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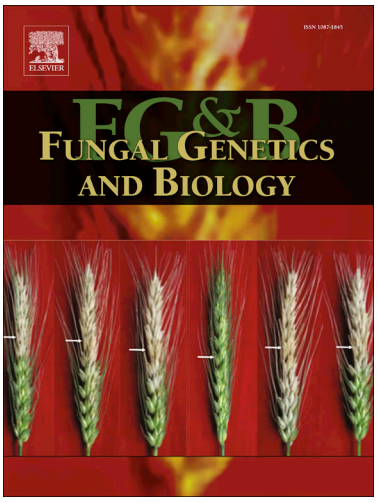


Resource

# Annotation Resource of Tandem Repeat-containing Secretory Proteins in Sixty Fungi

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# Annotation Resource of Tandem Repeat-containing Secretory Proteins in Sixty Fungi

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**Abstract**

Fungal secretory proteins that interact with host plants are regarded as effectors. Because fungal effectors rarely contain conserved sequence features, identification and annotation of fungal effectors from predicted secretory proteins are difficult using outward comparison methods such as BLAST or hidden Markov model. In desire of more sequence features to prioritize research interests of fungal secretory proteins, this study developed a pipeline to identify tandem repeat (TR) domain within putative secretory proteins and tested a hypothesis that at least one type of TR domain in non-orthologous secretory proteins has emerged from convergent evolution for plant pathogenicity. There were 2,804 types of TR domains and a total of 2,925 TR-containing secretory proteins found from 60 fungi. There was no conserved type of TR domain shared only by plant pathogens, indicating functional divergence for different types of TR domain and TR-containing secretory proteins. The annotation resource of putative fungal TR-containing secretory proteins provides new sequence features that will be useful for the community interested in fungal effector biology.

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