The Vaginal Microbiome during Pregnancy and its Impact on Preterm Birth -A Systematic Review

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BACKGROUND

- Preterm birth (PTB) has a global incidence of 11% and is a major (1), determinant of morbidity in infants and children (2).
- The aetiology of PTB is multifactorial, one influencing factor is infection and inflammation. Bacteria that can precipitate PTB can ascend from the lower genital tract (3).
- The culture independent DNA extraction and the sequencing of 16S ribosomal RNA (rRNA) has allowed comprehensive identification of the vaginal microbiome (4).

METHOD

- performed Search in PubMed, MEDLINE and EMBASE between 01Jan2006 and 08Dec2016.
- Search terms were: "Pregnan* AND Vagin* AND Microbio* AND (16S OR Metageno* OR Culture Independent OR PCR)".
- Studies were chosen based on inclusion and exclusion criteria.
- National Heart, Lung & Blood Institute Quality Assessment of Studies and the Cochrane Risk of Bias Tools were applied to assess the quality of studies.

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RESULTS

- 412 studies screened, 18 met the inclusion criteria.
- А large number of bacterial taxa were identified using 16S rRNA methods.
- There was no identifiable relationship between bacteria in the vagina and PTB or full term birth (FTB).
- All women who had a FTB had the presence of bacterial genera , Lactobacillus and Prevotella.
- There was no identifiable relationship between bacteria in the vagina at varied trimesters when stratified birth by outcome.

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CONCLUSIONS

- We cannot conclude the clinical significance of the bacteria found in the vagina of pregnant women.
- There is not enough data. and too much heterogeneity between studies, to conclude a relationship between bacteria in the vagina detected by 16S rRNA methods and;
 - Preterm birth;
 - Pregnancy outcomes (PTB or FTB) or;
 - Pregnant outcome and Trimesters.

FUTURE DIRECTIONS



RESEARCH THAT DIRECTLY ADDRESSES THE CLINICAL QUESTION "Does the vaginal microbiome during pregnancy play a role in PTB?"

WELL DESIGNED CLINICAL

STUDIES Studies that have adequate power, have considered the known risk factors for PTB, and take vaginal samples from



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the same women longitudinally.

Further research regarding the clinical significance of bacteria in the vagina identified by 16s rRNA methods.

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