

## Introduction

*Streptococcus agalactiae* (Group B *Streptococcus*; GBS) is a gram positive bacterium that commonly colonise the gastrointestinal tracts. Globally, GBS is responsible for 319 000 infant invasive disease and 90 000 infant deaths per year (1). The major risk factor for GBS disease in infants is maternal recto-vaginal colonisation. There is paucity of data on the association of vaginal microbiome composition and GBS colonisation in pregnant women. Understanding the relationship between the vaginal microbiome and GBS colonisation is essential to informing potential preventative strategies against GBS disease.

**Objective:** To determine the vaginal microbiome associated with GBS colonisation in pregnant women from South Africa, Kenya and Ethiopia.

## Method

### Study cohort

- Pregnant women aged 18 to 45 years were enrolled in a GBS Multicentre study, between 2016 and 2018.
- Vaginal swabs were collected before or during delivery and screened for the presence of GBS using culture methods and stored in STGG media (-70°C) at Wits-VIDA.
- For this study, 94 vaginal swabs that were either culture-positive or negative for GBS were randomly selected for each site.

### Laboratory Methods

- Total nucleic acids were extracted from the vaginal swabs using Easymag extraction machine
- Nucleic acids were analysed using a 56 target Open array quantitative polymerase chain reaction (qPCR) method,



### Statistical analysis

- Logistic regression was performed for Univariate analysis.
- Statistical analyses was performed using Stata, version 13 software.

## Results

**Table Vaginal microbiome association with GBS colonised and non-colonised group**

Target	Total (n=282)	GBS non-colonised (n=141)	GBS colonised (n=141)	OR (95% CI)	P-value
<i>Candida albicans</i>	99 (35.1%)	29 (20.6%)	70 (49.7%)	3.81 (2.25-6.44)	0.0001*
<i>Mobiluncus curtisii</i>	21 (7.5%)	17 (12.1%)	4 (2.8%)	0.21 (0.07-0.65)	0.007
<i>Mobiluncus mulieris</i>	15 (5.3%)	12 (8.5%)	3 (2.1%)	0.23 (0.06-0.85)	0.027
<i>Megasphaera 1</i>	65 (23.1%)	42 (29.8%)	23 (16.3%)	0.46 (0.26-0.82)	0.008
<i>Peptostreptococcus anaerobius</i>	128 (45.4%)	53 (37.6%)	75 (53.2%)	1.89 (1.17-3.03)	0.009*
<i>Prevotella bivia</i>	133 (47.2%)	55 (39%)	78 (55.3%)	1.94 (1.21-3.11)	0.006*
<i>Staphylococcus aureus</i>	62 (22%)	7 (5%)	55 (39%)	12.24 (5.33-28.1)	0.0001*
<i>Trichomonas vaginalis</i>	16 (5.7%)	3 (2.1%)	13 (9.2%)	4.67 (1.3-16.77)	0.018*
<i>Ureaplasma urealyticum</i>	183 (64.9%)	84 (59.6%)	99 (70.21%)	1.60 (0.98-2.62)	0.062
<i>Veillonella parvula</i>	224 (79.4%)	101 (71.6%)	123 (87.2%)	2.71 (1.46-5.01)	0.002*

<sup>a</sup> Data are no (%) of total participants, <sup>b, c</sup> Data are row %. \* Significant association with GBS colonisation.

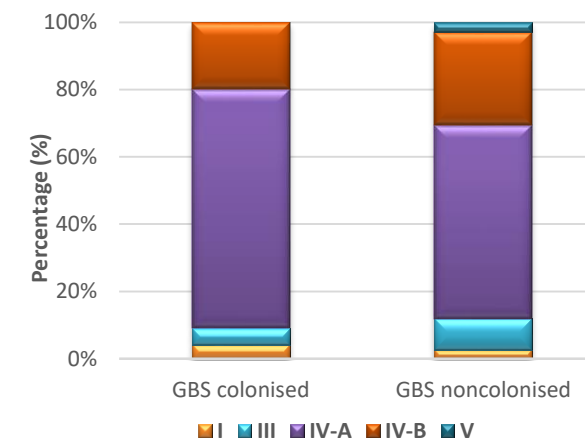
## Discussion

- 6 organisms were positively associated with GBS colonised group, indicating that GBS colonisation is influenced by vaginal organisms.
- Conversely, *Mobiluncus curtisii*, *Mobiluncus mulieris* and *Megashpaera 1* common in women with bacterial vaginosis were positively associated with GBS non-colonised group.
- CST V was only detected in GBS noncolonised group, suggesting that *Lactobacillus jensenii* may offer protection against GBS colonisation.

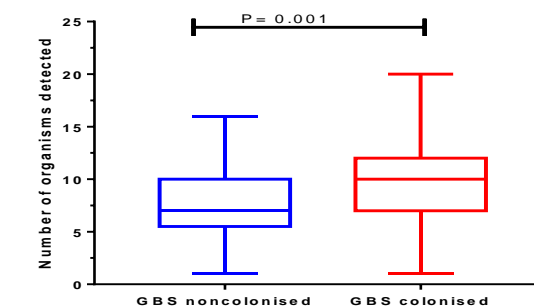
• **Conclusion;** the association between vaginal microbiome and GBS colonisation warrants further investigation to determine if interventions directed at the vaginal microbiome could reduce the risk for GBS disease in the women and their offspring.

## Reference

1. Seale AC, Bianchi-Jassir F, Russell NJ, Kohli-Lynch M, Tann CJ, Hall J, et al. Estimates of the Burden of Group B Streptococcal Disease Worldwide for Pregnant Women, Stillbirths, and Children. *Clinical infectious diseases* : an official publication of the Infectious Diseases Society of America. 2017;65(suppl\_2):S200-S19



**Figure 1;** Distribution of Community State types in two groups.



**Figure 2;** Number of vaginal organisms detected in a swab of GBS colonised and non-colonised women. A high number of multiple organisms was detected in GBS colonised (t-test,  $p < 0,05$ ).

## Acknowledgements

