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A mr tence on hind xxx movies here.. icy kandico pussy or getting banged by black mate in sex club buddy sex hind cdp 3gp fat virgin hind download you porn hind full movie 1-evolution model, which considers the rapid generation of antibiotic resistance genes by single-stranded DNA or circular plasmids, avoids the overestimation of antibiotic resistance genes caused by multiple copies of these genes ([@B31]). Microbial community analysis was performed based on the 16S rRNA gene. The results obtained for the archaea were similar to those of the 16S rRNA gene analysis, indicating that most of the archaeal community members are members of the domain Euryarchaeota. The phylogenetic group Arcl was not detected. This group is described as associated with cold habitats, such as Antarctica ([@B41]), and was considered a possible contributor to the biosynthesis of the nanomaterial for treatment of skin wounds ([@B41], [@B42]). The phylogenetic groups ArclI and ArclIII were detected and represented 8.51% and 1.57% of all sequences, respectively, with *L. lactis* subsp. *cremoris* as the dominant member. These results are similar to those reported for the dairy environment ([@B43]). The results of the analysis of the bacterial community indicate that *P. acnes* and *S. epidermidis* were the two main members of the skin surface microbiome. The highest number of sequences were affiliated to the genus *Pseudomonas* (11.28%), followed by *Staphylococcus* (10.01%) and *Micrococcus* (2.61%), which contributed relatively low amounts of sequences. The presence of these species is commonly associated with skin, and their presence in the same proportion suggests that they are probably more important in terms of their abundance than the number of sequences. Other species found in relative high amounts were *Propionibacterium* (6.29%), which is an anaerobic bacteria and is considered a metabolically versatile species, capable of fermenting a variety of sugars and producing hydrogen ([@B44]). In this study, the human skin microbiota was analysed from a region of the body that is highly exposed to microorganisms, which could explain the high abundance of bacterial species. In general, the core microbiomes were shared by the different individuals included in the study. However 6d1f23a050

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