**S\_Text 8. Gene family expansions**

*Secretory lipases (PF01764)*:Secretory lipases can be divided into two PFam families: PF03583 and PF01764. The Lipase 3 (PF01764) family includes the previously characterized *M. globosa* LIP1 gene [1]. Members of this family are also known as triglyceride lipases, and are widely distributed in prokaryotes, plants, animals (http://pfam.xfam.org/family/PF01764), and fungi (**S\_Table 3**) [2]. Our analysis revealed there are eight such lipase genes in *M. globosa,* six in *M. restricta*, and seven in *M. sympodialis* (**S\_Table 3**). The number of genes in other species is comparable, except in diploid *M. furfur* strains and in *M. slooffiae* (12 copies).

*Acid sphingomyelinase*:The PFam database does not have a corresponding category for acid sphingomyelinase. Therefore, we used a sequence similarity-based approach to identify these genes in the *Malassezia* proteome based on the *C. albicans* acid sphingomyelinase. We found them to be highly conserved (4-5 copies in haploids) (**S\_Table 3**).

*Proteases and peptidases*:Proteases are known to be associated with virulence in pathogenic fungi [3]. The aspartyl protease family (PF00026) is among the largest domain families in the *Malassezia* genus (**S\_Table 3**). The numbers of aspartyl proteases in each species vary (**S\_Table 3**). For example, *M. globosa* and *M. restricta* genomes harbor more copies of this gene compared to *M. sympodialis* (**S\_Table 3**). Beyond aspartyl proteases, the *Malassezia* genomes also contain a range of other proteases or peptidases (including cysteine peptidases, metallopeptidases and serine peptidases) many of which have widely varying copy numbers in different species (**S\_Table 3**) and could contribute to niche specificity in *Malassezia*.

**References**

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