

An update on Gardnerella vaginalis associated bacterial vaginosis in Malaysia

ABSTRACT

Objective: To update the status of Gardnerella vaginalis (*G. vaginalis*) as a causative agent of bacterial vaginosis (BV) in Malaysia and to define its epidemiology, metronidazole resistance and virulence properties. **Methods:** It is a single-centre (Gynaecology clinic at the Hospital Kuala Lumpur, Malaysia) prospective study with laboratory-based microbiological follow up and analyses. Vaginal swabs collected from the patients suspected for BV were subjected to clinical BV diagnosis, isolation and identification of *G. vaginalis*, metronidazole susceptibility testing, vaginolysin and sialidase gene PCR, Piot's biotyping and amplified ribosomal DNA restriction analysis genotyping. **Results:** Among the 207 patients suspected for BV, *G. vaginalis* was isolated from 47 subjects. *G. vaginalis* coexisted with *Trichomonas vaginalis* and *Candida albicans* in 26 samples. Three *G. vaginalis* isolates were resistant to metronidazole. Biotyping revealed 1 and 7 as the common types. Amplified ribosomal DNA restriction analysis genotype II was found to be more common (n = 22; 46%) than I (n = 12; 25.53%) and III (n = 13; 27.6%). All genotype I and III isolates carried the sialidase gene, while 91.6% and 84.6% contained the vaginolysin gene. Genotype I was significantly associated with post-gynaecological surgical complications and abortions (P = 0.002). **Conclusions:** The existence of pathogenic *G. vaginalis* clones in Malaysia including drug resistant strains should not be taken lightly and needs to be monitored as these may bring more complications especially among women of child bearing age and pregnant women.

Keyword: Gardnerella vaginalis; Piot's biotype; ARDRA; Vaginolysin; Sialidase