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Unraveling plant disease susceptibility to fungal pathogens

Multi-layered defense barriers ensure that a plant is the host to only a few adapted pathogens. Thus, the host range of a particular plant pathogen relies on its ability to fully suppress plant defense responses such as the pattern-triggered immunity (PTI). One of the common pathogen strategies to overcome PTI is the production of a plant defense suppressor. In the case of *Mycosphaerella pinodes*, a causal agent of Mycosphaerella blight on pea, this fungus can avoid host defense responses by secreting at least two suppressors named suppressins A and B (Fig. 1), which manipulate the physiology of the host cells, including JA biosynthesis through targeting the host's ATPase. In parallel, a constituent(s) similar to the fungal suppressins has been discovered in healthy leaves of pea. Such a constituent was also found in the healthy leaves of barley and Arabidopsis plants, and collectively referred to as an endogenous suppressor (ES). Actually, the purified ES can suppress or delay PTI, enabling the non-adapted pathogen to cause disease symptom on corresponding plants. Interestingly, the action of the pea ES is quite similar to that of the suppressins A and B secreted by *M. pinodes*. Consistently, the ES can severely inhibit host's ATPase, temporarily reducing the ability of the host cell to defend itself. The putative role of the ES is assumed to be involved in the trade-offs between plant growth and defense by preventing excessive defense responses against pathogen attack. Alternatively, it is likely used by a pathogen to promote disease susceptibility. We are now focusing on the host cell physiology altered by a pathogen- and/or plant-derived suppressors in relation to the convergent evolution between pathogen and host.

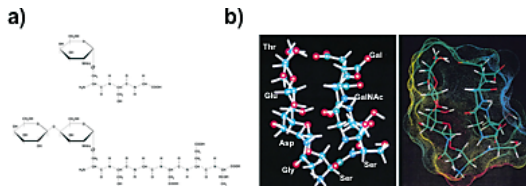


Fig. 1. Chemical structures of Suppressins A and B from *Mycosphaerella pinodes*. (a) Chemical structures of Suppressin A (upper) and B (lower). The common moiety consisting of O-glycosyl portion attached to the serine (GalNAc-Ser-Ser-Gly) is proposed to be essential for suppressor activity. (b) A predicted structure (left) of the Suppressin B, a major suppressor of *M. pinodes* and its distribution of charge around this molecule (right).