P1628
Paper Poster Session
Fungal diagnosis: from culture to molecular techniques

Distribution of bis(methylthio)gliotoxin production within the Aspergillus genus

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Background: Several species of the genus *Aspergillus* can cause invasive aspergillosis (IA) an opportunistic infection associated with high mortality. During host infection, the secondary metabolites gliotoxin (GT) and bis-methylthio-gliotoxin (bmGT) are produced by several species of the genus *Aspergillus* in the hyphae stage. GT is encoded by a gen cluster named *gli*, meanwhile its inactive derivative bmGT is generated by methylation. The gene *gtmA* encodes the methyltransferase involved in the production of bmGT. Both GT and bmGT have been proposed as potential biomarkers of this disease but only bmGT seems to be a reliable IA diagnosis biomarker. Although there are several studies reporting GT production within different species of the genus *Aspergillus*, studies assessing frequency and distribution of bmGT-producing *Aspergillus* isolates are lacking. Here we have analysed bmGT production by several *Aspergillus* spp in order to assess the efficacy of bmGT in the diagnosis of IA produced by different *Aspergillus* species.

Material/methods: *In vitro* GT and bmGT production by 241 different environmental and clinical isolates of five *Aspergillus* species (*Aspergillus* section *Fumigati, n= 115; A. niger, n= 37; A. flavus, n= 35; A. terreus, n= 33; and A. nidulans, n= 21)* was analysed. A 12 McF conidial suspension was made in sterile water. 1ml of this suspension was added to 9ml of liquid medium (RPMI 1640 + glucose 20g/l + glutamine 2mM + HEPES 25mM) and placed in culture flasks. Liquid cultures were incubated at 37ºC for 96h. Then, GT and bmGT detection and quantification were performed by High Performance Thin Layer Chromathography (HPTLC) on culture supernatants. The influence of *gliP* and *gtmA* RNA expression in GT and bmGT production is being analysed by PCR.

Results: GT was detected on several isolates from the species studied (*Aspergillus* section *Fumigati 73%, A. terreus 31%, A. nidulans 27%, A. flavus 11% y A. niger 10%).* bmGT was detected on isolates from *Aspergillus* section *Fumigati* (80%)*, A. nidulans* (27%) and *A. flavus* (14%). It is suspected that PCR results show a correlation between *gliP* and *gtmA* expression and GT and bmGT production on the isolates analysed. Figure 1.

Conclusions: The results indicate that bmGT is produced by most of the *Aspergillus* section *Fumigati* that are responsible of most cases of IA. In contrast this biomarker might not be useful to detect the

infection caused by other less frequent species as *A. niger* or *A. terreus* that were not able to generate this regulatory metabolite.

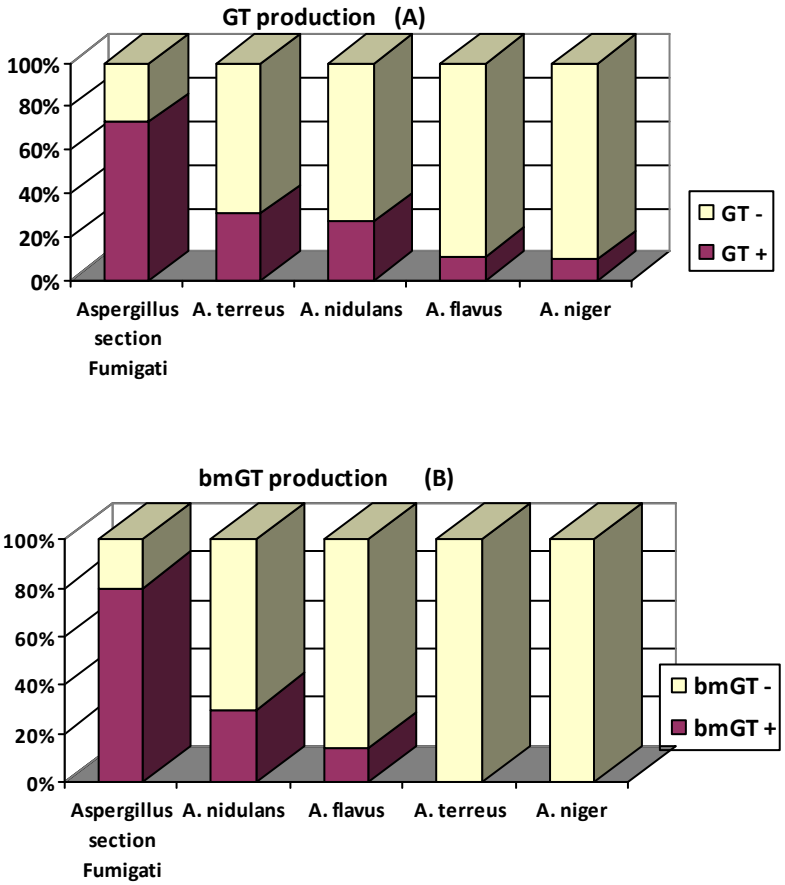

FIGURE 1: frequency of GT (A) and bmGT (B) production in different isolates of several *Aspergillus* species.