

Structure based investigation of phytoplasma PHYL1 interacting proteins

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Abstract

Phytoplasmas are cell wall-deficient bacteria, which causes severe symptoms such as phyllody, dwarfism and leaf yellowing in the infected plant (1,2). Phytoplasmas targets many important crops such as including peanut, papaya, loofah and pear, and they have caused a serious loss in agriculture (1,2). Therefore, it is important to discover treatment methods for this bacteria. During the infection, phytoplasmas secrete many effectors to control the plant development (3). One of these effectors, PHYL1 (Phytoplasmal effector causing phyllody 1), plays an important role for phytoplasma-caused symptoms (4). Functionally, PHYL1 alters the biological function of MADS transcription factors which have essential roles in the development of floral quartets. This results in abnormal plant developments such as phyllody (4). In 2019, we reported the crystal structure of PHYL1 from Peanut witches'-broom phytoplasma (4). By using structural and proteomic approaches, we investigated the interaction between PHYL1 and the K domain of SEPALLATA3 MADS transcription factor (SEP3_K) (4). Interestingly, our subsequent study further indicates that PHYL1 also has ability to interact with other proteins, including another MADS transcription factor SVP and two unknown phytoplasmal proteins PnE1 and PnE2. To understand the biological meaning of these PHYL1-interacting proteins, we will investigate their structures in the near future. We anticipate the results of this study will be useful for understanding the pathogenesis of phytoplasmas.

Keywords – Phytoplasma, Phytoplasmal effector causing phyllody 1, MADS transcription factor, phyllody.

References

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