SEARCH FOR BIOACTIVE COMPOUNDS PRODUCED BY A *Magnolia dealbata* Zucc.-ASSOCIATED FUNGI

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Key words: bioactive compounds, fungi. Geomyces.

Introduction. Bioactive natural products are defined as those having an effect over another organism, including antibiotics, fungicides, herbicides, antiparasitic, antitumor, etc. They can be obtained from plants, animals, insects and microorganisms (1). Plants offer a great diversity of habitats for microorganisms, and therefore have raised physiological and ecological interactions with them. In addition, plants produce secondary metabolites, which add some complexity to this relationship, and result in an abundant source of bioactive compounds (2). Knowing that plants are good source of new microbial species, we focused on some endemic plants of Mexico, used in traditional medicine. Therefore, the aim of this work was to search for *Magnolia dealbata* Zucc.-associated fungi, by their capacity to produce bioactive compounds.

Methods. Biological activities determined include the search for antimicrobial activity [using the Kirby-Bauer test (3)], fungicide, herbicide, antiparasitic (trypanocidal) (by Neubauer chamber cell counting) and cytotoxic (by MTT assay). For identification of the selected fungi we amplified a region of ribosomal DNA comprising ITS1, 5.8S gene and ITS2 with the universal primers ITS1F and ITS4A. Later, separation of bioactive compounds will be performed by chromatographic and spectroscopic methods.

Results. Most of the isolated fungi which inhibited the susceptible microbial strains have similarities with the *Penicillium* genera, but the effect ranged between them. From these, we chose those with the broad spectrum to identify them (Fig. 1); both resulted to be *Penicillium chrysogenum.* Among other fungi tested, we were particularly interested in *Geomyces* sp., as it has shown to be a psychrotolerant specie. This fungus presents very small mycelia; its hyphae are septated and hyaline, with spherical conidia (Fig.2A). It grows moderately at 25° C, and secretes a red pigment. The microorganism showed partially inhibition of the *Micrococcus luteus, Bacillus subtilis* and *Saccharomyces cerevisiae* growth (Fig.2B).

Amplification, sequencing and blasting of the 5.8S gene (Fig. 2C) supported the fungus as belonging to the *Geomyces* genera. Morphological studies have discarded the fungus as a member of the *Geomyces destructans* species, responsible for causing a global affection in bats, known as the White Nose Syndrome (WNS). This fungus has curve and larger conidia and non-septate hyphae (Blehert *et al.,* 2009).

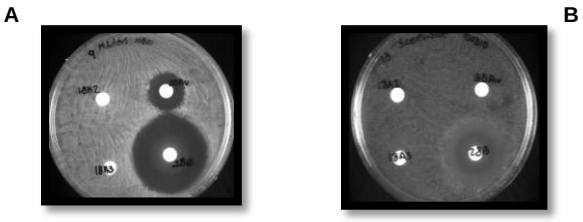

Fig. 1 A) *Penicillium chrysogenum* Kirby-Bauer test in nutrient agar vs *Micrococcus luteus*. B) *Penicillium chrysogenum* Kirby-Bauer test in nutrient agar vs *Saccharomyces cerevisiae.*

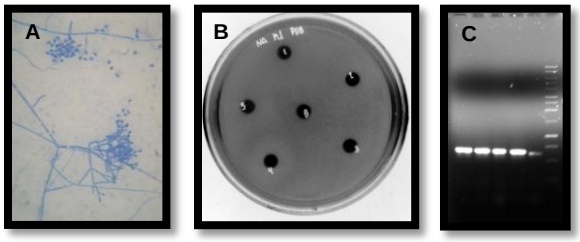

Fig. 2 A) *Geomyces* sp. stained with cotton blue; it has a conidiogenic structure with hyalin and septate mycelia (in 100x). B) Kirby-Bauer test in nutrient agar vs *Micrococcus luteus*. C) A 0.8% agarose gel showing a PCR product of the *Geomyces* sp. amplification (600bp).

Conclusions. We have isolated fungi belonging to the *Geomyces, Fusarium* and *Penicillium* genera. *Geomyces* showed a moderate antibiotic spectra and its phenotype does not agree with *Geomyces destructans*, and likely belongs to a new specie.

Acknowledgements. Allan Espinosa is supported by a postgraduate fellowship from CONACYT, Mexico.

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