Analisis Diversitas Mikrobiom Kulit Wajah Sehat Berdasarkan Parameter pH dan Kelembaban Kulit menggunakan Next Generation Sequencing 16s rRNA = Diversity analysis of healthy skin microbiome based on skin pH and moisture level using Next Generation Sequencing 16s-rRNA

Windy Dwininda, author

Abstrak

Keseimbangan berbagai jenis bakteri pada kulit sangat penting dalam menjaga kesehatan kulit. Permasalahan pada kulit wajah yang muncul salah satunya disebabkan oleh disbiosis mikroba. Penelitian dilakukan untuk menganalisis keberagaman mikrobiom bakteri yang terdapat pada kulit wajah dengan kondisi pH dan kelembaban beragam. Metode analisis diversitas dengan Next Generation Sequencing 16s rRNA. Jumlah responden yang digunakan pada penelitian ini sebanyak 144 sampel. Hasil analisis pada penelitian ini ditemukan bahwa kelas filum bakteri tertinggi Actinobacterium (49,72%), Proteobacterium (29,86%) dan Firmicutes (18,64%). Pada genus Cutibacterium (41,48%), Neisseriaceae (20,29), Staphylococcus (10,16%) ditemukan terbanyak pada kulit wajah dengan nilai kondisi pH dan kelembaban berbeda. Analisis diversitas alfa dengan indeks Chao1 (p=0,05) dan Faith PD(p=0.004) menunjukan kelimpahan mikrobiom signifikan lebih tinggi ditemukan pada pH tinggi dibandingkan pH normal. Analisis diversitas Alfa pada kelembaban tidak ditemukan signifikan terhadap kelimpahan bakteri mikrobiom wajah. Hasil diversitas beta ditemukan perbedaan kelimpahan mikrobiom bakteri pada sepuluh genus tertinggi yang ditemukan pada pH normal dan pH tinggi serta kelompok kelembaban dengan sangat lembab, lembab dan kering. Kesimpulan penelitian profil genus Cutibacterium, Neisseriaceae, Staphylococcus bakteri paling banyak ditemukan pada pH tinggi dan pH normal seta kelembaban sangat lembab, lembab dan kering. Cutibacterium, Neisseriaceae dan Staphylococcus menunjukan adanya peningkatan pH kulit maka kelimpahan bakteri tersebut semakin meningkat. Pada kelembaban kulit, kelimpahan Cutibacterium dan Staphylococcus menurun seiring penurunan nilai kelembaban kulit.

......Balancing various types of bacteria on the skin is crucial for maintaining skin health. One of the issues that arise with facial skin is caused by microbial dysbiosis. Research was conducted to analyze the diversity of bacterial microbiomes on the facial skin with varying pH and moisture conditions. The diversity analysis method used Next Generation Sequencing 16s rRNA, and the study included 144 samples. The results of this research revealed that the highest bacterial phylum classes were Actinobacterium (49.72%), Proteobacterium (29.86%), and Firmicutes (18.64%). The genera Cutibacterium (41.48%), Neisseriaceae (20.29%), and Staphylococcus (10.16%) were the most abundant on the facial skin with different pH and moisture conditions. Alpha diversity analysis using Chao1 index (p=0.05) and Faith PD (p=0.004) indicated significantly higher microbial abundance found in high pH compared to normal pH. However, there was no significant difference in alpha diversity concerning the moisture level and facial bacterial microbiome abundance. Beta diversity analysis showed differences in bacterial microbiome abundance in the top ten genera found between normal pH and high pH, as well as between moisture groups categorized as very moist, moist, and dry. In conclusion, the research profiled the genera Cutibacterium, Neisseriaceae, and Staphylococcus as the most found bacteria in high pH and normal pH conditions, as well as very moist,

moist, and dry moisture levels. Cutibacterium, Neisseriaceae, and Staphylococcus showed an increase in skin pH resulting in an increase in the abundance of these bacteria. On the other hand, the abundance of Cutibacterium and Staphylococcus decreased with decreasing skin moisture levels.