

# Epidemiological aspects and genotypic characterization of *T. violaceum* strains collected during a Belgian National survey on anthropophilic tinea

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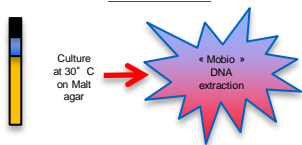
## Objectives

- To investigate the epidemiological determinants responsible for the high number of anthropophilic dermatophytes received by the National Reference Centre for Mycosis of Liège (NRCL), during the last years. Indeed, the last two years, clinical cases of tinea capitis caused by *Microsporum audouinii* (*M. audouinii*) and *Trichophyton violaceum* (*T. violaceum*), have increased in Belgium.
- To perform a genotypic characterization by the Diversilab® system focusing on *T. violaceum*.
- To present results of the national survey launched between February 2013 and March 2014.

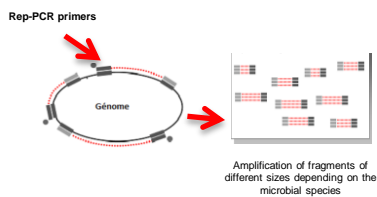
## Methods

**Population:** A total of 23 strains of *T. violaceum* (23 clinical+ 1 reference strains) collected between March 2013 and February 2014 were included in the study. The strains were collected from different laboratories through Belgium. **Figure 1** describes the Diversilab® system (bioMérieux) used for genomic analysis of *T. violaceum* strains.

### Step 1: Fungal culture + DNA extraction



### Step 2: Rep-PCR



### Step 3: Diversilab® analysis

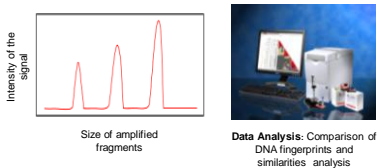


Figure 1: Description of the Diversilab® method.

## Results

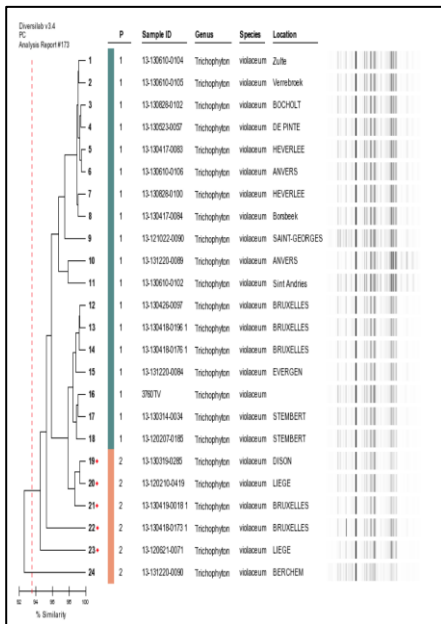


Figure 2: Dendrogram obtained after Diversilab® analysis of the strains N° 1 to 24

The 24 strains have been genotypically characterised by Diversilab® fingerprinting to visualize genomic variants between *T. violaceum* species. **Figure 2** represents the DNA fingerprints of these strains (Strains 1 to 24).

**Figure 3** represents the scatterplot of all strains analysed showing the differentiation into 2 different groups. The genotypic analysis led thus to the distinction of two genotypic variants of *T. violaceum*.

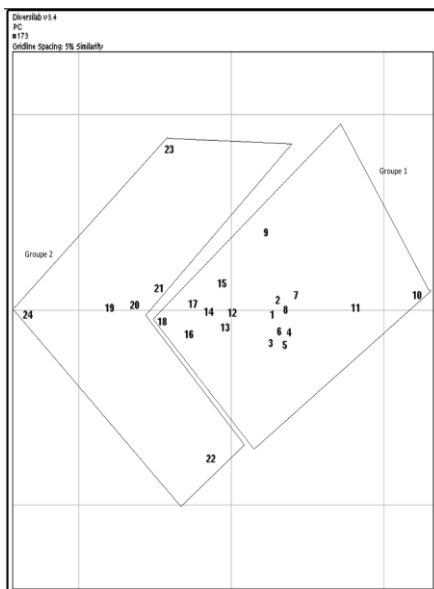


Figure 3: Scatterplots obtained after genomic analysis of strains by Diversilab® showing 2 different groups amongst *T. violaceum* strains.

The major group was composed of 17 strains which were mainly collected in the North of Belgium and included also the reference strain (18/23, 83,3%). The other group (6 strains) was close to the major group but the analysis of the spectral superposition showed some differences between these two groups, defining two distinct variants of *T. violaceum* in the Belgian population. This second variant was mainly recovered from South Belgium (5/6, 83,3%). Analysis of the epidemiological characteristics of the infected population shows that the main age category concerns 0-4 year-old children (n=9, 39,1%) with a sex-ratio M/F of 1.875. Data concerning the geographic origin of the family were present in 82,6% of the cases and reveal that patients were mainly of Ethiopian origin (n=8, 57,9% of known cases). One patient was also from Burundi showing that *T. violaceum* strains probably circulate mainly in East Africa.

Variable	T. violaceum		
	Origine géographique Province	N	Number (%) p-value
		23	
	Liège	6	(26.1) 0,31
	Bruxelles	5	(21.7)
	Brabant flamand	2	(8.7)
	Limbourg	1	(4.3)
	Anvers	4	(17.4)
	Flandre occidentale	1	(4.3)
	Flandre orientale	4	(17.4)
	Hainaut	0	(0.0)
	Brabant wallon	0	(0.0)
Age (années)		23	
	0-4	9	(39.1) 0,13
	5-9	8	(34.8)
	10-14	4	(17.4)
	>15	2	(8.7)
Sexe		23	
	Femme	8	(34.8) 0,14
	Homme	15	(65.2)
Origine ethnique		12	
	Belgique	0	(0.0) 0,0039
	Burundi	1	(8.3)
	Congo	0	(0.0)
	Guinée	0	(0.0)
	Cameroon	0	(0.0)
	Maroc	0	(0.0)
	Mauritanie	0	(0.0)
	Rwanda	0	(0.0)
	Afrique du sud	0	(0.0)
	Ethiopie	11	(91.7)

Table 1: Epidemiological analysis of the data obtained during the national survey.

## Conclusions

The Diversilab® system proved to be an efficient method to investigate the molecular epidemiology of dermatophytes infections as reported previously for *M. audouinii*. These results show that two distinct isolates co-exist in Belgium providing evidence of genetic heterogeneity and a possible spread of one genotypic variant in a restricted geographic area or the co-existence of two variants circulating in different African communities. However, no clear correlation could be established between the appartenance to a group and epidemiological factors, such as age or ethnical origin.