



Category: Metagenomics

Diversity of cultivable vaginal microbiota in asymptomatic women of reproductive age in Mumbai, India

Rinku Pramanick¹, Shraddha Parab¹, Niranjan Mayadeo², Himangi Warke² and Clara Aranha^{1*}

¹National Institute for Research in Reproductive Health (Indian Council of Medical Research, Parel, Mumbai, INDIA

²Department of Obstetrics and Gynecology, King Edward Memorial Hospital and Seth Gordhandas Sunderdas Medical College, Parel, Mumbai, INDIA

Presenting author: rinku.pramanick@gmail.com; *Corresponding author: aranhac@nirrh.res.in

Abstract

Microbes in the vaginal microbiota form a mutual relation with its constituent members and its host. In recent years our acquaintance with vaginal microbiota has widened, however, insufficient knowledge is available in Indian scenario. In the present study, the diversity of cultivable vaginal microbiota in asymptomatic women of the reproductive age group from Mumbai was investigated using multiplex PCR and species specific PCR, validated by 16sRNA Sanger sequencing. Vaginal samples taken from 199 women were classified according to Nugent score as normal (n=147), intermediate (n=23) and bacterial vaginosis (n=29) indicating 14.5% asymptomatic BV. Cultivable Lactobacilli were recovered from 97.9% (195) participants. The abundance of vaginal Lactobacilli was reduced in women with BV. Of 147 women, 110 were considered healthy, as 37 women colonized vaginal *Candida*. The most predominant vaginal *Lactobacillus* spp. in healthy women were *L. iners* (70.9%), *L. crispatus* (26.4%), *L. reuteri* (20.9%), *L. gasseri* (18.2%), and *L. jensenii* (15.5%). Our data demonstrated a profound shift in the prevalent vaginal *Lactobacillus* spp. when comparing women with healthy and diseased conditions. In women with normal flora colonizing *Candida*, *L. rhamnosus* (24.3%) was one of the prevalent Lactobacilli. *L. crispatus* was identified as a specific species present only in the healthy state. *L. iners* was found to be the most frequent vaginal *Lactobacillus* irrespective of the vaginal health. Majority of the women harbored heterogeneous population of *Lactobacillus* indicating their cumulative effect in maintaining the vaginal niche. Among the single species population, distinct diversity of Lactobacilli were found in women with Normal, Intermediate and BV microflora. Though most frequently identified, *L. iners*, significantly coexisted with other *Lactobacillus* spp., suggesting its minimal protective role alone in the vaginal niche. About one third of study population colonized *Candida*, most of which were Non *albicans Candida*; whereas BV related genera viz., *Gardnerella*, *Atopobium*, *Prevotella* and *Megasphaera* was observed at high prevalence even in women with healthy microflora. This recommends the use of in-depth analysis wherein detection of a specific species can be employed as a disease marker. Our study provides an insight into the overall structure of vaginal community that may provide fundamental information for future investigations using metagenomics, *in-vitro* approaches and metaproteomics.

Citation: Pramanick, R., Parab, S., Mayadeo, N., Warke, H. and Aranha, C. Diversity of cultivable vaginal microbiota in asymptomatic women of reproductive age in Mumbai, India [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 129. <https://doi.org/10.24870/cjb.2017-a115>