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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 *Gardnerellavaginalis*. 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 thorough 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.