High vaginal load of *Atopobium vaginae* reduces the interval time to delivery in high risk pregnancies


**Background:** Bacterial vaginosis (BV) has been suggested to be a risk factor of prematurity. However, the current methods for its diagnosis are mainly based on clinical score and/or Gram staining. They are fastidious, lack of precision, and difficult to reproduce. The aim of this study was to rationally evaluate the link between vaginal flora anomalies and prematurity using molecular methods.

**Methods & Materials:** A prospective multicenter national study was performed: 813 high risk pregnant women with late abortion, previous preterm delivery, and/or short cervix diagnosed by ultrasound were included. Quantitative molecular analyses were performed using specific real-time polymerase chain reaction assays and serial dilutions of a plasmid suspension targeting *Atopobium vaginae*, *Gardnerella vaginalis*, *Mycoplasma hominis*, *Lactobacillus*, and *A. vaginae*, and a human gene.

**Results:** High vaginal loads of *A. vaginae* (≥10^5/ml) was systematically and significantly linked before 22, 28, and 32 weeks to a shorter interval for delivery. This time was: 152.1 and 413.2 days (p = 0.003; Hazard ratio [HR], 6.6; 95% Confidence Interval [CI] 1.9-22.6) before 22 weeks, 149.2 and 400.6 days (p = 0.036; HR, 2.8; 95% CI, 1.1-7.6) before 28 weeks, and 132.5 and 365.1 days (p = 0.017; HR, 2.3; 95% CI, 1.2-4.5) before 32 weeks. High vaginal loads of *G. vaginalis* (≥10^5/ml) was significantly linked to a shorter interval time to delivery before 22 weeks only; the mean interval was 174.1 and 412.9 days (p = 0.028; HR 3.9; 95% CI, 1.2-13.5). Low vaginal loads of *Lactobacilli* (≤10^2/ml) were also significantly linked to a shorter interval time to delivery before 22 weeks only; the mean interval was 169.4 and 415.4 days (p = 0.024; HR 0.2; 95% CI, 0.1-0.8). The differences remain significant only for high vaginal loads of *A. vaginae* (≥10^5/ml) and delivery before 22 weeks (p = 0.014) after multivariate analysis.

**Conclusion:** In high risk women, there is a specific link between high vaginal loads of *A. vaginae* and abortion before 22 weeks.

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Molecular epidemiology of methicillin-resistant *Staphylococcus aureus* in Africa: A systematic review of the published literature

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**Background:** Methicillin-resistant *Staphylococcus aureus* (MRSA) infections are a serious global problem with considerable impact on morbidity and mortality, and health care costs. The epidemiology of MRSA in hospital and community settings in the developed world has been extensively studied. However, in lower and middle-income countries, and in Africa in particular, it remains largely understudied.

**Methods & Materials:** We conducted a systematic review for published articles (up until November 2013) on the molecular epidemiology and population structure of MRSA in Africa. English and French language eligible articles available in PubMed, EBSCOhost, ISI Web of knowledge and Scopus were retrieved. In addition, African Journals Online database was screened to identify eligible articles which are not indexed in the above databases.

**Results:** Seventy five eligible studies were identified, primarily from Tunisia, Egypt, Nigeria and South Africa. Twenty five studies from 12 countries reported complete data on MRSA clones (Multi Locus Sequence type and Staphylococcal Chromosomal Cassette mec element).

The community clones ST8-IV (USA300) and ST88-IV-PVL + were identified both in hospitals and in the community in Gabon, Senegal, Morocco, Cameroon, Madagascar, Nigeria and South Africa. The European clone ST80-IV-PVL +, also a community clone, was limited to Algeria, Tunisia and Egypt. “The early ancient clones” ST250-I and ST247-I thought to be declining world-wide, were identified in Nigeria and Tunisia. A new clone ST612-IV-PVL+ has been recently reported in a South African hospital. The epidemic MRSA clone ST39-II (EMRSA- 16) circulating in hospitals was identified in the community in Algeria. Besides, in a single study conducted in Senegal, animal-human transmission has been reported for the paediatric clone ST5-IV. A novel clone (ST239-IVa) that has not been reported elsewhere, appears to have resulted from SCCmec type IVa replacing SCCmec type III in the hospital clone ST239-III in Algeria.

**Conclusion:** In summary, identified MRSA clones in Africa include the major lineages circulating worldwide, while some clones appear to be over-represented or display specific epidemiological traits, such as zoonotic or community transmission.

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