Insight into Plant-Fungal interactions through Secretome analysis

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Plants possess the ability to distinguish between beneficial and harmful organisms entering the plant from the external environment, and respond accordingly. Effectors are specific elicitor proteins secreted by pathogenic organisms to suppress plant defense systems and facilitate the pathogenesis process (infection and colonization). Simultaneously, plants use these effector proteins to identify the intruding organisms and activate a second line of defense known as effector triggered immunity (ETI). Therefore it is plausible to assume that effector proteins secreted by intruding organisms play a significant role in deciding the final outcome of an interaction with a host plant (e.g. pathogenic or endophytic). Thus this study aimed at conducting an *in silico* study to investigate the effector proteins of fungi that belong to three different life strategies, viz, pathogenic, endophytic and free-living. Representing the three life strategies, proteomes of nine fungal species (3 species representing each life strategy) were selected for the study. Using an optimized analytical pipeline, the secretome for each proteome was predicted followed by the effector proteins based on the predicted secretome. The results revealed that, in general, the number of effector proteins of pathogenic fungi is greater than that of endophytic and free living fungi.An analysis on conserved functional domains of effector proteins (across all 9 fungal proteomes selected) revealed that pathogenic fungi possess a higher number of enzymatic, toxic, pathogenesis, necrosis and binding related functional domains compared to that of endophytic fungi, followed by the free living fungi. Endophytic fungi, that generally maintain a mutually beneficial interaction without harming host seemed to lack effector proteins with functional domains associated with toxicity, pathogenesis and necrosis. A number of important conserved domains such as Hce, Cerato-platanin, Kp4 and Enterotoxin were seen only in effector proteins derived from pathogenic fungi. A conserved motifanalysis conducted for the total set of effector proteins of all 9 proteomes revealed 2 motifs ("MKFSTLLLLL" and "LAALALAAPV") that were mostly conserved across all 9 proteomes studied, indicating the presence of an effector protein specific motif. This preliminary *in silico* study has provided insight into how a host-fungus interaction is determined at genome level.