

***Beauveria bassiana* proteomics: understanding fungi-host mechanisms for development of novel strategies on *Callosobruchus maculatus* biocontrol.**

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Callosobruchus maculatus is the main cowpea (*Vigna unguiculata*) predator, causing severe losses to poor farmers in South America and Africa. Several control strategies have been utilized toward insect-pests as the use of entomopathogenic microorganisms, which produces hydrolase's that cleave insect exoskeleton and peritrophic membrane. An initial *in vivo* insecticidal screening of several fungi was carry, showing that several isolates of *Beauveria bassiana* have higher lethal activity against *C. maculatus*. For this reason, our report describes the proteomical analysis of *B. bassiana* secretion in response to the presence of cowpea weevil cuticle. 1.0×10^7 spores of *B. bassiana*, obtained from Cenargen/Embrapa, were grown in TM medium. After three days of incubation, mycelium was divided and half secretion was transferred to minimal medium. The other part was transferred to minimal medium added by 0.5% (w:v) of dehydrated macerated *C. maculatus* exoskeleton. Both were incubated for three days at 29°C. The supernatant was double filtered, lyophilized and stored at -20°C. Protein concentrations were measured by Bradford method and both samples ($200 \mu\text{g} \cdot \text{ml}^{-1}$) were submitted to two-dimensional gel analyses. After electrophoresis, the gels were silver stained using Bio-Rad staining kit, and analyzed. Several different spots could be observed at insect shells induced secretion with broad range of pI and molecular mass. These different spots were excised and treated with bovine trypsin gold and identified by peptide mass finger printing analysis. These results will be useful to understand pathogenic processes of *B. bassiana* and might be used for development of novel bio-insecticides.

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