Molecular and conventional identification of Malassezia spp. in Malassezia spp.-associated dermatoses

**Background**
Malassezia spp. yeasts are known to be associated with pityriasis versicolor, seborrheic dermatitis, dandruff, and Malassezia folliculitis. Recently, their pathogenicity is being expanded to other skin disorders, such as atopic dermatitis, psoriasis, and acne vulgaris. Identification of Malassezia spp. yeasts has been carried out mostly through morphological and biochemical analyses. Various molecular biological techniques are now available and being preferred as they are species-specific, and therefore are more accurate and less time-consuming.

**Objective**
The purpose of this study was to elucidate the pathogenic role of Malassezia spp. in Malassezia spp.-related skin diseases, and to evaluate the reliability of PCR as a molecular diagnostic tool in identification compared with conventional methods.

**Patients and methods**
Conventional identification of Malassezia spp. and molecular analysis using PCR-restriction fragment polymorphism (PCR-RFLP) was carried out on some Malassezia spp.-associated dermatoses.

**Results**
Three Malassezia spp. were identified (Malassezia furfur, Malassezia globosa, and Malassezia sympodialis), and the results of the conventional identification were in
accordance with the pattern obtained from 26S rDNA (or large subunit ribosomal DNA) PCR-RFLP.

**Conclusion**

26S rDNA PCR-RFLP method confirmed the conventional identification of *Malassezia* spp. in *Malassezia* spp.-associated dermatoses in our study. Further species-specific and strain-specific identification may help elucidate the role of the individual species in various diseases.

**Keywords:**

Malassezia spp., Malassezia spp.-associated dermatoses, PCR-restriction fragment polymorphism