Molecular Epidemiology of *Ureaplasma* Species Isolated from Neonates in the Global Multi-Center Child Health and Mortality Prevention Surveillance Network (CHAMPS)

**BACKGROUND**

*Ureaplasma* species, including *U. urealyticum* and *U. parvum*, are infectious causes of stillbirth, neonatal sepsis, and preterm labor. Recent studies in South Asia and South Africa suggest *Ureaplasma* species are an underrecognized cause of neonatal infections in low- and middle-income countries. Diagnostic testing of neonatal clinical specimen for *Ureaplasma* is rarely done, and bacterial factors associated with birth complication and infection remain unclear.

**METHODS**

We performed additional testing on post-mortem blood, cerebrospinal fluid (CSF), and tissue specimens from Child Health and Mortality Prevention Surveillance (CHAMPS) cases in South Africa from May 2017 to January 2018. *Ureaplasma* species were initially detected by real-time reverse transcription polymerase chain reaction (RT-PCR) using custom TaqMan Array Cards. Specimens from CHAMPS cases in which *Ureaplasma* was detected in one or more specimen types were transferred to the Centers for Disease Control and Prevention (CDC) for culture, real-time PCR, and whole genome sequencing (WGS).

**RESULTS**

Ten isolates (5 *U. urealyticum*, 5 *U. parvum*) were recovered from 22 primary specimens, including lung tissue (n=5), blood (n=2), and CSF (n=3), from 6 cases where *Ureaplasma* was detected but did not attributed to the cause of death. Genome assemblies were generated for 8 isolates from 6 cases where *Ureaplasma* detection was confirmed in one or more specimen types. Novel allelic profiles were identified in all isolates.

**GRAPHICS**

- **U. parvum**
- **U. urealyticum**

*Ureaplasma* species are an underrecognized cause of neonatal infections. Genome assemblies revealed allelic profile diversity and potential indication of tetracycline resistance. Additional sequencing could uncover unique features impacting illness severity.