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Introduction:

The association of microbiota changes with sensitive skin remains controversial until now. Although a strong correlation is detected between skin microbiota distribution and biophysical parameters, there is little knowledge on the link between sensitive skin and skin microbiota in Chinese women¹²³. This study aimed to unravel the correlation between facial skin microbiota distribution and skin barriers in Chinese women with sensitive skin.

Materials & Methods:

Totally 34 volunteers were enrolled, including 24 subjects with sensitive skin (SS group) and 10 subjects with non-sensitive skin (NS group). The cuticle moisture content, transepidermal water loss (TEWL) and facial skin sebum secretion were measured, and the facial skin surface morphology was evaluated. Sensitive skin samples were collected from the facial (SS-F group) and chest skin of subjects in the SS group (SS-C group), while non-sensitive skin samples were collected from the facial skin of subjects in the NS group (NS-F group). All skin samples were subjected to 16S rRNA sequencing.

Results & Discussion:

16S rRNA sequencing detected Actinobacteria, Firmicutes and Proteobacteria as the three most common microbiota phyla and *Propionibacterium*, *Paracoccus*, and *Corynebacterium* as the three most common microbiota genera, and there were no significant differences in the relative frequency of Actinobacteria, Firmicutes or Proteobacteria, or *Propionibacterium*, *Paracoccus* or *Corynebacterium* among the SS-F, SS-C and NS-F groups ($P > 0.05$)(Fig.1). We detected no significant difference in the diversity of bacterial communities among the SS-F, SS-C and NS-F groups; however, the Shannon's diversity index was significantly higher in the NS-F group than in the SS-C group (Fig.2). In addition, Spearman correlation analysis showed a correlation between the microbiota genera and skin physiological parameters ($P < 0.05$). (Fig.3)

References:

- 1.Ma YF, Yuan C, Jiang WC, Wang XL, Humbert P. Reflectance confocal microscopy for the evaluation of sensitive skin. *Skin Res Technol.* 2017; 23(2): 227-234.
- 2.Li X, Yuan C, Xing L, Humbert P. Topographical diversity of common skin microflora and its association with skin environment type: An observational study in Chinese women. *Sci Rep.* 2017; 7(1): 18046.
- 3.Chen SY, Yin J, Wang XM, Liu YQ, Gao YR, Liu XP. A new discussion of the cutaneous vascular reactivity in sensitive skin: A sub-group of SS? *Skin Res Technol.* 2018; 24(3): 432-439.

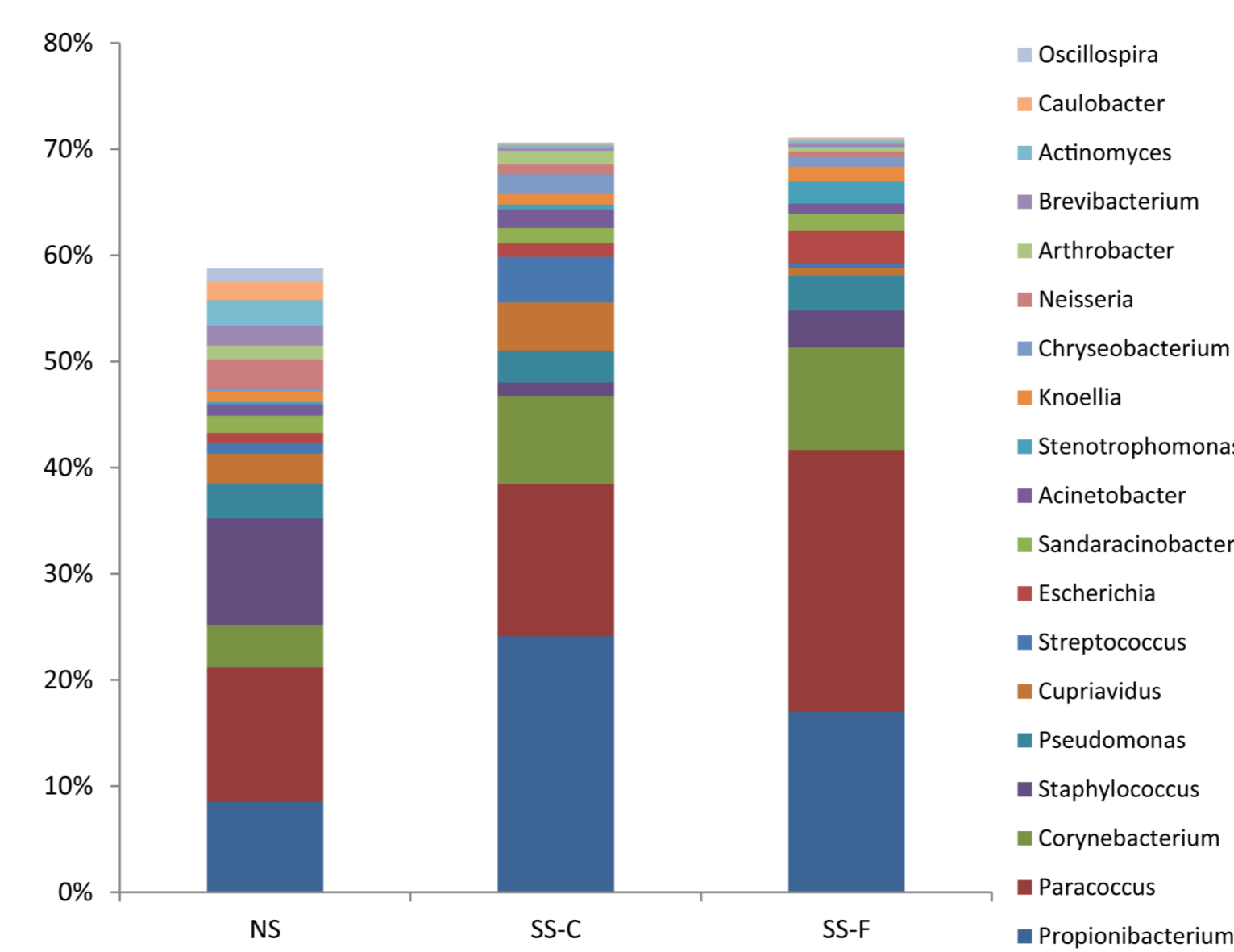


Figure 1. 16S rRNA sequencing detects genus-wide distribution of microbes on the facial and chest skin of subjects with sensitive skin and facial skin of subjects without sensitive skin.

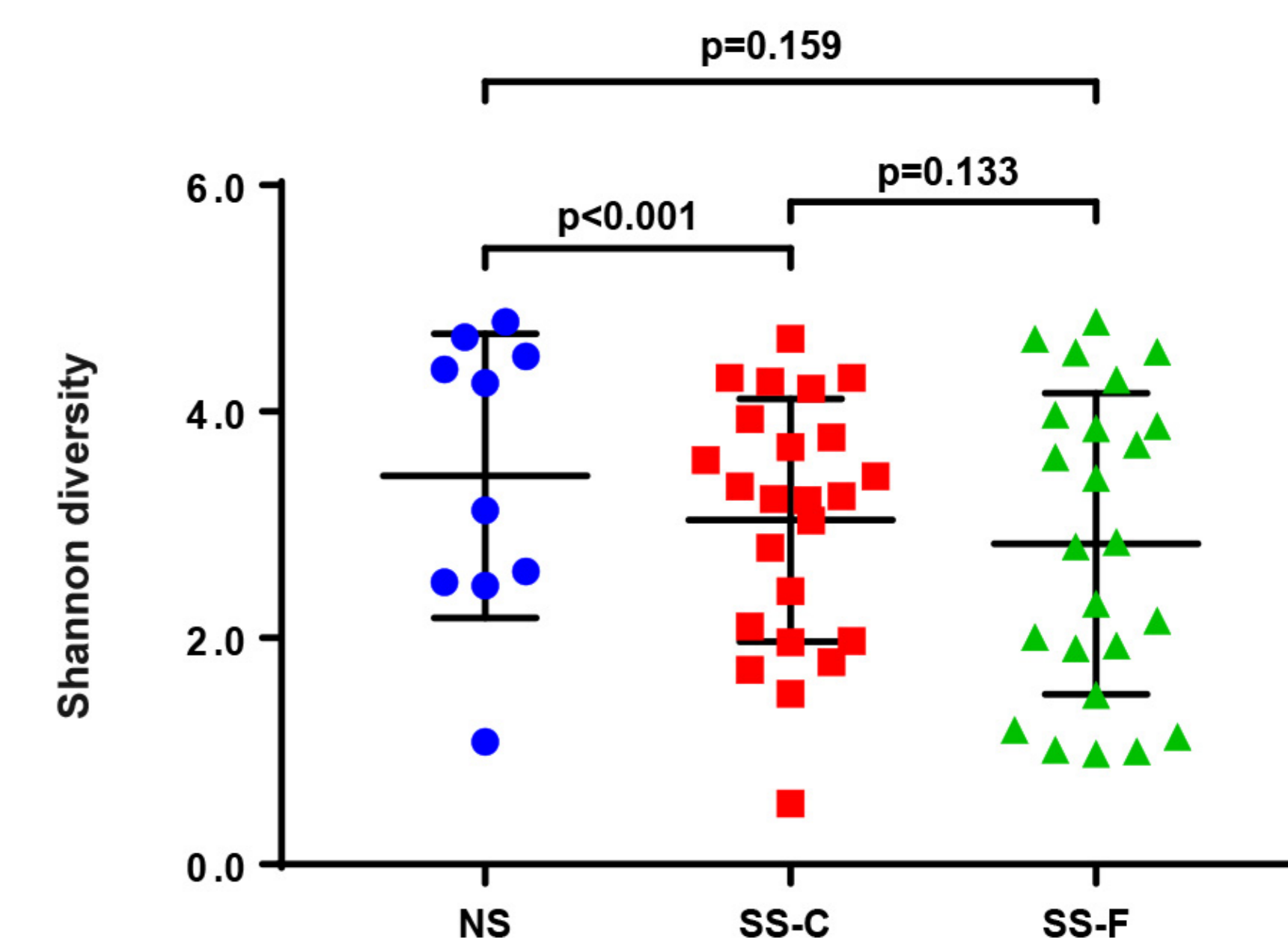


Figure 2. Comparison of Shannon's diversity index among the SS-F, SS-C and NS-F groups.

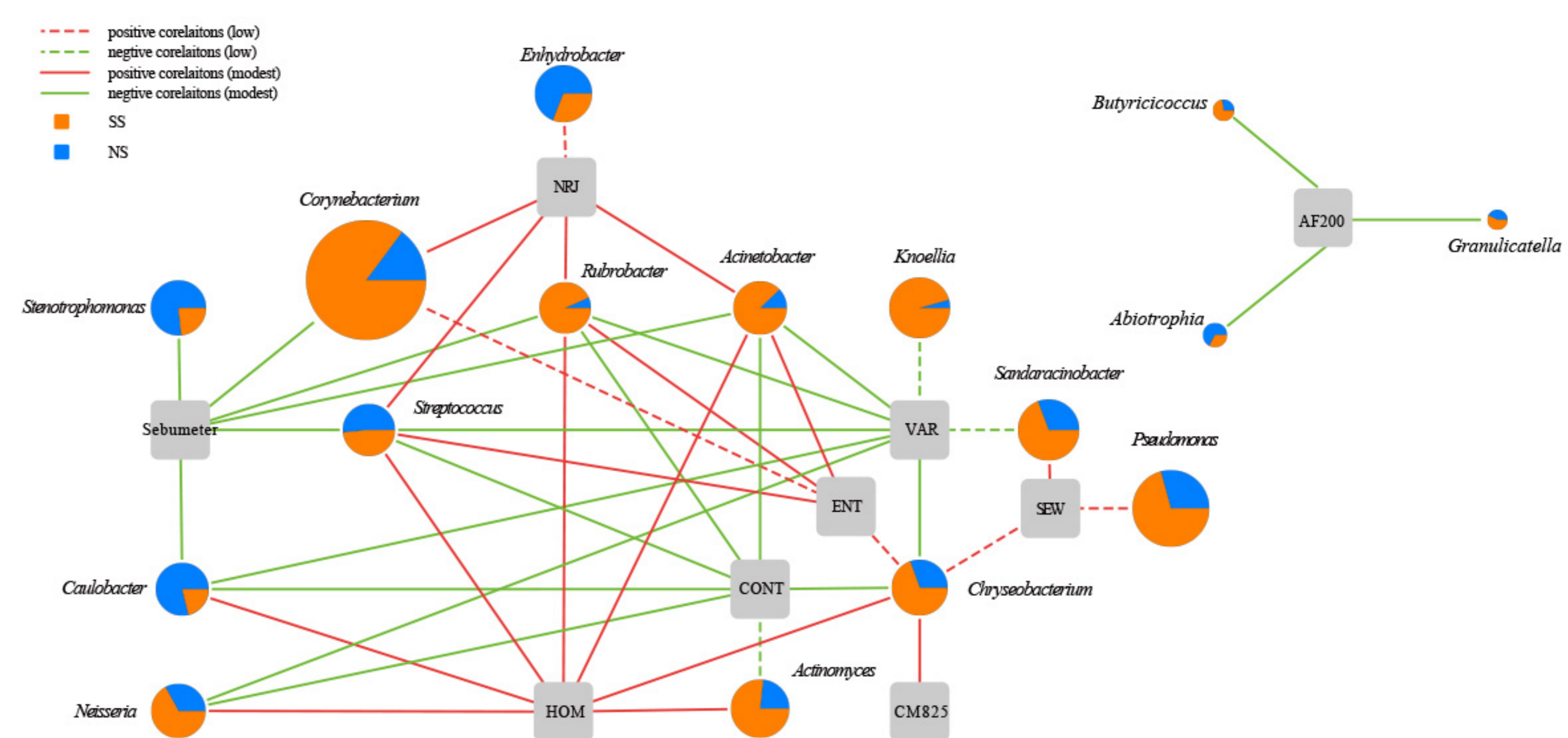


Figure 3. Correlation between skin microbiota and physiological parameters of skin. Dashed lines indicate a weak correlation (correlation coefficient of < 0.35 or > -0.35), and solid line denote a medium correlation (correlation coefficient of > 0.35 and < 0.68 or > -0.68 and < -0.35). Sebumeter, skin sebum secretion; NRJ, energy; HOM, homology; CONT, contrast; ENT, entropy; VAR, variety; CM825, cuticle moisture content; SEW, surface evaluation of wrinkles; AF200, transepidermal water loss.

Conclusions:

This study preliminarily unravels the skin microbiota of sensitive skin using a high-throughput tool, and there are no microbiota genera with strong associations with skin physiological parameters.