destructive disease on soybean production. In the plant transcription regulation system, one of the major regulators is the RNA polymerase II system who transcribes all protein-coding and most non-coding RNA genes and is globally regulated by Mediator - a large, conformationally flexible protein complex with a variable subunit composition. We performed genome-wide analysis of the soybean mediator subunits and a total of 95 mediator subunits have been identified. These 95 soybean mediator subunits are unevenly located on all the 20 soybean chromosomes and only segmental duplication is found among all the subunits. Every subunit shows a tissue-specific expression pattern. We divide the soybean mediator subunits into five subfamilies and 13 subgroups, which potential functions belong to multiple biological processes. We further obtained the *MED16* genes in soybean through homologous cloning and performed preliminary study on its functional participation in soybean-*Phytophthora sojae* interaction. From the treatment by *Phytophthora sojae* and plant hormones, we found that *MED16* genes in soybean could response to *Phytophthora sojae* infection as well as plant hormone treatment. Using the RNAi technology to perform soybean hairy root transformation mediated by *Agrobacterium rhizogenes*, we found that silencing of the *MED16* genes in soybean can make it easier for the hyphae accumulation in the silencing tissues and make soybean more susceptible to *Phytophthora sojae*. Moreover, zoospores were used to treat the silenced hairy roots and control ones, we found that marker genes related to the hormone signaling pathways showed significantly change in the silenced tissues after inoculation. Above all, our results showed that the *GmMED16* genes participate in soybean-*Phytophthora sojae* interaction through the regulation of hormone signal pathways.