Molecular adaptations to hypersaline environments in *Hortaea werneckii* and some other selected fungi – I.

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(Hyper)saline environment

Salts dissolved in water → Lowered water potential

\[ \Psi \] – less water is available to organisms

\[ \Psi_s = - CiRT \]

Hypertonic environment

\[ \text{Loss of } H_2O \]
Isolation and detection of fungi

**Samples:** brine, immersed wood, surface of halophites, soil, microbial mats

**Classic isolation:** filtering, direct inoculation, very selective media (17-32% NaCl), aerobic, microaerophilic, anaerobic incubation

**Molecular methods:** DNA isolation from natural samples, PCR, Temporal Temperature Gradient gel electrophoresis (TGGE), Clone Sequencing Libraries
Salt as source of contamination of food with fungi
Fungi are inhabitants of solar salterns and salty lakes around the world.
Population dynamics of fungal communities in hypersaline environments *(Statistical canonical correspondence analysis)*

– temporal factor,
– water activity,
– nutrients (P, N)

Numbers: hypersaline water up to 40.000 CFU/l

For comparison: ocean water 10 CFU/l, polluted sea water 5.000 CFU/l
Emericella Fusarium
Acremonium, Aspergillus, Penicillium, yeasts
Eurotium
Aternaria Cladosporium
Black yeasts
Wallemia

3% 17% 35%
Halotolerant and halophilic black yeasts

- Growth within a wide range of NaCl (0 - 32%)
- Constant presence in salterns/ rare occurrence elsewhere

- **Extremophilic ecotype:** slow, often meristematic growth, proliferation with endoconidiation, thick, melanized cell walls
Understanding life at low water activity – important for agronomy and biotechnology

Almost 400 Mha of land is salinized (Nachtergaele and Young, 2000)

20% of irrigated soil is salinized (Yeo, 1999)

On a global scale we lose every minute 10 hectares of arable land, 3 due to salinization (Kovda, 1983)
Model organisms for adaptations to hypersaline conditions

Saccharomyces cerevisiae

- Aspergillus nidulans
- Candida sorbitophila
- Candida versatilis
- Debaryomyces hansenii
- Pichia guillermondii
- Rhodotorula mucilaginosa
- Zygosaccharomyces rouxii
New model organisms needed!!!
Halotolerant model - *Aureobasidium pullulans*
var. pullulans: plant, Salterns, osmotic subst.

var. melanogenum: glaciers, water, deep sea

var. subglaciale: glaciers

var. namibiae: desert
Freezing – dehydration of cells due to ice formation and diminished water absorption
High salinity - dehydration of cells due to osmotic disbalances
10th European Conference on Fungal Genetics: Dothideomycetes Comparative Genomics Workshop, March 29, 2010

US Department of Energy Joint Genomes Institute (DOE JGI), Walnut Creek, Ca, USA.

Genomes of 4 A. pullulans varieties?
Hortaea werneckii – extremely halotolerant model organism
Hortaea werneckii
Ecological niches
Genom of *H. werneckii* already in progress...
Wallemia ichthyophaga – obligate halophile
Wallemia sebi (up to 2005)
Groth of 3 *Wallemia* species on media with different water activity

![Graph showing the growth of Wallemia species on media with different water activities](image-url)
BASIDIOMYCOTA

TS Trichosporonales
TL Tremellales
FB Filobasidiales
CFB Cystofilobasidiales
DM Dacrymycetales
MZ Malasseziales
TT Tilletiales
ET Entylomatales
GF Georgiomyceliales
EB Exobasidiales

AFTOL project:
Hibbett et al.:
BGI Genomics Institute Shenzhen; China
**H. werneckii** and other fungi adapt to high concentrations of NaCl on many levels

**Melanisation of cell walls is salt dependent (distribution of granules, expression of genes)**


**High levels of compatible solutes (glycerol, erythritol, arabitol, manitol) are synthesized**


**Differential expression of many genes**


**Membrane fluidity changes**
