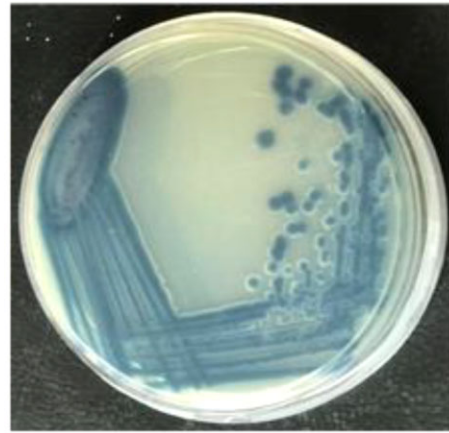
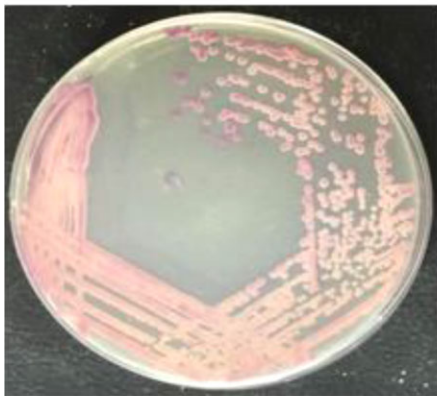


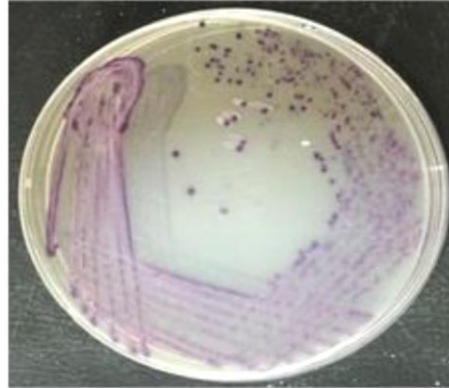
Candida albicans



Candida tropicalis



Candida krusei



Candida glabrata

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Genetic recombination between the main human skin commensal fungus, *Malassezia restricta*, and *M. globosa* using an *Agrobacterium tumefaciens*-mediated gene transfer system

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Objects: *Malassezia restricta* and *M. globosa* cause or exacerbate *Malassezia*-associated skin, seborrheic, and atopic dermatitis, as well as pityriasis versicolor, 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 pAg1-Δfkb1::NAT1 was introduced into *M. restricta* CBS 7877 and *M. globosa* CBS 7966 via ATMT; FKB1 was replaced. Then, FKB1 was re-introduced into the mutants to counteract the deficiencies.

Results and Discussion: The medium acetosyringone concentration 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 FKB1 gene (which encodes the FKBP12 protein that binds to the calcineurin inhibitor tacrolimus). Wild-type *M. restricta* and *M. globosa* were tacrolimus-sensitive, while the FKB1 mutants were tacrolimus-resistant; drug susceptibility was restored by reintroducing FKB1.

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

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

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Objectives: The present study employed data collected during the Mycosands survey to investigate the environmental factors influencing yeasts and molds 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) down-

loaded 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 comparing occurrence data on shores for *Aspergillus* spp., *Aspergillus fumigatus*, *A. flavus*, *A. niger*, *Fusarium* spp., dematiaceous fungi, and considering all molds, to climatic datasets showed the highest probability of presence along Eastern and South-Central Mediterranean coasts, whereas comparison of water occurrence data to water features 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 Ireland sea, and Kuri Lagoon in Lithuania. The main variables contributing to the models were minimum temperatures in winter, water temperature during spring, and chlorophyll concentration. The comparison with soil datasets showed a high tolerance of soils with a high concentration of CaCO₃ and basic 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., *Rhodotorula* spp., 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 coasts, Kuri 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 Ireland Sea, Western Atlantic coast of France, and the Northern European coasts from France to western 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 cadmium.

Conclusions: All together our results suggest a different probability of distribution of yeasts and molds along European shores. Yeasts seem to tolerate low temperatures better during winter 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 cadmium resulting in a distribution mainly at the mouths of European rivers or lagoons, where these metals accumulate in river sediments.

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Mold infections in solid organ transplant recipients in indian setting

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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 invasive mold infections (IMI).