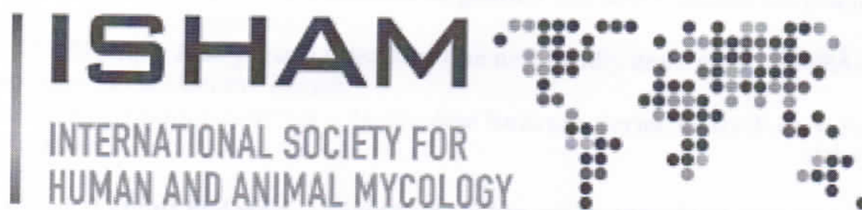
Diversity and pathogenicity of Onygenales

A pre-congress workshop of 20st ISHAM, 28-29 June 2018, Amsterdam, The Netherlands



11:00 – 11:15 - ***Coccidioides* in Mexico** – **Raquel Salazar** (*Ensenada, Mexico*).
11:15 – 11:30 - **Emerging Onygenales species in Southern USA wildlife** – **Marcus Teixeira** (*Flagstaff, USA*).
11:30 – 11:45 - **Coccidioidomycosis in Northeastern Brazil** – **Rossana Cordeiro** (*Fortaleza, Brazil*).
11:45 – 12:00 - **Comparative genomics and evolution of virulence in dimorphic human pathogenic fungi** – **Jose Muñoz** (*Boston, USA*).
12:00 – 12:15 - **Integrated genome–phenome framework for fungal outbreak investigation**– **Vishnu Chaturvedi** (*San Francisco, USA*).

12:15 – 13:30 - **Lunch**

Session 7
Chair: Ann Packeu

13:30 – 13:45 - **Majocchi's granuloma: current perspectives** – **Murat Durdu** (*Adana, Turkey*).
13:45 – 14:00 - **Antifungal drug resistance of *Trichophyton* clinical isolates** – **Michel Monod** (*Lausanne, Switzerland*).
14:00 – 14:15 - **Urease Activity Among the Onygenales**– **Alf Botha** (*South Africa*).
14:15 – 14:30 - **Multifunctional activities of fungal extracellular vesicles** – **Leonardo Nimrichter** (*Stony Brook, USA*).
14:30 – 14:45 - **Cryptic populations of *Histoplasma* in bats in Mexico** – **Daniel Estrada Bárcenas** (*Mexico DC, Mexico*).
14:45 – 15:00 - **Recent advances in genetic tools of dermatophytes** – **T. Yamada** (*Tokyo, Japan*).

15:00 – 15:30 - **Coffee Break**

Session 8
Chair: Marcus Teixeira

15:30 – 15:45 - **Proteolytic activity-associated genes in dermatophytes** – **Aylin Döğen** (*Mersin, Turkey*).
15:45 – 16:00 - **Macrophage activation by IFN-γ triggers restriction of phagosomal copper from intracellular pathogens** - **Qian Shen** *(Ohio, USA)*.
16:00 – 16:15 - **Changing epidemiology of dermatophytoses in Slovenia** – **Maja Subelj** (*Ljubljana, Slovenia*).
16:15 – 16:30 - **Implementation of a multiplex real-time PCR assay in the diagnostic algorithm of dermatophytoses in Liège (Belgium)** - **A. Wakpo** (*Cotonu, Benin*).

16:30 – 17:00 - ***Closing remarks the ISHAM Working Group; next meeting*** – **Marcus Teixeira, Tom Chiller, Vit Hubka, Sybren de Hoog**.

Proteolytic activity-associated genes in dermatophytes

Aylin Dogen[1], Engin Kaplan[2], Serpil Gonca[1], Hazal Boral[3], Suleyha Hilmioglu-Polat[4], Macit Ilkit[3], Reiko Tanaka[5], Takashi Yaguchi[5], Silke Uhrlaβ[6], Pietro Nenoff[6]
[1]*Mersin University, MERSIN, Turkey;* [2]*Bulent Ecevit University, Zonguldak, Turkey;* [3]*Cukurova University, Adana, Turkey;* [4]*Ege University, Izmir, Turkey;* [5]*Chiba University, Chiba, Japan;* [6]*Laboratory for Medical Microbiology, Mölbis, Germany*

Objectives Dermatophytes are among the most successful human pathogens, but their virulence mechanisms are not yet well characterized. Dermatophytic fungi secrete proteases in vivo, and these enzymes are deemed responsible for fungal colonization and degradation of keratinized tissue during infection. In the present study, we used PCR to investigate the presence of genes encoding metalloproteases or fungalysins (MEP) and subtilisins (SUB) in three dermatophyte species whose incidence has been increasing in Europe
Methods Dermatophyte isolates (n = 97), including those of *T. rubrum* (n = 58), *M. canis* (n =33), and *T. benhamiae* (n = 6), were analyzed in the present study. All isolates had beenpreviously identified by conventional ITS sequencing.These dermatophytic fungiwere recovered from both humans and animals (cat and guinea pig), as well assymptomatic and asymptomatic infections.The isolates were cultured on Sabouraud glucose agar (SGA; Merck, Darmstadt,Germany) and incubated at 28°C for 7–15 days.All PCRamplifications were performed in a Techne Prime thermal cycler, in a total reaction volume of 25 uL. contained 12.5 uL of 2x master mix. Positive and negative controls were used for each PCR reaction.The PCR products were resolved by agarose gel (1%, w/v) electrophoresis 0.5 × TBE buffer.
Statistical analysis was conducted using the Statistical Package SPSS, version 19 (SPSS Inc., Chicago, IL, USA). of $p < 0.05$ were considered to indicate statistically significant differences.
Results The distribution of the MEP1–5, SUB1, SUB4, SUB5, and SUB7 genes in the anthropophilic and zoophilic species was found to be significantly different ($p < 0.05$). In addition, the positivity rates of MEP1–5 and SUB1–3 in the human clinical and asymptomatic carrier cat isolates of *M. canis* differed significantly ($p < 0.05$). MEP2 and SUB4 were mostly detected in *T. rubrum* isolates; MEP3 and SUB1 were mostly harbored by *M. canis* isolates; and MEP1, 2, and 4 and SUB3–7 were most frequently harbored by *T. benhamiae* isolates ($p < 0.05$). Furthermore, MEP1–5 and SUB1–3 genes were significantly more prevalent in human clinical isolates of *M. canis* (n = 17) than in asymptomatic cat isolates of *M. canis* (n = 16; $p < 0.05$).
Conclusion The presented overview of the incidence of the MEP and SUB virulence genes in three dermatophyte species of diverse origin provides insights into the host-fungus interaction and dermatophyte pathogenesis.