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COMPARISON OF VAGINAL MICROBIOTA FINGERPRINTS FROM HEALTHY AND BACTERIAL VAGINOSIS–POSITIVE PORTUGUESE WOMEN

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Bacterial Vaginosis (BV) is a common disease in women of reproductive age and is characterized by the substitution of Lactobacillus species, which are predominant in the normal vaginal microbiota, by rapidly proliferating anaerobic bacteria, particularly Gardnerella vaginalis. The aim of this study was to study microbial communities’ structure in the vaginal microbiota of healthy and BV–positive Portuguese women. To this end, DNA obtained from vaginal samples of 22 BV–negative and 19 BV–positive women was analyzed using a PCR–DGGE approach. Total bacterial communities were amplified using general 16S rRNA gene primers. Group–specific primers were also used targeting Lactobacillus and Bifidobacterium genera and G. vaginalis. DGGE profiles were compared using the BioNumerics™ software package (Applied Maths, Belgium). Similarity between DGGE profiles was determined by calculating similarity indices of the densitometric curves of the compared profiles, using the Dice product–moment correlation. Different DGGE profiles could be obtained for BV–positive and BV–negative samples and this was verified for all primers sets utilized, suggesting that alteration of microbial community structure of BV–positive and –negative samples could be detected by PCR–DGGE. DGGE profiles obtained from samples of BV–positive women were more diverse than the ones from healthy women (as determined by a higher number of DGGE bands). The analysis of the standard electrophoretic bands for bacteria reveals an intrinsic diversity even within the two groups studied: similarities in bacterial DGGE profiles vary between 14–78% and 47–100% in BV–positive and BV–negative samples, respectively. Among the 19 BV–positive women studied 18 were colonized with G. vaginalis. G. vaginalis was not detected in any of the healthy women samples. The analysis of Lactobacillus communities revealed a higher diversity in BV–negative women than in BV–positive ones, which confirms the association of Lactobacillus in healthy vaginal microbial communities. A more thoroughly comparison between BV–negative and BV–positive, including the retrieval of sequencing data from these samples, is necessary for getting more insight on BV influence on vaginal microbiota.