Genome mining and transcriptomic analysis of iron metabolism genes in *Scedosporium apiospermum*

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Background & purpose

Scedosporium apiospermum

- Increasingly important opportunistic pathogen
- Mechanisms of pathogenesis poorly understood
- The role of iron-uptake systems, especially siderophore production and reductive iron assimilation (RIA), may be critical for establishment of *Scedosporium* infections

Purpose

To identify the **genes potentially involved in iron metabolism** in the recently sequenced genome of *S. apiospermum* strain IHEM 14462 [1]

Material & methods

Genome mining

- In silico search for **iron-related genes** (tblastn) [2]
- **Synten**y with *A. fumigatus* Af293, *A. nidulans* FGSC A4, *C. higginsianum* IMI 349063, and *T. reesei* QM6a genomes

Transcriptomic study

- Culture at 37°C for 48 h in **iron-depleted** (200 µM BPS) or **-overloaded** (20 µM FeSO₄, FeCl₃ or transferrin-bound iron) YEPD media
- Gene expression: RT-qPCR (ΔΔCt)

Results

❖ 39 genes putatively involved in:

- siderophore biosynthesis (n = 10)
- siderophore-iron transport (n = 10)
- RIA (n = 14)
- regulation of iron metabolism (n = 5)

❖ Organization in **2 clusters**, each containing a **Non-Ribosomal Peptide Synthetase** as core member (Fig. 1)

Scedosporium apiospermum (SAPIO_CDSxxxx)

Aspergillus fumigatus

Aspergillus nidulans (ANID_0xxxx)

Colletotrichum higginsianum (CH63R_xxxx)

Trichoderma reesei (TRIREDRAFT_xxxxx)

Fig.1 | Genes organization in siderophore-producing clusters in *S. apiospermum*, *A. fumigatus*, *A. nidulans*, *C. higginsianum*, and *T. reesei* genomes. Orthologous genes, taking *A. fumigatus* as reference, are identically colored.

❖ Siderophore biosynthesis and RIA genes are differentially expressed according to iron availability (Fig. 2)

Fig. 2 | Heat map analysis of iron homeostasis genes in *S. apiospermum* IHEM 14462. Expression levels were determined by qPCR after 48 h of culture under iron carency or iron excess conditions. Relative fold-changes were log₂ transformed for data analysis.

Conclusions

S. apiospermum possesses genetic information needed for **iron uptake and regulation**.

Studies are now undertaken to **identify all the siderophores** produced by the fungus according to the iron status, and to determine the relative contribution of both siderophore production and reductive assimilation systems in its **virulence**.

References:

- [1] Vandeputte *et al.*, Genome Announc. 2014;2:e00988-14
- [2] Haas H., Front Microbiol. 2012;3:28

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