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# ECFG10

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MEETING ABSTRACTS

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### PR3.26

#### The black truffle of perigord responds to cold stress with an extensive reprogramming of its transcriptional activity

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Free-living fungi often encounter different kinds of environmental stresses, including changes in temperature, osmolarity, pH, humidity, availability of O<sub>2</sub> and nutrients, exposure to toxins, UV or heavy metals, as well as competition with other organisms. To understand the cell adaptation and the survivor in non-ideal conditions, a better comprehension of many basic events is required. *Tuber melanosporum* can be subjected to different stress conditions, considering its life cycle. In this work, the genome sequence of the ectomycorrhizal ascomycete *Tuber melanosporum* was analysed with the aim to identify and characterize genes involved in environmental stress response. As a second step whole genome arrays were used to verify the transcriptional profiling in the presence of a cold shock (4°C for 7 days). In a whole genome microarray (7496 genes/probe), 423 genes resulted significantly differentially expressed (> 2.5 fold; p-value < 0.05) in stressed mycelia compared to the control ones. After 4°C exposure for 7 days the number of up-regulated genes was 187; the down-regulated genes were 236. The 50-60% of the up- or down-regulated transcripts had no KOG classification and were clustered as unclassified proteins, which represent the most abundant category both in up- and down-regulated genes. A gene subset, concerning a range of biological functions, was chosen to validate the microarray experiment using qRT-PCR. Sixteen out of 22 considered genes confirmed the array data. At our knowledge this is the first work, which considers the global gene expression profiling in a filamentous fungus under cold stress condition.

### PR3.27

#### Screening and sequence analysis of zhd101 (zearalenone lactonohydrolase) homologues in *Trichoderma/Clonostachys* sp.

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Zearalenones are economically important group of *Fusarium* sp. mycotoxins, exhibiting estrogenic activity and chemical structure consisting of a resorcinol moiety fused to a 14-membered macrocyclic lactone. These compounds are converted into a far less estrogenic product by incubation with *Clonostachys rosea* IFO 7063 expressing *zhd101* zearalenone lactonohydrolase gene. In the present study we described screening of *Trichoderma/Clonostachys* combined collection for new strains with functional lactonohydrolase homologues. In the screened samples, we observed degradation reactions in 10 of 79 total *Trichoderma* sp. and *Clonostachys* sp. isolates and have been able to determine new lactonohydrolase homologue sequences with average sequence identity of 90%.