Place of *Trichophyton soudanense* in the *Trichophyton rubrum* complex : a clinical isolates analysis

Introduction

Development of molecular laboratory tools has led to a complete revision of *Arthrodermataceae* classification and a consequent reduction of species number within this family. However, the phylogenetic place of *Trichophyton soudanense* remains uncertain inside the *Trichophyton rubrum* complex. *Trichophyton soudanense* is synonym either to *T. rubrum* or *T. violaceum* according to the authors, while, more recently, De Hoog *et al.* gave it the status of « borderline species » [1]. *T. soudanense* remains one of the major etiological agents of *tinea capitis* in our hospital [2] and its epidemiological, clinical and phenotypic features led us to consider *T. soudanense*, *T. rubrum* and *T. violaceum* as separate entities. All studies that have been interested in this issue have only used collection strains.

Objectives

The main aim of our study was to determine the phylogenetic place of *T. soudanense* using clinical samples obtained in dermatology consultation at Saint Louis Hospital, Paris, France. Furthermore, this study aimed at evaluating the quality of identifications by phenotypic methods in our laboratory and to determine the discriminating power of different loci used in molecular identification of dermatophytes.

Methods

We sequenced all the isolates obtained between April and September 2016 using four loci: ITS1-ITS4, β 2-tubulin gene, α 1 elongation factor gene and chitin synthase gene. Molecular identification of isolates was obtained by comparing ITS sequences to the Mycobank® database. The sequences of the 4 loci were concatenated and a phylogenetic analysis was performed. In parallel, we photographed each culture on Sabouraud agar medium. The colors of the photographs were extracted and compared according to the RGB color model.

Figure 1: Colors distribution of the front (left) and back (right) of the cultures by species

Results

122 clinical isolates phenotypically identified as :

- *T. rubrum* (n=48),
- *Trichophyton mentagrophytes/interdigitale* (n=34),
- *T. soudanense* (n=10),
- *Trichophyton tonsurans* (n=22),
- *Trichophyton sp.* (n=1),
- *Microsporum audouinii* (n=6)
- *Microsporum canis* (n=1).

The concordance of phenotypic and molecular identifications was 94%.

The color coding of the isolates objectified the pleomorphism of the dermatophytes (Figure 1).

The phylogenetic organization of the genus *Trichophyton* was identical to that obtained by De Hoog *et al.* [1]

Isolates of *T. soudanense* appear to be separated from those of *T. rubrum*, and took an intermediate place between *T. rubrum* and *T. violaceum* when comparison of ITS sequences alone (Figure 2).

The majority of isolates identified as *T. interdigitale* or *T. mentagrophytes* present identical ITS sequences, probably corresponding to the species *T. interdigitale*

Figure 2: Position of *T. soudanense* inside the *T. rubrum* complex by ITS sequence comparison

Conclusion

The sequence differences between *T. rubrum* and *T. soudanense* remain tenuous whereas they are easily differentiated on a clinical presentation. The comparison of their transcriptome could help to understand the origin of their differences.

[1] De Hoog *et al.*, « Toward a Novel Multilocus Phylogenetic Taxonomy for the Dermatophytes », 2017

[2] Gits-Muselli *et al.*, « Continuous Increase of *Trichophyton tonsurans* as a Cause of *Tinea Capitis* in the Urban Area of Paris, France: A 5-Year-Long Study », 2017