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# **Fungal genetics, host pathogen interaction and evolutionary ecology**

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## **PROGRAM & ABSTRACTS**



lignin from spruce wood prior to depolymerization of plant cell wall polysaccharides, thus possessing potential in biotechnological applications such as pretreatment of wood in pulp and paper industry. The genome-sequenced monokaryotic *O. rivulosa* strain 3A-2 derived from the dikaryon T241i, expressed a constitutive set of genes encoding putative plant cell wall degrading enzymes during 8-weeks cultivation on spruce wood. High level of expression of the genes targeted towards all plant cell wall polymers was detected at 2-week time point, after which majority of the genes showed reduced expression. This implicated non-selective degradation of lignin by the *O. rivulosa* monokaryon and suggests high variation between mono- and dikaryotic strains of the white-rot fungi with respect to their abilities to convert plant cell wall polymers.

## Integrating field surveys and molecular data to assess the phytosanitary status of cashew in Guinea-Bissau (West Africa)

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Cashew is a major agriculture commodity in Guinea-Bissau, providing significant export earnings and households' income and food security at the smallholder level. Thus, evaluation of the cashew orchard diseases is of chief importance for sustainable production of this crop. For three years, a series of field surveys was conducted throughout Guinea-Bissau. Data collected included ecology of orchards, social organization of households, evaluation of the incidence and severity of relevant cashew-related diseases, and understory vegetation. A total of 25 cashew orchards were evaluated, covering main administrative cashew-producing regions (i.e. Biombo, Bafatá, Cacheu, Oio, Quinara, Gabú and Bolama). Our results show that cashew orchards are a monoculture cropping system with irregularly spaced trees, in most cases with more than 20 years old. Several diseases' symptoms related to gummosis, anthracnose, and dieback were positively identified, which seem to be uneven distributed along dry/rainy seasons. From infected tissues (trunk, bark, leaf, flowers, apple and nut) close to 200 fungi were isolated and morphologically identified followed by ITS sequencing for confirmation. Reported causal agents of gummosis and dieback were identified in all surveyed regions, namely genera from *Botryosphaeriaceae* (*Lasiodiplodia* sp., *Neofusicoccum* sp., *Cophinforma* sp.); while

the anthracnose agent *Colletotrichum* spp. seems to be restricted to Bolama region. Pathogenicity tests are under progress to relate possible causal agent to the diseases identified. These preliminary results suggest that gummosis is the major cashew disease, and further studies using ecological, biological and environmental data are currently underway to determine main factors associated to the expansion of fungal diseases. This work represents the first assessment of the cashew diseases in Guinea-Bissau, a main step towards sustainable production.

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## Fungal highway and bacterial toll

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Microbes ubiquitously live in nearly every ecological niche. Different species coexist in certain habitats and share available metabolites. A novel mutualistic growth mechanism is discovered between models of filamentous fungus and bacteria, *Aspergillus nidulans* and *Bacillus subtilis*. The bacterial cells move faster along fungal highway and disperse farther on fungal growth, while bacterial cells deliver thiamine to tips of fungal hyphae and support the fungal growth. The simultaneous spatial and metabolic interactions indicate a mutualism that facilitates the bacterial-fungal species to compete for environmental niche and nutrient respectively. The bacterial cells move along fungal highway and pay thiamine as a toll to extend fungal highway. An example of co-isolated bacterial- fungal species from nature supports the ecological relevance of the mutualistic interaction.

## Functional validation of Carbohydrate Esterase family 1 subfamily 1 and 2 by characterization of fungal esterases from uncharacterized branches

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The fungal members of Carbohydrate Esterase family 1 (CE1) from the CAZy database include both acetyl xylan esterases (AXEs) and feruloyl esterases (FAEs). AXEs and FAEs play significant roles as accessory enzymes in biomass saccharification for the