INSIGHTS INTO *CLAVICEPS PASPALI* SECRETOME: A FIRST APPROACH INTO EFFECTOR MOLECULES EXPRESSED DURING *CLAVICEPS PASPALI-PASPALUM DILATATUM* INTERACTION

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The ascomycete *Claviceps paspali* is a biotrophic flower pathogen of *Paspalum* spp. genus. This fungus has become a serious problem threatening the forage potential of some susceptible species like *P. dilatatum*. Infections with this pathogen lead to the formation of a sclerotia instead of seed in the infected flower, drastically reducing the seed production of these plants almost to no commercial use. Also, infected seeds had toxic effects on grazing animals reducing performance. Filamentous plant pathogens that establish biotrophic interactions need to avoid plant immune responses. Colonization is governed in all systems by hundreds of secreted fungal effector molecules. These effectors suppress plant defense responses and modulate plant physiology to accommodate fungal invaders and provide them with nutrients. Using a computational pipeline integrating data from RNA-seq during infection of *C. paspali* in *P. dilatatum* and bioinformatic predictions, we have identified secreted proteins of this fungus. Small secreted and effector-like proteins similar to agents of fungal-plant pathogenesis were also identified within the secretome. In particular, we predicts 8122 genes with coding potential from the draft genome of *C. paspali* obtained from NCBI database. From the total proteome, 367 (4,5%) were predicted as secreted proteins. From this predicted secreted proteins, 25 (6,8%) had known functions as enzymes that degrade cell walls and 134 (36,5%) had annotated PFAM domains. Also, a total of 220 (60 %) proteins could be predicted as effectors. Based on RNA-seq expression analysis we also determine that at least 6 of these secreted proteins are in the Top50 differential expressed genes within the first 96 hrs post infection in the stigma of *P. dilatatum*. With this study, we provide new insights that will provide a basis for a better understanding of this pathosystem. Also, we present a collection of candidate genes to be evaluated for functional roles in this plant–microbe interaction.

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