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Friends and foes - comparative genomics of 23 *Aspergillus Flavi* species

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A. oryzae is widely used in food fermentation for the production of soy sauce, sake and miso in addition to enzyme production and it has GRAS status. A close relative *A. flavus* on the other hand produces some highly toxic compounds such as aflatoxin and is an opportunistic pathogen. Both species belong to section *Flavi* consisting of at least 29 species¹.

In this study, we have whole genome-sequenced 19 novel *Flavi* species to examine the core of this section and the differences based on comparative genomics. The genomes reveal a highly diverse section with the number of predicted genes ranging from 9,078 to 14,216 in *A. coremiiformis* and *A. transmontanensi* respectively. We have identified 1,119 *Flavi* specific core protein families corresponding to approximately 9% of the proteome while the number of species specific protein families ranges from 395 for *A. nomius* NRRL 13137 to 2,219 for *A. leporis*.

Of particular interest is enzymes for degradation of carbohydrates, due to their essentiality both for food fermentation, plant pathogenicity, and biotechnology. Thus, the Carbohydrate-Active enZymes (CAZY) potential was investigated ranging from 353 to 617 identified proteins belonging to a CAZy family for *A. coremiiformis* and *A. novoparasiticus* respectively.

In addition, we have investigated the secondary metabolite (SM) potential of this section since it is vital for food safety but also represents potential useful bioactive compounds. The total number of predicted SM clusters in the *Flavi* section is 1,527 constituting 283 cluster families with an average of 73 clusters per species. No SM gene cluster family is shared between the all the *Flavi* species however 106 unique cluster families are only found in one species. Overall this investigation paints a picture of a highly diverse section encompassing friends and foes.

¹Varga *et al.* 2011 Studies in Mycology 69:57-80