Differential gene expression of species from *Trichophyton benhamiae* clade

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Introduction

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Introduction

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Trichophyton benhamiae

= Arthroderma benhamiae

- Arthrodermataceae
- Onygenales
- Ascomycota
Trichophyton benhamiae

- Clinical manifestation

Experimentally infected guinea pig

Lesion caused by *T. benhamiae*, young women
Trichophyton benhamiae

Cluster 1
- EUROPE (235)
- JAPAN (1)

Cluster 2
- USA (4)
- unknown (1)

Cluster 3
- USA (14)

Cluster 4
- JAPAN (9)
- EUROPE (13)

Cluster 5
- EUROPE (40)

Cluster 6
- Polynesia (1)
- Fiji (1), Indonesia (1)

T. benhamiae var. luteum / T. benhamiae var. benhamiae C2 / T. benhamiae var. benhamiae C3
T. japonicum / T. europaeum / T. concentricum
Trichophyton benhamiae

T. benhamiae / T. japonicum / T. europaeum / T. concentricum
**Trichophyton benhamiae**

**Yellow Phenotype**
- 2002 – 2012: **Switzerland**
  - Symoens et al. (2015)

**White Phenotype**
- before 1967: **USA**
  - Ajello & Cheng (1967)

- 1960 – 1970: **Belgium, Spain, France**
  - Takashio (1974)

- 1977 – 1980: **Finland**
  - Ahola (1980)

- 1989: **Czechia**
  - Hajtnanek & Hajtnanková (1989)

- 1989 – 2009: **USA**
  - Sieklucki et al. (2014)

- since 1996: **Japan**
  - Kimura et al. (2015), Takahashi et al. (2008)

- 2002 – 2004: **France, Switzerland**
  - Fumeaux et al. (2004), Fréalle et al. (2007)

**Epidemic Spread in Europe**
- 2012: **Japan**
  - Hituma et al. (2015)

- 2016: **Brazil**
  - de Frestas et al. (2019)

**Various European Countries**
- before 2010: **Taiwan**
  - Sun et al. (2010)

- 2011 – 2014: **Iran, Russia**
  - Rozai-Motehkozvaei et al. (2013), Pchelin et al. (2016)

- 2010 – 2017: **USA**
  - Needle et al. (2019)
Aims of the study

• To answer:
  
  What stands behind epidemic spread of yellow phenotype?

  How does gene expression of virulence factors differ?
RNA Sequencing-Based Genome Reannotation of the Dermatophyte Arthroderma benhamiae and Characterization of Its Secretome and Whole Gene Expression Profile during Infection

Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi

Differential gene expression in the pathogenic dermatophyte Arthroderma benhamiae in vitro versus during infection

Peter Staib, Christophe Zaugg, Bernard Mignon, Johann Weber, Maria Grumbt, Sylvain Pradervand, Keith Harshman, and Michel Monod

Burmeister et al. Genome Biology 2011, 12:R7
https://genomebiology.com/2011/12/1/R7

Microbiology (2010), 156, 884–895
DOI 10.1099/mic.0.033464-0
Current knowledge - gene expression

Putative virulence factors:
- Secreted proteases
- Transporters
- Hydrophobins

Enzymes from metabolic pathways:
- Non-ribosomal peptide synthase
- Polyketide synthase
- Isocitrate lyase
- Malate synthase
Methods

• Cultivation:
  liquid medium
  mouse skin explants

• Transcriptome analysis:
  RNAseq
  RT-qPCR
Mouse skin explants

- skin tissue
- sterilization
- 3x
- ATB
- cultivation medium
Mouse skin explants

*T. luteum cultivated on MSE:* A) freshly inoculated, B) after 4 days, C) after 6 days, D) after 8 days; grown at 30°C

*T. japonicum cultivated on MSE:* A) freshly inoculated, B) after 4 days, C) after 6 days, D) after 8 days; grown at 30°C
RNAseq – preliminary data

White phenotype
1Len-red = mouse skin after 6 days
4Len-red = liquid medium after 6 days
11Len-red = liquid medium after 8 days

Yellow phenotype
3Len-yellow = mouse skin after 6 days
2Len-yellow = liquid medium after 6 days
RNAseq – preliminary data

White phenotype
1Len-red = mouse skin after 6 days
4Len-red = liquid medium after 6 days
11Len-red = liquid medium after 8 days

Yellow phenotype
3Len-yellow = mouse skin after 6 days
2Len-yellow = liquid medium after 6 days
Take home message

- *T. benhamie* clade consists of several clusters
- One of the clusters is epidemically spreading in Europe
- This cluster probably differs from others in gene expression
Thank you for your attention

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References


