Fungal candidate genes implicated in plant pathogenesis identified via transcriptome analyses

Grain mold is a serious disease of sorghum that affects grain quality and utilization. It is caused by several fungal species, of which *Fusarium*, *Curvularia*, and *Alternaria* spp. are the most common Several factors contribute to grain mold resistance in sorghum and may act additively or synergistically: pigmented testa, red pericarp , endosperm texture, cell wall composition, presence of phenolic compounds and antifungal proteins (β-1,3-glucanases, chitinases, RIPs - ribosome-inactivating proteins, and sormatin). To overcome plant defense compounds the colonizing fungi activate several detoxifying mechanisms, where orphan cytochromes P450 likely play decisive roles and function as virulence factors.

To understand key processes in *C. lunatus* plant pathogenesis and to identify fungal candidate genes implicated in sorghum infection, we exposed fungal mycelia to a synthetic cocktail mimicking sorghum defense compounds for 90 min and 48 h. Transcriptomes were sequenced by next-generation high-throughput sequencing technology on the 454 GS FLX platform (Roche) and Ion Torrent PGM sequencer. Sequences were mapped to the *C. lunatus* genome v2 using Bowtie 2 tool, and differentially expressed genes were identified by EdgeR. Candidate genes encoding hydrolitic enzymes, cytochrome P450s (CYPs), transporters and regulatory proteins were identified bioinformatically via comparative genomics with other closely related and/or pathogenic fungal species. Finding specific genes and mechanisms underlying sorghum infection by *C. lunatus* provided additional knowledge about fungal-plant interactions and offered potential fungal specific targets for antifungal drug design.