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Multiplex PCR for the discrimination of vaginal bacterial population**Ana Margarida Magalhães, Joana Castro, Ana Filipa Henriques, Nuno Cerca**

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Bacterial vaginosis is one of the most common disorders in women of reproductive age worldwide and while not life-threatening, it leads to increased risk of more serious gynecologic infections and pre-term labor. It is a pathology which has been recognized to possess several microorganisms involved such as *Lactobacillus* species, *Gardnerella vaginalis*, *Atopobium vaginae*, and other anaerobic bacteria of difficult identification, whose fragile balance may determine the appearance or not the pathology. Currently diagnosis is made mostly based on symptoms and is variable dependent on the symptoms which the physician judge to be most important for diagnosis, and laboratory culture techniques for the identification of bacterial strains present is very time consuming and not always successful in identifying most microorganisms present. In order to have a better understanding of the aetiology of BV and thus be able to identify better tools for the correct diagnosis of this pathology, more effective tools for identification of bacteria commonly associated with the vaginal flora are needed. The use of new molecular biology techniques, such as PCR, has begun to be extensively developed for the study of pathologies such as BV. Besides conventional PCR there have been key developments made to this techniques such as multiplex PCR (allowing the detection of the presence of several strains of organisms in a single reaction) and qPCR which allows the fast quantification of organism which would otherwise take many days to quantify using traditional microbiology techniques. Here we describe the development of a multiplex PCR assay for the identification of 3 of the most commonly studied bacterial strains for the diagnosis of BV: *Lactobacillus* spp., *G. vaginalis* and *A. vaginae*.

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