Hepatitis A is an important sexually transmitted enteric infection in MSM and an effective vaccination is available. It has been estimated that 70% of MSM need to be immune to hepatitis A in order to provide adequate herd immunity. In the UK, hepatitis A transmission in MSM is associated with high risk behaviours such as anonymous sex, multiple sexual partners, sex-on-premises venues and dating apps. European Centre of Disease Prevention and Control (ECDC) and the British Association for Sexual Health and HIV (BASHH) recommend opportunist vaccination for all MSM.

We aimed to estimate the proportion of MSM who were susceptible to hepatitis A over a 10-year period (from 2010–2019) and to determine if there are any demographic factors associated with susceptibility which may provide useful information for future vaccination programmes.

6884 MSM attended for the first time during the study period. 1401/6884 (20%) were tested for hepatitis A IgG at this first attendance. Testing rates increased significantly between 2010–2019 (OR=67.79, 95%CI=39–118, p=0.0001). 626/1401 (45%, 95% CI=42–47) were susceptible to hepatitis A (confirmed by a negative IgG). Susceptibility rates did not change significantly during the study period (OR=0.98, 95% CI=0.33–2.89, p=0.98). MSM aged 35 years and under had significantly higher susceptibility vs MSM over 35 years (OR=3.42, 95% CI=2.71 to 4.31, p<0.0001). UK-born MSM had significantly higher susceptibility vs non-UK born MSM (OR=1.5, 95%CI=1.21–1.86, p=0.0002). There was no difference in the presence of a sexually transmitted infection (chlamydia, gonorrhoea, syphilis, HIV) at their first attendance between susceptible and immune MSM (OR=1.2, 95% CI=0.95–1.62, p=0.1099).

Susceptibility of Hepatitis A in MSM is much lower than necessary to control future outbreaks. It is important that effective targeting of MSM, particularly young MSM occur at all levels of healthcare, rather than waiting until opportunistic presentation at a sexual health clinic.

Objectives This study reported on prevalence of common, and often curable, Chlamydia trachomatis (CT), Neisseria gonorrhoea (NG), Trichomonas vaginalis (TV), Mycoplasma genitalium (MG), human papillomavirus (HPV) infections, and on VMB composition among common women and post-delivery women in Pemba Island, Tanzania.

Methods Vaginal swabs were collected at two timepoints during pregnancy and once after delivery by Pemba Biobank. Molecular assays were used to detect HPV, CT, NG, TV, and MG in samples from 438 individual women. IS-pro kit was used to characterize the VMB in a subset of women (n=90) based on 16S rDNA intersperser region length. VMB were defined based on dominant species. Shannon diversity index, for number (richness) and relative abundance of species, was calculated and Mann-Whitney test used for analysis.

Results In samples from 20.5% of the women, at least one pathogen was detected. Infection with HPV was the most prevalent (10.3%), followed by TV (7.1%), CT (4.6%), MG (2.1%), and NG (0%). The most common VMB were Lactobacillus-dominant during pregnancy (77% at first, and 81% at second timepoint), and non-Lactobacillus-dominant (73.9%) postdelivery. The Shannon diversity was lower during pregnancy than postdelivery (p=0.03). A decrease in VMB richness (p=0.02) was observed during pregnancy. Klebsiella species and Streptococcus anginosus were the most common microorganisms with pathogenic potential (pathobionts) at all timepoints. A high abundance of pathobionts was seen in women with non-Lactobacillus-dominant VMB. At second timepoint during pregnancy, 67% of the women carrying a genital pathogen had Lactobacillus iners-dominant VMB.

Conclusion This study contributes knowledge on VMB composition and its changes during pregnancy and post-delivery, as well as simultaneous presence of pathobionts and genital pathogens.