**Irmer**

In vitro model of aspergillosis, in Media and Blood

M = media

B = blood

30 = after 30 minutes

180 = after 180 minutes

**Hillmann**

Cells cultivated in 02 controlled fermeter, essay at

* 0 min, 100% O2
* 15 min, 5% O2
* 30 min, 5% 02
* 75 min, 100% 02

**Hagiwara**

Fungal conidia are dormant unless condition for germination are present.

* Germ are germinated conidia (1h cultured conidia)
* Atfa is a transcription factor, from conidia
* afs35 is the reference strain for aspergillus fumigatus (CTR), it’s from conidia

**Liu**

Grown in a medium without zinc and nitrate. Samples are WT and mutation ace1 gene, a transcription factor

**Kowalski**

Expression in normoxia and hypoxia (lack of oxygen), using WT and a fumigatus strain (EVOL20) with reduced ability to grow in low oxygen

* hrmA Hypoxia Responsive Morphology factor A
* EVOL are EVOL20 strain
* Hyp is hypoxia
* Nor is normoxia
* hrmA REV is the EVOL strain with delta hrmA
* OE is over expression

**Kurucz**

Tratement with hydrogen peroxide and iron deficiency

**Niu**

Response to antifungin treatment, both datasets are mycelium

* Hode is treatment with 5 ug/mL 5,8-dihydroxyoctadecadienoic acid
* Etoh is 0.005% ethanol

**Valero**

Treatment with caspofungin and mutants for fhdA, transcription factor important for mitochondrial function and iron metabolism

**Danion**

Akub(KU80) is a strain with increased frequency of homologous recombination. It does so by disrupting the homologous gene to human KU80. It’s grown in minimum medium and in a medium with D-glucose (G), Ammonium tartrate (A) and KH2PO4 (P), GAP

**Lind and Lind2**

Dataset with mutants in VeA (stimulates product of diverse type of Small Metabolites) and MtfA a VeA depended regulator for Small Metabolites)

**Losada**

Experiment in hypoxia (5% C02 and 1% 02) at time 0h, 12h, 24h and 36h

**Bowyer**

Trascriptome of fumigatus A1160, hapB mutant and 29.9 in presence of itraconazole. 29.9 is not explained (neither is hapB but that is at least a known gene and an often used mutant)

**Furukawa**

Response to itraconazole in WT and mutant delta nctA and nctB (Negative CofactorTwo A and B)

STRATEGY FOR HEATMAP 1 - DONE

Remove similar datasets: Kowalski has a lot of dublicated datasets that cluster together cause they are very similar

Remove complex samples: multiple mutants samples are probably not very useful to study general genes

Remove badly annotated datasets: Bowyer has not additional info and no article avaiable

STRATEGY FOR HEATMAP 2

Write code for Log2FoldChange

What to keep?

* Irmer vs blood 180 and medium 180
* Hillmann 30 vs 0
* Hagiwara hyphae vs conidia, germ vs conidia, atfa vs conidia
* Liu mutant vs CTR
* Kowalski hypoxia vs nor\_WT\_CTR, nor\_hrma\_delta vs nor\_WT\_CTR (maybe add different strain vs CTR)
* Kuruc festarv vs CTR, oxstress vs CTR
* Niu hode 120 vs 30, hode vs 30 (but not a lot changes, also the 30 is not WT)
* Valero WT\_cas vs CTR, fhda\_delta vs CTR
* Danion GPA vs min (but min is not WT)
* Lind delta vs CTR
* Lind2 delta vs CTR
* Losada 12 vs CTR, 36 vs CTR (maybe just keep 36 vs CTR?)
* Bowyer a1160\_itra vs CTR, hapb\_noitra vs CTR, 29\_no itra vs CTR (but 29 not explained)
* Furukawa WT\_itra vs CTR, nctB\_noitra vs CTR, nctA vs CTR