Table 1. Genotype, phagocytosis and proliferation index for 21 strains of Cryptococcus spp.

| Strain | ST* | Genotype | Clonal complex | Phagocytosis | Proliferation (PI)** |
|--------|-----|----------|----------------|--------------|---------------------|
| A      | 23  | VNI      | 23             | Low          | PI ≤ 1.0            |
| R      | 23  | VNI      | 23             | Intermediate | PI ≤ 1.0            |
| B      | 63  | VNI      | 23             | Low          | PI ≤ 1.0            |
| F      | 63  | VNI      | 23             | Low          | PI ≤ 1.0            |
| J      | 311 | singletone| 2             | High         | PI > 1.0            |
| E      | 608 | singletone| 2             | Low          | PI ≤ 1.0            |
| Q      | 612 | singletone| 2             | Low          | PI ≤ 1.0            |
| N      | 32  | singletone| 2             | Low          | PI ≤ 1.0            |
| O      | 32  | singletone| 2             | Low          | PI ≤ 1.0            |
| M      | 607 | singletone| 2             | Low          | PI ≤ 1.0            |
| P      | 32  | singletone| 2             | Low          | PI ≤ 1.0            |
| S      | 338 | singletone| 2             | Intermediate | PI ≤ 1.0            |
| L      | 610 | singletone| 2             | Low          | PI ≤ 1.0            |
| I      | 606 | singletone| 2             | Low          | PI ≤ 1.0            |
| D      | 609 | singletone| 2             | Low          | PI ≤ 1.0            |
| G      | 611 | singletone| 2             | Low          | PI ≤ 1.0            |
| K      | 20  | VGI      | 2             | Low          | PI ≤ 1.0            |
| T      | 132 | VGI      | 2             | Low          | PI ≤ 1.0            |
| S      | 157 | VGI      | 2             | Low          | PI ≤ 1.0            |

*ST: Sequence type. **PI: Proliferation index.

Conclusions: Candida albicans was the common species isolated in our study. Candida Chrome Agar can be used as a routine media for rapid identification and Candida speciation. ART needs to be done routinely to know the susceptibility pattern of isolates and initiate proper treatment of patients. Oral yeast colonization was associated with low CD4+ count (<200 cells/μL). Thus, oral lesions can serve as early markers for HIV infection.
PS81
Genetic recombination between the main human skin commensal fungus, Malasseza restricta, and M. globosa using an Agrobacterium tumefaciens-mediated gene transfer system

Otami Cho1, Yasuhiro Matsumoto1, Tatsuyoshi Yamada2, Taisei Sugita1
1Meiji Pharmaceutical University, Kyoide, Japan
2Nakayama University of Medical Mycology, Hachiouji, Japan

Poster session 3, September 23, 2012, 12:30 PM – 1:30 PM

Objectives: Malassezia restricta and M. globosa cause or exacerbate Malassezia-associated skin, seborrheic, and atopic dermatitis, as well as pruritus varioliforme, but the virulence factors remain unclear because between-species genetic recombination has not yet been achieved. We built an Agrobacterium tumefaciens-mediated gene transfer (ATMT) system that generated gene-knockout mutants of both Malassezia species.

Materials and Methods: The binary vector pPG1-A1tk1-NAT1 was introduced into M. restricta CBS 7877 and M. globosa CBS 7966 via ATMT. FKR1 was re-introduced into the mutants to counteract the deficiencies.

Results and Discussion: The medium acetoacetate concentrations and temperature, as well as the co-cultivation ratios of A. tumefaciens and the Malassezia strains, affected recombination efficacy. We generated a mutant of the FKR1 gene (which encodes the FK506-binding protein A) that leads to the calcium resistance mutant. Wild-type M. restricta and M. globosa were toxicologically non-toxic, while the FKR1 mutants were toxicologically resistant, drug susceptibility was retained by re-introducing FKR1.

Conclusion: Studies on recombination between M. restricta and M. globosa will aid elucidation of the molecular mechanisms underlying Malassezia-associated dermatitis.

PS82
Molds and yeasts on the beach: environmental factors influencing distribution of fungi along european shores

Massimo Cogliani1, Anna Puglisi1, Maria Carmela Esposto1, Luisa Romano1, Joao Brandao2, Mycoscanda Working Group
1Dipt. Biomedical Sciences for Health, Università degli Studi di Milano, Milan, Italy
2Dipt. of Environmental Health, National Institute of Health Dr. Ricardo Jorge, Lisbon, Portugal

Poster session 3, September 23, 2012, 12:30 PM – 1:30 PM

Objectives: The present study employed data collected during the Mycoscanda survey to investigate the environmental factors influencing marine and soil distribution along European shores by applying a species distribution modeling approach.

Methods: Occurrence data were compared to climatic datasets (temperature, precipitation, and solar radiation), soil datasets (chemical and physical properties), and water datasets (temperature, salinity, and chlorophyll concentration) downloaded from web databases. All dataset layers were edited and formatted by QGIS software and analyses were performed by Maxent software.

Results: The distribution maps inferred computing occurrence data on shores for Aspergillus spp., A. niger, Penicillium spp., dermatophytes fungi, and considering all mollusks, to climatic datasets showed the highest probability of presence along Eastern and South-Central Mediterranean coasts, whereas comparison of water occurrence data to water furmures identified a high suitability along Eastern Mediterranean coasts, Gulf of Lion, Southern coasts of Spain, and Southern and Central Atlantic coast of Portugal, Southern Atlantic coast of France, Netherlands coasts, the mouth of Danube, coasts of the Island sea, and Kari Lagoon in Lebanon. The main variables contributing to the models were minimum temperatures in winter, water temperatures during spring, and chlorophyll concentration. The comparison of soil datasets showed a high tolerance of soils with a high concentration of CaCO3 and pH. Nitrogen concentration was tolerated at values below 1 g/kg and phosphorus concentration at values <20 mg/kg and >40 mg/kg. In addition, the model identified a high tolerance to soils rich in nickel.

The same analyses were performed for the following groups of occurrence data: Candida spp., A. niger, P. verrucosum, and all yeasts. Results showed the highest probability of presence on shores located along the coasts of Eastern Mediterranean Sea, Southern-Central Mediterranean Sea, Northern Adriatic Sea, Kari Lagoon, and Northern European coasts from France to Denmark. In waters, high suitability areas were located along the coasts of Northern Black Sea, Northern Adriatic Sea, coasts of Island Sea, Western Adriatic coast of France, and the Northern European coasts from France to waters Denmark. The most relevant variables contributing to the model were minimum temperatures during winter and water chlorophyll concentration. The comparison with soil features showed similar results to those obtained for molds, except a high tolerance for soils rich in carbonates.

Conclusions: All together our results suggest a different probability of distribution of yeasts and molds along European shores. Yeasts seem to evolve less temperature bears during warmer than molds and this reflects a higher suitability for the Northern European coasts. This difference is more evident considering suitability in waters. Both distributions of molds and yeasts are influenced by basic soil pH, probably because acidic soils are more favorable to bacterial growth. Soils with high nitrogen concentrations are not suitable for fungal growth, which, in contrast, are optimal for plant growth, favored by this environment. Finally, molds show affinity with soil rich in nickel and yeasts with soils rich in calcium resulting in a distribution mainly at the mouths of European rivers or lagoons, where these metals accumulate in river sediments.

PS84
Mold infections in solid organ transplant recipients in Indian setting

Niveditha Enaganti, Kripa Sridhar, Rajkumar J, Subramaniam Swaminathan S, Joy Verghese, Sreenivas Reddy, Selva, Muthukumar, Balaji, Lokeshwar, Moulikeswaran
Glenwood Global Health City, Chennai, India

Poster session 3, September 23, 2012, 12:30 PM – 1:30 PM

Background: Fungi are ubiquitous in nature and the risk of infection rises when a person is immunosuppressed. Prior studies have shown that 70% of all invasive fungal infections in transplant recipients were mucous mold infections (MMI).