Development of a multi-locus sequence typing scheme for *Ureaplasma parvum:* towards accurately identifying isolates associated with preterm birth.

Research overview

Ureaplasma sp. are tiny a bacteria that are present in the vagina of 40-50% of women during pregnancy. Our research suggests they are capable of triggering intra-amniotic and fetal inflammatory responses and they have been widely reported to be associated with preterm birth. However, not all women colonised with Ureaplasma spp. deliver preterm. The aim of this project is to analyse the genetic structure of a range of *Ureaplasma sp.* isolates, from both preterm and term pregnancies, in order to design a new classification system based on the identification of specific genes and/or genetic markers. This system may then be used to identify isolates associated with preterm birth.

Research highlights

- Vaginal swab samples were collected from 191 pregnant women over three time points during pregnancy (13-26wks, ~28 wks and ~36 wks GA)
- *Ureaplasma spp.* were detected in 48% of recruitment samples and showed minimal variance over the three time points
    - *Ureaplasma parvum* was the dominant species detected (81% of cases)
    - *U. parvum* was significantly associated with preterm birth

      17 cases of preterm birth, 71% positive for Ureaplasma spp., 92% of these positive for *U. parvum*

      Six cases of preterm birth <34 wks GA, all positive for *U. parvum*
- 21 preterm *U. parvum* isolates and 36 term U. parvum isolates selected for genetic analysis
- Protein analysis of the major *Ureaplasma sp.* antigen demonstrated similar profiles in terms of band number and size.

Progress report

Sample collection for this study was completed in 2014 and the selection of isolates for inclusion in the genetic analysis component was finalised in early 2015. We have opted to exclude *Ureaplasma urealyticum* isolates from the project based on the results of our prevalence study which showed no association between *U. urealyticum* and preterm birth (only one isolate from 12 cases) and low vaginal prevalence of this species overall. Selected *U. parvum* isolates were purified and sent to Dr Brad Spiller in Cardiff, UK to conduct screening of the multiple-banded antigen protein to look for differences in band pattern and size. This work has now been completed and DNA is currently about to be extracted from all purified isolates for whole genome sequencing. We expect this to be completed by the end of 2015, with data analysis completed by early 2016.

THE TEAM

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