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**Evaluation of differences in C acnes, S epidermidis and Demodex between rosacea subjects and normal controls**

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The role of the microbiome in the etiology and exacerbation of rosacea has been highlighted in recent studies. Increased *Demodex* mite density is frequently reported in association with rosacea, but multiple studies have failed to correlate *Demodex* and rosacea severity. *S. epidermidis* has been isolated from rosacea pustules, and decreased abundance of C*. acnes*, dominant on healthy facial skin, has been demonstrated in rosacea subjects. We sought to better understand these players in the rosacea microbiome and to elucidate the differences between rosacea and normal control subjects. In our study, 13 subjects with papulopustular rosacea were compared to 3 normal subjects. Rosacea subjects had at least one papule and mild erythema. Lesional (L) and nonlesional (NL) facial swabs of rosacea subjects and swabs of normal subjects were obtained and analyzed for abundance of bacterial and *Demodex* DNA by qPCR. *C. acnes* rCFU showed no significant difference between normal subjects and L and NL rosacea skin. *Demodex* copy number also exhibited no difference between rosacea subjects L and NL skin, but there was a slight trend ($p=0.0622$) toward lower copy number in NL rosacea subjects when compared with normal. *S. epidermidis* exhibited no difference between normal subjects and rosacea subjects L and NL skin, but there was a slight trend toward a significant difference between *S. epidermidis* L and NL skin ($p=0.0594$). The results of our study show no significant difference between normal subjects and rosacea subjects at baseline in their L and NL skin. The trend toward significance between normal skin and NL rosacea subjects; *Demodex* copy number, as well as the increase in *S. epidermidis* in L verses NL skin, will need to be further explored. Expansion of our healthy control subjects and improved uniformity in swab sites are currently underway to further explore these differences.