FUNGAL STUDY OF GUANO BAT SAMPLES

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Scedosporiosis is the human disease caused by *Pseudallescheria/Scedosporium* complex species (PSC). This group has been described as emerging fungal pathogens due to the increasing frequency in recent years that is often correlated with cases of environmental infection. PSC can cause a wide variety of infections in immunocompromised as well as in immunocompetent individuals as shown in **Fig. 1**. Species of the PSC are saprophytes in soil, wood, polluted water, agricultural land, sewers, ponds and sediments. The distribution patterns of PSC between countries can be seen at **Fig. 2**. However the current understanding of the role of PSC in the environment is still limited. Therefore, a better knowledge on the ecological niches of the fungus is necessary. We aim to study the fungal biota of bat guano by focusing on *Scedosporium* spp.

Fig. 1 – Diagram of manifestations of scedosporiosis.

Table 1 - Distribution of different groups of microorganisms for the positive samples according to culture medium

Culture medium	Number of positive samples for:						
	Mucorales	<i>Aspergillus</i> spp.	Other phialide bearing fungi	PSC	Other hyaline fungi	Dematiaceous fungi	Yeasts Other fungi *
Scedo-Select III	14	2	0	4	10	0	3 0
YPDA+C	30	34	6	1	7	1	3 10
YPDA+C+V	24	3	2	0	3	1	1 3
Total samples (54)	34	34	7	5	14	2	5 12

* Other fungi which were not recognized by macro and microscopy

In conclusion, the PSC occurrence is associated with human-impacted areas. Further studies are required to elucidate connections between environmental sources and clinical infections. We want to continue investigating PSC positive zones, if bats can be a vector of fungi and if there is any association with other emerging pathogens, like species of the genus *Rasamsonia*.

We examined guano bat samples collected in 18 different regions of France. The methodology applied for the fungal isolation is shown in **Fig. 3**. Of the 54 samples, 9 remained negative. The results of the 45 positive samples are shown in **Table 1**. Five samples were positive for *Scedosporium* spp. and these were concentrated around 3 regions (in the Pays-de-la-Loire region of France). Some fungi were selected for molecular identification. Sequencing of the ITS 1 and 2 regions of nuclear rRNA genes was used. At this moment, we are waiting for the results of the sequencing service.

Fig. 2 – Global distribution and relative burden of scedosporiosis infections from June 2007 to December 2016 (Luplertlop N., 2018).

Fig. 3 - Fungal isolation used for guano bats samples.

Luplertlop, N. *Pseudallescheria/Scedosporium* complex species: From saprobic to pathogenic fungus. *Journal de Mycologie Médicale* (2018).

Rougeron, A et.al.. Human-impacted areas of France are environmental reservoirs of the *Pseudallescheria boydii/Scedosporium apiospermum* species complex. *Environmental Microbiology* (2015) 17(4), 1039–1048.