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1 **The human *Ureaplasma* species as causative agents of chorioamnionitis**

2

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52 **SUMMARY**

53 The human *Ureaplasma* species are the most frequently isolated microorganisms from the
54 amniotic fluid and placentae of women who deliver preterm and are also associated with
55 spontaneous abortions or miscarriages, neonatal respiratory diseases and chorioamnionitis.
56 Despite the fact that these microorganisms have been habitually found within placentae of
57 pregnancies with chorioamnionitis, the role of *Ureaplasma* spp. as a causative agent has not
58 been satisfactorily explained. There is also controversy surrounding their role in disease,
59 particularly as not all women infected with *Ureaplasma* spp. develop chorioamnionitis. In
60 this review, we provide evidence that *Ureaplasma* spp. are associated with diseases of
61 pregnancy and discuss recent findings, which demonstrate that *Ureaplasma* spp. are
62 associated with chorioamnionitis, regardless of gestational age at the time of delivery. Here,
63 we also discuss the proposed major virulence factors of *Ureaplasma* spp., with a focus on the
64 multiple banded antigen (MBA), which may facilitate modulation/alteration of the host
65 immune response and potentially explain why only subpopulations of infected women
66 experience adverse pregnancy outcomes. The information presented within this review
67 confirms that *Ureaplasma* spp. are not simply ‘innocent bystanders’ in disease and highlights
68 that these microorganisms are an often underestimated pathogen of pregnancy.

69 **CLINICAL PERSPECTIVES ON CHORIOAMNIONITIS AND ITS SIGNIFICANCE**
70 **TO THE HEALTH OF THE PREGNANCY AND NEONATE**

71 Chorioamnionitis refers to inflammation of the fetal membranes, which comprise the chorion
72 and amnion. Although the chorioamnion is anatomically part of the placenta, it is derived
73 from the zygote and is considered to be of fetal origin (**Box 1**). The chorioamnion is also in
74 contact with the decidua, a tissue of maternal origin, and together these form the
75 maternal/fetal interface. Chorioamnionitis frequently occurs in parallel with microbial
76 infection of the chorioamnion and amniotic fluid (1-3); however, it may also occur in the
77 absence of demonstrable microorganisms (i.e. 'sterile inflammation' (2, 4), which will not be
78 discussed in this review). The clinical signs of chorioamnionitis include fever, uterine fundal
79 tenderness, maternal tachycardia (>100 beats/minute), fetal tachycardia (>160 beats/minute)
80 and purulent or foul-smelling amniotic fluid (5). However, it is becoming increasingly
81 apparent that a large proportion of chorioamnionitis cases are sub-clinical and are not
82 diagnosed until retrospective analysis of the placenta (6) (**Box 2**). Upon histological
83 examination, acute chorioamnionitis is defined as diffuse influx of neutrophils into the
84 chorioamnion/decidua, and the severity of the maternal and fetal immune response can be
85 classified according to published standards (7). Chronic chorioamnionitis is less well-defined,
86 but has been characterized by an infiltration of maternally-derived mononuclear cells, usually
87 macrophages and T lymphocytes, into the chorioamnion or chorionic plate (the fetal surface
88 of the placenta that directly connects to the uterine wall, where the chorionic villi are formed)
89 (7, 8).

90 Since amniotic fluid, but not the placenta, is accessible prior to delivery in women at risk for
91 preterm labor, most clinical studies have correlated intraamniotic infection or inflammation
92 rather than chorioamnionitis with preterm labor/delivery. However, intraamniotic infection,
93 defined as microorganisms detected in the amniotic fluid (9), may not always be concordant

94 with retrospective diagnosis of histological chorioamnionitis. Recently, a National Institutes
95 of Health workshop recommended that the term ‘chorioamnionitis’ be replaced with
96 ‘intrauterine infection or inflammation or both’ (abbreviated to ‘Triple I’ and characterized as
97 being either proven or suspected), or isolated maternal fever (10). For the purposes of this
98 review, we have used the terms ‘chorioamnionitis’ and ‘intraamniotic infection’ according to
99 their traditional definitions, as described above.

100 Clinical chorioamnionitis and histological chorioamnionitis affect 1-4% and 23.6% of term
101 births (37-42 weeks of gestation) respectively (5, 11, 12). However, it has been well
102 established that the frequency (13-15) and severity (15, 16) of chorioamnionitis is inversely
103 related to gestational age at the time of delivery. In a study of 7505 placentae from singleton
104 pregnancies, Russell (13) reported that the frequency of chorioamnionitis in patients who
105 delivered between 21-24 weeks of gestation was 94.4% (17/18 patients). More recently, Stoll
106 *et al.* (14) demonstrated that histological chorioamnionitis was present in 70% (295/421) of
107 pregnancies that delivered at 22 weeks of gestation. The frequency of histological
108 chorioamnionitis was significantly higher in women who delivered after the spontaneous
109 onset of labor compared to those who had induction of labor at term or delivered *via*
110 Caesarean section in the absence of labor (17, 18). Furthermore, the frequency of histological
111 chorioamnionitis increases in patients with prolonged duration of labor (19) and premature
112 rupture of membranes (20). Additional risk factors for chorioamnionitis include: multiple
113 digital examinations, nulliparity, bacterial vaginosis, alcohol and tobacco use, group B
114 *Streptococcus* colonization, meconium-stained amniotic fluid and epidural anesthesia (20-
115 23).

116 **Chorioamnionitis: a major predictor of preterm birth**

117 Preterm birth, defined as delivery at <37 weeks of gestation, is the leading cause of neonatal
118 death worldwide (24). In addition, complications arising from preterm birth are a leading

119 cause of death in children under the age of 5, second only to pneumonia (25).
120 Microbiological studies have demonstrated that intrauterine infection may be responsible for
121 25-40% of preterm births (26); however, this is likely to be underreported due to difficulties
122 in detecting fastidious microorganisms using conventional culture methods. Histological
123 chorioamnionitis complicates 40-70% of all preterm births (5) suggesting that
124 chorioamnionitis may be an important, and potentially preventable, antecedent of preterm
125 birth.

126 *Parturition in normal pregnancy versus chorioamnionitis*

127 Figure 1 compares the key events that occur during normal parturition and inflammation-
128 induced preterm delivery. The normal initiation of parturition in humans is a complex process
129 that involves fetal hypothalamic-pituitary-adrenal (HPA) axis activation and increased
130 placental synthesis of corticotropin releasing hormone (CRH) (Figure 1). Maternal CRH
131 plasma levels increase throughout the duration of pregnancy and peak at term (27). Increased
132 CRH levels drive the production of corticotropin and cortisol in the mother and fetus, which
133 promotes fetal lung maturation and prostaglandin (PG) synthesis (e.g. PGE2 and PGF2 α)
134 within the amnion (28). PG production is enhanced by the concomitant downregulation of
135 prostaglandin dehydrogenase (PGDH) within the chorion (29) and the production of
136 prostaglandin-endoperoxide synthase-2 (PGS2, formerly cyclooxygenase-2) (30). Both CRH
137 and PGE2 stimulate the release of matrix metalloproteases (31, 32) (MMPs; e.g. MMP-2 and
138 MMP-9), which weaken the chorioamnion and facilitate membrane rupture and cervical
139 ripening. In parallel, activation of the fetal HPA axis and uterine stretching caused by fetal
140 growth leads to the upregulation of contraction-associated proteins and myometrial activation
141 (28). Progesterone withdrawal coupled with increased estrogen production is also a key
142 feature of parturition and further promotes uterine contractility (33-35).

143 In patients with chorioamnionitis, parturition may be accelerated by a maternal and/or fetal
144 inflammatory response, which is thought to be mediated by Toll-like receptor (TLR)
145 signaling (Figure 1). A recent prospective study of human pregnancies demonstrated that the
146 expression of TLR-1 and TLR-2 was significantly increased in chorion obtained from
147 preterm deliveries with histological chorioamnionitis compared to chorion from preterm
148 deliveries without histological chorioamnionitis (36). Similar results were reported in a
149 separate studies by Moço *et al.* (37) and Kim *et al.* (38), suggesting that the upregulation of
150 TLRs plays an important role in the pathogenesis of chorioamnionitis.

151 Bacterial endotoxins, such as lipopolysaccharide (LPS) (39), and live microorganisms (40)
152 have been shown to upregulate placental/chorioamnion TLRs, which are expressed by
153 amnion epithelial cells, decidual cells, intermediate trophoblasts in the chorion, macrophages
154 and neutrophils (38). *In vitro* studies have demonstrated that human primary amnion
155 epithelial cells express functional TLR-2, TLR-4, TLR-5 and TLR-6, and that stimulation
156 with TLR-5 and TLR-2/6 agonists leads to activation of nuclear factor-kappa B signaling, and
157 the production of proinflammatory cytokines, MMP-9 and PGS2 (41). These findings are
158 consistent with human studies and animal models of chorioamnionitis/intrauterine infection,
159 which demonstrate an increase in interleukin (IL)-1 β and IL-6 (42, 43), IL-8 (36) tumor
160 necrosis factor (TNF)- α (44), monocyte chemotactic proteins (45) and granulocyte colony-
161 stimulating factor (G-CSF) (46) in preterm fetal membranes, amniotic fluid and/or cord
162 blood. These inflammatory cytokines and chemokines stimulate PG production (47, 48),
163 neutrophil infiltration and the release of MMPs (49), thus leading to cervical ripening and
164 weakening/rupture of the fetal membranes. Indeed, the levels of MMPs (50) and PGs (40, 51)
165 are significantly increased within the amniotic fluid and fetal membranes during
166 chorioamnionitis.

167 **Neonatal sequelae of chorioamnionitis**

168 During chorioamnionitis, the fetus may be directly exposed to microorganisms and
169 inflammatory mediators within infected amniotic fluid. The fetus inspires, swallows and is
170 bathed in amniotic fluid, therefore the fetal lungs (52, 53), gastrointestinal tract (54, 55) and
171 skin (56) are primary sites of inflammation-mediated injury. Exposure to inflammatory
172 mediators may also occur *via* the placental-fetal circulation, resulting in immunomodulation
173 within the fetal blood (57-59), lymphoid tissues (60-62), and distant organs such as the brain
174 (63, 64). The systemic response of the fetus to chorioamnionitis, termed the fetal
175 inflammatory response syndrome (FIRS), is a severe inflammatory condition that is
176 characterized by elevated inflammatory cytokines within fetal plasma, particularly IL-6 (65,
177 66), and increased fetal plasma white blood cell counts (67). FIRS is associated with multi-
178 organ injury and is associated with severe neonatal morbidity and mortality (66). The fetal
179 immune response to chorioamnionitis has been reviewed in detail elsewhere (68, 69).

180 In human studies, chorioamnionitis has been associated with neonatal death (11, 70), early-
181 onset neonatal sepsis (70-72), intrauterine growth restriction (73), poor neonatal growth (74),
182 neurologic impairment/injury (75, 76), intraventricular hemorrhage (70), bronchopulmonary
183 dysplasia (77-79), patent ductus arteriosus (70, 73, 77, 80), retinopathy of prematurity (73,
184 81, 82), cardiovascular abnormalities (83, 84), necrotizing enterocolitis (85, 86), and
185 dermatitis (87). However, low gestational age is often a significant contributing factor (88-
186 90) and therefore it is difficult to attribute these sequelae solely to chorioamnionitis.
187 Nonetheless, when controlling for gestational age in a multivariable analysis, a recent study
188 of 3,082 extremely preterm infants (<27 weeks of gestation) demonstrated that fetal exposure
189 to histological chorioamnionitis and clinical chorioamnionitis was associated with an
190 increased risk of cognitive impairment at 18-22 months corrected age compared to infants
191 exposed to no chorioamnionitis or histological chorioamnionitis alone (91). When adjusting
192 for gestational age, other studies have confirmed that chorioamnionitis is an independent risk

193 factor for early-onset neonatal sepsis (92, 93), bronchopulmonary dysplasia (79), adverse
194 neurodevelopmental outcome at 3 years (94) and necrotizing enterocolitis (92). Interestingly,
195 the severity of chorioamnionitis has been shown to correlate with an increased frequency of
196 chronic lung disease and necrotizing enterocolitis (95), but has an inverse relationship with
197 the development of respiratory distress syndrome (96).

198 **HOST DEFENSES AND PATHWAYS OF MICROBIAL INVASION OF THE** 199 **CHORIOAMNION AND AMNIOTIC FLUID**

200 Traditionally, the normal intrauterine environment is considered to be a sterile site with the
201 chorioamnion representing the major physical and immunological barrier to the developing
202 fetus. The chorioamnion expresses TLRs, which detect pathogen associated molecular
203 patterns and signal to coordinate cellular immune responses. The chorioamnion also secretes
204 numerous natural antimicrobial peptides and defensins to protect against microbial invasion
205 (97). *In vitro*, human chorion and amnion from healthy pregnancies that delivered at term
206 inhibited the growth of a wide range of pathogenic bacteria, including group B *Streptococcus*,
207 group A *Streptococcus*, *Staphylococcus aureus* and *S. saprophyticus* (98). Parthasarathy *et al.*
208 also reported that human fetal membranes possess strong antimicrobial effects against
209 *Escherichia coli*, *Shigella* spp., and the fungal pathogens *Aspergillus niger* and *A. nidulans*
210 (99). Nonetheless, a wide range of microbes are capable of invading the fetal membranes and
211 amniotic cavity, and causing chorioamnionitis. Specific routes by which microorganisms are
212 thought to access the upper genital tract during pregnancy include: (i) retrograde spread from
213 the peritoneal cavity (*via* the Fallopian tubes); (ii) hematogenous dissemination *via* the
214 placenta and maternal blood supply; (iii) iatrogenic contamination at the time of invasive
215 medical procedures (such as chorionic villus sampling or amniocentesis) and (iv) ascending
216 invasive infections from the lower genital tract (26). While other studies have suggested that
217 bacteria (specifically, *Ureaplasma* spp.) may also gain access to the upper genital tract

218 attached to spermatozoa (100, 101), the most widely accepted route is that microorganisms
219 originating from the lower genital tract ascend through the cervix into the choriodecidual
220 space and cross the chorioamnion membrane, thereby reaching the amniotic fluid and fetus
221 (102).

222 Recent deep sequencing studies have demonstrated that the placental parenchyma harbors a
223 unique microbiome comprising non-pathogenic bacteria from the *Firmicutes*, *Tenericutes*,
224 *Proteobacteria*, and *Fusobacteria* phyla, with distinct similarities to the adult oral microbiota
225 (103). Furthermore, whole genome shotgun sequencing of placental membranes (fetal
226 chorion and/or villous placental membranes) from term deliveries without chorioamnionitis
227 demonstrated the presence of a diverse range of bacteria, including *Enterobacter* spp., *E. coli*,
228 *Acinetobacter lwoffii*, *A. johnsonii* and *Lactobacillus crispatus* (104). These findings redefine
229 our understanding of the placental microenvironment and challenge the view that the fetus
230 exists normally within a sterile compartment. It is therefore possible that the commensal
231 microorganisms of the placental parenchyma and fetal membranes represent a previously
232 unrecognized source of bacteria, which under certain conditions, may initiate an
233 inflammatory response leading to chorioamnionitis. This may also be important for the
234 establishment of the fetal/neonate microbiota (103) and normal immune development of the
235 fetus (105).

236 **CAUSATIVE AGENTS OF CHORIOAMNIONITIS**

237 A range of microorganisms, including bacteria, viruses and (less frequently) yeast and fungi
238 have been implicated in chorioamnionitis. The bacterial pathogens that are most frequently
239 isolated in cases of chorioamnionitis include: the human *Ureaplasma* species (*U. parvum* and
240 *U. urealyticum*), *Fusobacterium* spp., *Streptococcus* spp., and less frequently, *Gardnerella*
241 spp., *Mycoplasma* spp. and *Bacteroides* spp. (1, 46, 104, 106-108). Other studies have

242 identified that the sexually transmitted pathogens *Chlamydia trachomatis* and *Neisseria*
243 *gonorrhoeae*, along with the uropathogen *E.coli* and yeast *Candida*, are also infrequently
244 associated with chorioamnionitis (106, 109-112). Viral etiologies of chorioamnionitis
245 include: adenovirus, cytomegalovirus, enterovirus and, less frequently, respiratory syncytial
246 virus and Epstein-Barr virus (113-116). Of the microorganisms associated with
247 chorioamnionitis, the human *Ureaplasma* spp. are consistently identified as the most
248 common microorganisms within the amniotic fluid and placentae of women with
249 chorioamnionitis (1, 46, 107, 117, 118), funisitis (104, 119, 120) and preterm birth (1, 121).

250 **THE HUMAN UREAPLASMA SPP.**

251 The human *Ureaplasma* spp. were first discovered in 1954 in agar cultures of urethral
252 exudates from male patients with non-gonococcal urethritis (122). Due to their small colony
253 size (5 – 20 µm) and their resemblance to the human *Mycoplasma* spp., *Ureaplasma* spp.
254 were initially identified as tiny-form pleuropneumonia-like organisms and referred to as ‘T-
255 mycoplasmas’ (122). However, *Ureaplasma* can be distinguished from *Mycoplasma* spp.
256 (123) by the presence of a urease enzyme, which hydrolyses urea to produce 95% of their
257 energy requirements. The hydrolysis of urea produces ammonia, which leads to an increase in
258 proton electrochemical potential and *de novo* ATP synthesis (124). The production of
259 ammonia is a distinguishing feature for the identification of *Ureaplasma* spp. in culture, and
260 these tiny bacteria are detected, not by turbidity within broth, but by an alkaline shift and pH
261 indicator color change in both broth and agar culture media (125, 126). Due to this distinctive
262 urease activity, the *Ureaplasma* spp. were reclassified into their own genus within the
263 *Mycoplasmataceae* family in 1974 (123). As members of the class *Mollicutes*, *Ureaplasma*
264 spp. do not possess a cell wall and are surrounded only by a plasma membrane. Due to this
265 lack of structural integrity, *Ureaplasma* are pleomorphic and individual organisms can range

266 in size from 100 nm to 1 μ m (127). As such, the *Ureaplasma* spp. are considered to be among
267 the smallest self-replicating microorganisms.

268 **Taxonomic classification**

269 The human *Ureaplasma* spp. are divided into two species, which contain at least 14 serovars:
270 *U. parvum* (serovars 1, 3, 6 and 14) and *U. urealyticum* (serovars 2, 4, 5, 7-13) (128). *U.*
271 *parvum* possesses a smaller genome (0.75 – 0.78 Mbp) than *U. urealyticum* (0.84 – 0.95
272 Mbp) (129) and these two species can also be distinguished based on restriction fragment
273 length polymorphisms, DNA-DNA hybridization, multi-locus sequence typing and sequences
274 of 16S rRNA, multiple banded antigen (*mba*) and urease genes (130-135). Whilst this
275 taxonomic classification was formally accepted in 2002, it has not been universally adopted
276 within the literature, and often the 14 serovars are still erroneously referred to as *U.*
277 *urealyticum*.

278 Several methods for serotyping *Ureaplasma* spp. have been described, including growth
279 inhibition tests (136, 137), immunoperoxidase tests (138), enzyme-linked immunosorbent
280 assays (139, 140) and colony indirect epi-immunofluorescence (141), which utilize rabbit
281 antisera. These tests performed poorly due to a lack of standardized reagents and the presence
282 of multiple cross-reactions between serovars. These approaches also poorly discriminate
283 clinical samples containing more than one *Ureaplasma* serovar. Therefore, serotyping of
284 *Ureaplasma* for diagnostic and epidemiological purposes has historically been technically
285 challenging. Molecular-based typing methods based on sequencing of the upstream region of
286 the *mba* (135), conventional PCR of the *mba* (142-144) and random amplified polymorphic
287 DNA PCR (142) have also been described. However, these methods do not fully discriminate
288 all 14 *Ureaplasma* serovars. In addition, the *mba* was recently shown to be part of a phase
289 variable gene super-family (129), suggesting its use as a diagnostic target may be limited.

290 Following the release of full genome sequences of *Ureaplasma* American Type Culture
291 Collection (ATCC) strains, Xiao *et al.* designed 14 separate mono-plex real-time PCR assays,
292 which successfully typed all 14 ATCC type strains without cross-reactivity between serovars
293 (145). However, when these real-time PCRs were used to type clinical human *Ureaplasma*
294 isolates, 6% of isolates failed to amplify and could not be typed according to any of the
295 known 14 serovars (146). Whole-genome shotgun sequencing of a selection of these isolates
296 revealed that the gene targets for real-time PCR were completely absent or had been
297 significantly modified, such that one of the primers was unable to bind. Even more intriguing
298 was that following filtering and sub-culture of single *Ureaplasma* colonies isolated from
299 samples thought to contain mixtures of multiple serovars, several isolates continued to
300 express loci from more than one serovar. DNA sequencing revealed that these isolates were
301 in fact ‘hybrids’ or genetic mosaics that carried multiple serovar markers. Screening of 271
302 clinical samples initially believed to contain multiple serovar mixtures demonstrated that 75
303 (28%) were hybrids, which carried markers of up to 4 different serovars (146). These data, in
304 combination with recent comparative genome sequencing studies, demonstrate that there is
305 extensive evidence of horizontal gene transfer in *Ureaplasma* spp., suggesting that typing
306 these microorganisms into defined serovar groups may be of limited value for diagnostic
307 purposes (146) and that *Ureaplasma* exist as quasi-species (129). On the other hand, it is
308 possible that there are more stable gene targets that have yet to be identified, which could be
309 utilized for the discrimination of *Ureaplasma* serovars or pathogenic versus commensal
310 subtypes. Large scale comparative genome sequencing studies are required to clarify this
311 issue.

312 ***Ureaplasma* spp. are commensals of the female lower genital tract**

313 *Ureaplasma* can be isolated from the mucosal surfaces of the vagina or cervix from 40-80%
314 of sexually active females (147). *U. parvum* is isolated more frequently from the lower

315 genital tract of females than *U. urealyticum* (142, 143, 148-150), and serovar 3 is the most
316 common serovar isolated from females in the United States and Australia (100, 142, 147).
317 *Ureaplasma* colonization of the female lower genital tract has been associated with numerous
318 factors including ethnicity (particularly African-American, Central/West African and
319 Indigenous Australian women) (107, 151, 152), age (most prevalent in the 14 – 25 year age
320 group and carriage declines with increasing age) (149, 151), the number of recent sexual
321 partners (107, 152), the use of non-barrier contraceptives (107), level of education (151), age
322 of first sexual intercourse (107) and intrauterine devices (151, 153). *Ureaplasma* spp. are
323 considered to be commensal organisms within the female lower genital tract due to: (i) their
324 high prevalence and (ii) studies demonstrating no differences in the rates of endocervical
325 *Ureaplasma* colonization between women of reproductive age with or without symptoms of
326 genital infection (149, 150). However, others have reported that *Ureaplasma* spp. can cause
327 lower urogenital tract infections, such as symptomatic vaginitis (154, 155), cervicitis (156),
328 bacterial vaginosis (157), pelvic infections (158, 159) and urinary tract infections (160-162).

329 **Lower genital tract *Ureaplasma* colonization association with chorioamnionitis and**
330 **adverse pregnancy outcomes**

331 It has been proposed that the presence of *Ureaplasma* spp. in the female lower genital tract
332 may be a risk factor for chorioamnionitis and adverse pregnancy outcomes, such as preterm
333 birth (163-168). A prospective study of 2471 women attending an antenatal clinic
334 demonstrated that *Ureaplasma* spp. were isolated from vaginal swabs from 52/97 women
335 (53.6%) who delivered preterm, and that vaginal *Ureaplasma* colonization was an
336 independent risk factor for preterm birth (odds ratio 1.64, confidence interval 1.08 - 2.48, $p =$
337 0.02). Despite this statistical association, it should be noted that, in the same study,
338 *Ureaplasma* was also isolated from the lower genital tract of 783/1891 women (41.1%) who
339 delivered at term. Similarly, Kataoka *et al.* demonstrated that *U. parvum* was detected in

340 16/21 women (76.2%) who delivered preterm, and also in 440/856 women (51.4%) who
341 delivered at term ($p = 0.024$). Other authors have reported equally high carriage rates in
342 women who deliver at term and the majority of studies conclude that lower genital tract
343 *Ureaplasma* colonization is not a significant predictor of preterm birth or chorioamnionitis
344 (169-174).

345 ***Ureaplasma* can cause ascending asymptomatic infections of the upper genital tract**

346 Although *Ureaplasma* spp. are (in most instances) considered to be commensals within the
347 lower genital tract, these microorganisms are capable of causing ascending asymptomatic
348 infections of the upper genital tract. A recent study of fertile and infertile women undergoing
349 diagnostic laparoscopy (who had no symptoms of genital tract infection) demonstrated that
350 lower genital tract *Ureaplasma* colonization can lead to asymptomatic infection of the Pouch
351 of Douglas (175). Furthermore, *Ureaplasma* spp. have been isolated from the endometrium
352 and Fallopian tubes of non-pregnant women in the absence of clinical symptoms or abnormal
353 pathology (176, 177). While it was historically thought that the *Ureaplasma* spp. were of
354 'low virulence' and that their presence in the upper genital tract may be of little consequence,
355 there is now increasing evidence that these microorganisms are not simply innocent
356 bystanders. The presence of *Ureaplasma* spp. in the upper genital tract of non-pregnant
357 women suggests that these microorganisms may infect the embryo at the time of implantation
358 (147). Moreover, they are capable of inducing chorioamnionitis, which can adversely affect
359 the health of the pregnancy and neonate. Herein, we discuss the role of the human
360 *Ureaplasma* spp. as causative agents of chorioamnionitis.

361 **UREAPLASMA SPP. AS ETIOLOGICAL AGENTS OF CHORIOAMNIONITIS:**

362 The first study to identify an association between *Ureaplasma* spp. and chorioamnionitis was
363 published in 1975 and identified a link between carriage of *Ureaplasma* spp. in the lower

364 genital tract and an increased incidence of chorioamnionitis (178). While the majority of
365 studies since have demonstrated that lower genital tract colonization with *Ureaplasma* is not
366 predictive of adverse outcomes during pregnancy, the role of *Ureaplasma* spp. in
367 chorioamnionitis has remained controversial. Attempts to correlate infection with
368 *Ureaplasma* spp. to the presence of chorioamnionitis have been made by a variety of studies
369 and utilizing amniotic fluid, cord blood or placental samples. These studies have
370 demonstrated that *Ureaplasma* spp. are habitually found in placentae with chorioamnionitis
371 (Table 1). Despite the fact that up to 100% of placentae infected with *Ureaplasma* spp. have
372 evidence of histological chorioamnionitis (see Table 1), a causative role for these
373 microorganisms has not been satisfactorily explained and is complicated by a number of
374 factors.

375 A factor which complicates the role of *Ureaplasma* spp. in chorioamnionitis is that not all
376 women who are infected with these microorganisms develop chorioamnionitis or experience
377 adverse pregnancy outcomes. Gerber *et al.* tested the amniotic fluid from 254 asymptomatic
378 pregnant women at 15 - 17 weeks of gestation by PCR and detected *Ureaplasma* spp. in
379 29/254 (11.4%) of subjects (121). Significantly, this study identified that 24% of women
380 infected/colonized with *Ureaplasma* spp. delivered preterm, compared to 4.4% of women
381 who were not infected with *Ureaplasma* spp. However, this study failed to comment on the
382 vast majority (76%) of women in this study who were infected/colonized with *Ureaplasma*
383 that went on to deliver at term with no apparent adverse outcomes. Similarly, Horowitz *et al.*
384 detected intraamniotic *Ureaplasma* infections in six pregnant women (2.8%) but only three
385 (50%) of these women experienced preterm birth (179). Numerous studies have identified
386 that the severity of upper genital tract *Ureaplasma* infection/inflammation in pregnant
387 women is highly variable. Some studies have demonstrated that there may be immunological
388 evidence of severe inflammation (180, 181), while in others there may only be moderate

389 inflammation (182), or there may be no correlation between infection with *Ureaplasma* spp.
390 and inflammation (183) (Figure 2).

391 Although it remains unclear why some women infected with *Ureaplasma* spp. experience
392 adverse pregnancy outcomes, while others do not, some researchers have attributed these
393 differences in sequelae to the virulence of the infecting serovar (184), the bacterial load
394 present (185, 186), or genetic background/ethnicity (187, 188). However, these findings are
395 not always consistent, with a recent study by our group demonstrating no correlation between
396 the numbers of *Ureaplasma* present within placentae, the species/serovar present, or the
397 ethnicity of women infected with *Ureaplasma*, and the incidence or severity of histological
398 chorioamnionitis (46). Furthermore, animal model studies in which *Ureaplasma* spp.
399 infections have been established with the same strain and dose of *U. parvum* resulted in
400 divergent inflammatory responses within the chorioamnion (43, 189, 190) and within other
401 genital tract tissues (191), suggesting that the development or magnitude of host immune
402 responses may contribute to the severity of chorioamnionitis. Indeed, we have demonstrated
403 that the human *Ureaplasma* spp. can undergo immune evasive behavior *in vivo* by varying
404 the expression of their surface exposed antigens, and that the severity of chorioamnionitis is
405 inversely related to the number of antigenically distinct subtypes detected within amniotic
406 fluid (reviewed in detail below). Therefore, we hypothesize that the ability of some
407 *Ureaplasma* strains to ‘hide’ from the immune system may be an important predictor of
408 outcomes, and may potentially explain why some women do not develop chorioamnionitis
409 despite high bacterial loads within the amniotic fluid and chorioamnion.

410 Table 1 summarizes human studies, which have investigated the role of *Ureaplasma* spp. in
411 chorioamnionitis. These studies showed that the rates of *Ureaplasma*-associated
412 inflammation within the chorioamnion may vary between 0 – 100%, further highlighting the
413 diversity of histological chorioamnionitis and why it is so difficult to confirm the role of

414 these microorganisms as causative agents of chorioamnionitis. Additionally, the pathogenic
415 role of *Ureaplasma* spp. is often unclear as the majority of these infections are clinically
416 silent. *Ureaplasma* infections of the chorioamnion can persist asymptotically for up to two
417 months in humans (192) and *Ureaplasma* infected placentae cannot be distinguished
418 macroscopically from normal placentae (although there may be histological evidence of
419 chorioamnionitis that is detected following delivery). Due to the predominantly
420 asymptomatic nature of *Ureaplasma* infections, coupled with the fastidious growth
421 requirements of these microorganisms, pregnant women are not routinely screened for
422 *Ureaplasma* spp. and therefore these tiny bacteria are not always suspected (and are,
423 therefore, likely to be under-reported) as causative agents of chorioamnionitis.

424 One of the major reasons as to why the role of *Ureaplasma* spp. in chorioamnionitis has
425 remained unconfirmed is due to the polymicrobial nature of chorioamnionitis (5, 193). The
426 majority of studies investigating chorioamnionitis focus specifically on very preterm (< 28
427 weeks) and early preterm (28 – 32 weeks) pregnancies and these studies have demonstrated
428 that up to 67% of amniotic fluid or placental samples with chorioamnionitis contained at least
429 two detectable microorganisms (often *Ureaplasma* spp. and another microorganism) (Table
430 1). Because of this, researchers have not been able to confidently claim that *Ureaplasma* spp.
431 are true etiological agents of chorioamnionitis. However, a recent study by our research
432 group demonstrated that infections within late preterm (32 – 36 weeks) and term (\geq 37
433 weeks) placentae typically harbored only a single microorganism (90.5%) and that the
434 presence of *Ureaplasma* alone was significantly associated with histological
435 chorioamnionitis, at any gestational age (46). Further investigations confirmed the finding
436 that placental infections with *Ureaplasma* spp. are strongly associated with chorioamnionitis,
437 using whole genome shotgun sequencing of late preterm and term placentae (104). Similarly,
438 another study has reported that preterm placentae infected with *Ureaplasma* spp. alone are

439 independently associated with inflammation of the chorioamnion membranes. This study
440 demonstrated that there were no differences in the incidence of chorioamnionitis in placentae
441 infected with *Ureaplasma* spp. and other microorganisms, when compared to placentae
442 infected with *Ureaplasma* spp. alone (194). Taken together, these recent data suggest that not
443 only are *Ureaplasma* spp. likely to be a key etiological agent of chorioamnionitis in the
444 absence of other microorganisms, but these reports also support a causal role for *Ureaplasma*
445 in chorioamnionitis throughout pregnancy.

446 **ANIMAL MODELS HAVE HELPED TO ELUCIDATE THE PATHOGENESIS OF**
447 **UREAPLASMA CHORIOAMNIONITIS**

448 Studies in experimental animal models have confirmed that *Ureaplasma* spp. can cause
449 chorioamnionitis and fetal inflammation following intrauterine inoculation. Using a non-
450 human primate model, Novy *et al.* (195) inoculated 10^7 colony forming units of *U. parvum*
451 serovar 1 into the amniotic fluid of pregnant Rhesus macaques at day (d) 132 - 147 of
452 gestation (term = 155 – 172 d) *via* an indwelling catheter. Intraamniotic *U. parvum* caused a
453 significant influx of leukocytes into the amniotic fluid, and significant increases in the
454 amniotic fluid levels of: (i) TNF- α , IL-1 β , IL-1ra, IL-6 and IL-8; (ii) PGE2 and PGF2 α and
455 (iii) latent (92 kDa) and active (83 kDa) MMP-9 compared with pre-inoculation baseline
456 values. A progressive increase in uterine activity was also observed following *U. parvum*
457 intraamniotic inoculation and the mean inoculation-to-labor onset period was significantly
458 reduced in *U. parvum* infected animals, compared to those inoculated with sterile media or
459 saline. Histological examination of fetal membranes revealed acute chorioamnionitis that was
460 characterized by edematous thickening of the chorioamnion, neutrophil infiltration,
461 denudation of amnion epithelial cells, and necrosis and microabscess formation in chorion
462 trophoblast cells (195). Similarly, intraamniotic injection of *U. parvum* serovar 1 into the
463 amniotic cavity of pregnant baboons at day 122 - 123 of gestation (term is 185 d) resulted in

464 elevated levels of amniotic fluid IL-6 and IL-8 at the time of preterm delivery (125 d), and
465 histological evidence of acute chorioamnionitis (196). In contrast, more recent studies in
466 Rhesus macaques demonstrated that despite the presence of high numbers (3.9×10^7 CFU/mL)
467 of *U. parvum* serovar 1 within the amniotic fluid, no chorioamnionitis was detected after
468 acute durations (3 d and 7 d) of infection (197).

469 Whilst non-human primate models exhibit the closest resemblance to humans with respect to
470 gestational length, uterine anatomy and parturition, experimental intrauterine infection causes
471 preterm delivery (195, 198) and therefore it is only possible to study acute chorioamnionitis
472 in these models. In contrast, sheep do not experience inflammation-induced preterm birth, as
473 intraamniotic infection/inflammation does not cause significant activation of the fetal HPA
474 axis, cortisol production and subsequent progesterone withdrawal, which is required for the
475 initiation of labor in many species (199-201). This enables the study of chronic,
476 asymptomatic intrauterine infection and chorioamnionitis, which is not possible using other
477 animal models. In addition, fetal sheep are similar in size to human fetuses, which enables
478 instrumentation of the ewe and fetus (201) and thus makes the ovine model very useful for
479 the study of fetal development and neonatal outcomes following chorioamnionitis exposure.

480 We have demonstrated that human *U. parvum* clinical isolates injected into the amniotic
481 cavity of pregnant sheep at 55 d (term is 150 d) can chronically colonize the amniotic fluid
482 and fetus (43, 189, 199, 202). Following an intraamniotic injection of 2×10^4 CFU of *U.*
483 *parvum* serovar 6 at 55 d of gestation, temporal analysis demonstrated that the peak of
484 amniotic fluid infection occurred between 87 d and 101 d of gestation, and that the number
485 of CFU/mL remained high (approximately 10^7 CFU/mL) until the time of surgical delivery at
486 140 d (43). These data demonstrate that *Ureaplasma* can chronically colonize the amniotic
487 fluid for at least 85 d and suggest that amniotic fluid, a rich source of urea, can support the
488 long term growth of these microorganisms. We further demonstrated that *U. parvum* was

489 consistently isolated from the chorioamnion and fetal lung following chronic intraamniotic
490 infection (189, 199, 202-204), and was also isolated from the umbilical cord and other fetal
491 tissues including cerebrospinal fluid, gut, kidney, liver and spleen (189). These findings are
492 consistent with human studies that have reported that *Ureaplasma* spp. may systemically
493 infect the fetus, leading to neonatal morbidity and mortality (205-212).

494 Both chronic and acute intrauterine *Ureaplasma* infections were capable of causing
495 histological chorioamnionitis in pregnant sheep (43, 189, 190, 202, 203). Intraamniotic *U.*
496 *parvum* infection was also associated with increased expression of IL-1 β , IL-6 and IL-8
497 mRNA within the chorioamnion (43, 203) and an influx of neutrophils,
498 monocytes/macrophages and lymphocytes (43, 189, 202), compared to media controls.
499 Generally, the severity of chorioamnionitis correlated with increased duration of
500 intraamniotic *Ureaplasma* exposure (190); however, variability in the severity of
501 inflammation was a notable feature of these sheep studies (189, 190), consistent with findings
502 from human pathological investigations. Despite 100% of chorioamnion samples being
503 infected with *U. parvum*, the severity of chorioamnionitis ranged from moderate
504 (characterized by inflammatory cell infiltrate, fibrosis, scarring, sloughing of the amnion
505 epithelium and disruption to the normal tissue architecture) to no histological evidence of
506 chorioamnionitis (189). The severity of chorioamnionitis was not related to the bacterial load
507 within the chorioamnion at the time of delivery, the inoculating serovar, or the initial dose of
508 *U. parvum* (189).

509 In an attempt to explain the differences in severity of *Ureaplasma* chorioamnionitis and
510 address whether some *Ureaplasma* isolates are inherently more virulent than others, we
511 infected the amniotic cavity of pregnant sheep with clonal *U. parvum* serovar 6 isolates (43),
512 derived from placental isolates, that had caused severe histological chorioamnionitis
513 (virulent-derived strain) or no chorioamnionitis (avirulent-derived strain) in a previous ovine

514 study (189). Regardless of the inoculating clonal strain, moderate to severe chorioamnionitis
515 was observed in experimentally infected animals and there were no differences in the
516 chorioamnion expression of TLR-1, TLR-2, TLR-6, IL-1 β , IL-6, IL-8, IL-10 and TNF- α
517 between animals infected with the avirulent-derived strain or virulent-derived strain.
518 Similarly, there were no differences in the numbers of *U. parvum* isolated from the amniotic
519 fluid, chorioamnion, cord or fetal lung at 140 d (43). In the same study, we demonstrated that
520 only a sub-population of infected ewes from each group generated a serum IgG response to
521 intrauterine *U. parvum* infection. When cytokine expression was compared between animals
522 with/without anti-*Ureaplasma* serum IgG, the expression of IL-1 β , IL-6 and IL-8 was
523 significantly increased in the chorioamnion of anti-*Ureaplasma* IgG⁺ animals. In addition,
524 maternal anti-*Ureaplasma* serum IgG was associated with a significant increase in
525 meconium-stained amniotic fluid (43). These findings are also consistent with human studies
526 that have demonstrated that patients with anti-*Ureaplasma* antibodies are at a higher risk for
527 adverse pregnancy and neonatal outcomes compared to those who do not develop a humoral
528 immune response (213, 214). Taken together, this suggests that *Ureaplasma* strains are not
529 likely to be inherently virulent/avirulent, but that the host response to infection may affect the
530 pathogenesis of chorioamnionitis.

531 **The immune response to *Ureaplasma* chorioamnionitis: harmful or helpful?**

532 Studies in BALB/c and C57Bl/6 mice have provided unique insights into the potentially
533 harmful immune responses that may occur during *Ureaplasma* chorioamnionitis. BALB/c
534 mice typically display a Th1/M1-dominant immune profile, whereas the immune profile of
535 C57Bl/6 mice is consistent with a Th2/M2 bias (187). These differences have enabled
536 researchers to examine the immunopathogenic role of a skewed Th1/M1 or Th2/M2 response
537 in *Ureaplasma* chorioamnionitis. In a model of experimental intrauterine infection, von
538 Chamier *et al.* injected 10⁷ CFU of *U. parvum* into the uterine horns of pregnant BALB/c and

539 C57Bl/6 mice at 14 d (187). Examination of the fetal membranes at 72 hours post-infection
540 demonstrated that C57Bl/6 mice exhibited mild-moderate chorioamnionitis, whereas BALB/c
541 mice displayed severe necrotizing chorioamnionitis and extensive neutrophil infiltration.
542 These differences could not be attributed to differences in bacterial load; however, the
543 placental expression of cytokines and calgranulins was markedly different between the strains
544 (187). In a separate study, it was demonstrated that intrauterine *U. parvum* infection increased
545 the expression of TLR2 and CD14 on neutrophils in BALB/c but not C57Bl/6 mice (40).
546 TLR/CD14-mediated signaling triggered by bacterial lipoproteins has been shown to extend
547 the survival of apoptotic neutrophils in infected tissues, thereby increasing the duration of
548 inflammation (215). It is therefore possible that TLR2/CD14 signaling plays a role in the
549 extensive neutrophil infiltration and severe chorioamnionitis observed in BALB/c mice.
550 Interestingly, increased levels of soluble CD14 are also observed in the amniotic fluid of
551 women with intrauterine *Ureaplasma* infection (216), suggesting that CD14 signaling may be
552 an important area for future research. Combined, these studies demonstrate highlight that the
553 host immune response may be a key factor that modulates the pathogenesis of acute
554 *Ureaplasma* chorioamnionitis. Further studies using genetically modified/knock-out mouse
555 lines may significantly improve our understanding of protective versus pathogenic immune
556 responses to intrauterine *Ureaplasma* infection.

557 **Immune effects of *Ureaplasma* spp. on the fetus**

558 Animal model studies from our research group have investigated the fetal immune responses
559 to *U. parvum* exposure during gestation. In a series of experiments in pregnant sheep, it was
560 demonstrated that chronic (69 d), but not acute (7 d), *in utero* infections with *U. parvum*
561 suppressed innate immune responses in fetal sheep. Fetuses were challenged with *E. coli* LPS
562 2 days prior to delivery, and the fetuses that were chronically exposed to intraamniotic
563 *Ureaplasma* spp. demonstrated significant decreases in pro- and anti-inflammatory cytokine

564 expression, as well as fewer CD3⁺ T lymphocytes and myeloperoxidase⁺ cells within the
565 fetal lung when compared to the fetuses that were intraamniotically exposed to sterile culture
566 media (vehicle). Blood monocytes obtained from these same animals also had a significantly
567 decreased response to LPS *in vitro* (105), demonstrating that fetal exposure to *U. parvum in*
568 *utero* can markedly alter the neonatal immune responses following delivery. Similarly,
569 chronic exposure to *U. parvum* alone (with no LPS challenge) was sufficient to augment the
570 presence of transforming growth factor (TGF)- β within the fetal lung, which may also
571 contribute to the development of lung pathologies, such as bronchopulmonary dysplasia
572 (217).

573 In both Rhesus macaque and sheep models, intraamniotic *U. parvum* infections decreased the
574 populations of CD4⁺FOXP3⁺ regulatory T cells (Tregs) in the preterm fetus, in both the
575 thymus and periphery (197, 218). Furthermore, an interferon- γ response was seen in Tregs
576 exposed to *U. parvum* during gestation, and this response was absent in Tregs of fetuses
577 exposed to control (media) intraamniotic injections. Since it is well established that Tregs are
578 potent anti-inflammatory T-cells (219), these results suggest the existence of a subset of
579 Tregs that can develop a Th1 phenotype early in life, and that this response may be increased
580 in the presence of inflammation (e.g. chorioamnionitis).

581 **MANIPULATION OF HOST CELLS BY UREAPLASMA SPP.**

582 Compared to other *Mycoplasma* spp., the cytoadherence of *Ureaplasma* has not been
583 investigated in detail. *In vitro* studies have demonstrated that *Ureaplasma* spp. are adherent
584 to erythrocytes (220), placental endothelial cells (221) and human epithelial cells (222);
585 however, the adhesion mechanisms are unknown. Pretreatment of HeLa cells and
586 erythrocytes with neuraminidase significantly reduced ureaplasma adherence (222),
587 suggesting that *Ureaplasma* may bind to receptors containing sialic acid. In contrast, the

588 adhesion of *Ureaplasma* to spermatozoa is thought to be mediated by
589 sulfogalactoglycerolipid, which is expressed by the mammalian male germ cell membrane
590 (223).

591 The human *Ureaplasma* spp. have been shown to alter/manipulate host cells in several ways.
592 Allam *et al.* reported that *U. parvum* significantly increased filamin A phosphorylation at
593 serine ²¹⁵² in human benign prostate cells, and altered its intracellular distribution (224).
594 Filamin A is an actin-binding protein that regulates the cytoskeleton and is involved in
595 antimicrobial signaling pathways (225). Further investigation into the upstream and
596 downstream signaling events may therefore reveal novel insights into *Ureaplasma*-host
597 interactions. In endothelial cells isolated from normal and preeclamptic placentae, *U.*
598 *urealyticum* significantly reduced cell viability, altered the expression of heat shock protein
599 70 and significantly increased the intracellular concentration of calcium and iron. It was
600 suggested that these events occurred as part of the cellular stress response to infection and
601 may indicate that cells are progressing towards apoptosis (221). Additional studies have
602 demonstrated that *U. urealyticum* induces apoptosis in other cell types, including human lung
603 epithelial cells (A549) and THP-1-derived macrophages (226). *Ureaplasma*-infected cells
604 demonstrated an altered morphology, underwent DNA fragmentation and translocation of
605 phosphatidylserine to the outside surface of the cell (as determined by Annexin V staining
606 and flow cytometry) (226). *Ureaplasma* spp. further manipulate host cells by suppressing
607 innate host defense pathways. A recent study demonstrated that *Ureaplasma* infection
608 decreased the expression of antimicrobial peptide genes in THP-1 cells *in vitro*, in association
609 with a significant decrease in histone H3K9 acetylation (227). These findings suggest that
610 *Ureaplasma* may downregulate antimicrobial/host defense genes *via* epigenetic modifications
611 (227), which may be an important factor contributing to the ability of these microorganisms
612 to cause persistent infections. Further studies using a combination of *ex vivo* and *in vivo*

613 approaches are required to elucidate the host-pathogen interactions that occur during
614 *Ureaplasma* chorioamnionitis.

615 **UREAPLASMA VIRULENCE FACTORS**

616 While *Ureaplasma* spp. were traditionally portrayed as microorganisms of low virulence,
617 they are now recognized as the cause of serious disease. As such, *Ureaplasma* spp. have
618 evolved specific virulence mechanisms that contribute to their survival and disease
619 pathogenesis. Five proposed virulence factors have been identified: the multiple banded
620 antigen (MBA), phospholipases A and C, IgA protease and the urease gene of *Ureaplasma*
621 spp. Genetic manipulation of these microorganisms has remained elusive, and thus definitive
622 roles for these proposed virulence factors have not been determined. Furthermore, recent
623 genome sequencing studies have questioned the presence of some of these proposed virulence
624 factors.

625 **The multiple banded antigen**

626 The multiple banded antigen (MBA) was first described by Watson *et al.* (1990) and has
627 since been identified as one of the major virulence factors of the human *Ureaplasma* spp. The
628 *mba* gene, which encodes the MBA protein, contains no homology to any other known
629 prokaryotes and is unique to *Ureaplasma* spp. (228). The MBA protein is the major antigen
630 that is recognized by the host during infection, and elicits the production of cytokines by
631 activating nuclear factor-kappa B *via* TLR-1, -2, and 6 (229-231). The MBA protein consists
632 of three major domains: a typical prokaryotic signal peptide, an N-terminal transmembrane
633 domain that is conserved among all 14 serovars of *Ureaplasma* spp. and a C-terminal
634 (surface-exposed) variable domain that is composed of multiple repeating units, with both
635 serovar-specific and cross-reactive epitopes (232, 233). The C-terminal region of the MBA
636 that has been shown to alter, both by switching on/off of the gene (antigenic phase variation)

637 and more commonly to vary in size (antigenic size variation) (43, 189, 232-235). *U.*
638 *urealyticum* serovar 13 is the only *Ureaplasma* serovar that does not contain any tandem
639 repeat units in the C-terminal variable domain of the *mba* (129).

640 While some studies demonstrated differences in the size of the MBA protein (giving rise to
641 the name of the protein itself as the multiple banded antigen) (235, 236), the first study to
642 characterize MBA size variation demonstrated that differences in the size of the MBA protein
643 directly correlated with the number of tandem repeating units within the *mba* gene (133, 237).
644 More recently, Knox *et al.* identified *mba*/MBA size variation *in vivo* using an ovine model
645 (189). Pregnant ewes were chronically infected for 69 d with a non-clonal *U. parvum* isolate
646 and the size of the *mba*/MBA was assessed. This study demonstrated that the number of
647 *mba*/MBA size variants was inversely correlated with the severity of inflammation within the
648 chorioamnion: when > 9 *mba*/MBA size variants were identified, there was little or no
649 chorioamnionitis; however, when < 5 *mba*/MBA size variants were identified, there was
650 severe histological chorioamnionitis (189). Other ovine studies have identified that variation
651 in the size of the *mba*/MBA was not seen after three days of intraamniotic infection, while
652 some slight variation was seen after seven days of infection (190) and significant *mba*/MBA
653 size variation was seen after 69 days of chronic intraamniotic *U. parvum* infection (43, 189,
654 190). Dando *et al.* (2012) also demonstrated the ability of *Ureaplasma* spp. to vary their
655 *mba*/MBA throughout the course of gestation and suggested that size variation of the
656 *mba*/MBA (presumably by slipped-strand mispairing) may be a mechanism by which
657 *Ureaplasma* spp. may evade host immune recognition, allowing chronic asymptomatic
658 infections to develop (43).

659 More recently, we have demonstrated for the first time that *Ureaplasma* spp. clinical isolates
660 from human placentae were also able to vary the size of their *mba*/MBA (Sweeney *et al.*,
661 manuscript in preparation). Clinical isolates that varied the size of their *mba*/MBA were

662 associated with a reduced incidence of histological chorioamnionitis and significantly lower
663 levels of the cord blood cytokines G-CSF and IL-8. In contrast, *Ureaplasma* spp. isolated
664 from placentae that demonstrated no *mba*/MBA size variation had severe histological
665 chorioamnionitis and elevated cord blood cytokines. Further *in vitro* investigations using
666 recombinant MBA (rMBAs) proteins of differing sizes (i.e. different numbers of tandem
667 repeat units) and human macrophage cells lines demonstrated immune responses that varied
668 depending on the size of the rMBA. These results were confirmed by western blot; the
669 expression of nuclear factor-kappa B fragment p65 (an activator of transcription) varied when
670 stimulated with the different sized rMBA proteins (Sweeney *et al.*, manuscript in
671 preparation). Combined, these results confirm the ability of *Ureaplasma* spp. to vary their
672 surface-exposed MBA *in vivo*, and that this variation is associated with the modulation of the
673 host immune response both *in vivo* and *in vitro*.

674 Other studies have also demonstrated that the *mba*/MBA can undergo phase (on/off
675 switching) variation. Three studies have identified that selective antibody pressure directed
676 against the MBA can result in the generation of MBA-negative variants (*Ureaplasma* isolates
677 that do not express their MBA protein) in serial passage experiments (43, 234, 238). In these
678 studies, MBA-negative *Ureaplasma* isolates were detected following two to three serial
679 passages in culture medium containing MBA-specific antibodies (43, 234). More recently,
680 phase variation of the MBA occurred in the absence of any selective (antibody) pressures
681 (239), indicating that this antigen is capable of rapid phase variation. Zimmerman *et al.*
682 (2009) hypothesized that the expression of the MBA (locus UU375) is alternated with
683 expression of an adjacent locus (UU376), which encodes an *Ureaplasma*-specific conserved
684 hypothetical protein. Utilizing polyclonal rabbit antisera generated against the conserved (N-
685 terminal, non-repetitive) regions of the MBA and UU376, these authors identified that
686 antibody treatment led to the emergence of 'escape variants', which expressed the protein that

687 had not been the target of selective pressure. Following this, it was hypothesized that DNA-
688 inversion events – presumably occurring at short inversion sequences - were responsible for
689 the switching on/off of expression of these genes (238). Zimmerman and colleagues further
690 investigated the role of DNA-inversion sites within the *Ureaplasma* genome, and
691 demonstrated experimentally that the *mba* paralogues UU171, UU172 and the orthologue
692 UU144 were also involved in site-specific DNA inversion/recombination (240). Furthermore,
693 it was shown that the XerC tyrosine recombinase gene of *U. parvum* is the most likely
694 mediator of these DNA inversion events (241). Subsequent experimental investigation into
695 the ability of the XerC to process the recombination event proved successful, indicating that
696 this tyrosine recombinase is able to induce DNA inversion events (242), representing the first
697 evidence of a mechanism which may govern antigenic phase variation in *Ureaplasma* spp.

698 In a separate series of investigations, whole genome sequencing was carried out on
699 *Ureaplasma* spp. ATCC strains and a range of clinical isolates, and revealed the presence of
700 multiple additional tandem repeat domains within the *mba* locus of all *Ureaplasma* isolates
701 tested (129). Remarkably, it was shown that the *mba* was part of a large gene superfamily,
702 comprising 183 genes in *U. parvum* and *U. urealyticum*, and 22 gene subfamilies. This study
703 also identified the presence of putative recombination sites surrounding tandem repeating
704 domains, consistent with the theory that *Ureaplasma* spp. may undergo significant antigenic
705 phase and size variation, dependent on which sequences within the genome are expressed.
706 Whilst there is convincing molecular evidence that the *mba* is part of a complex phase
707 variable system it should be noted that, to the best of our knowledge, MBA-negative
708 *Ureaplasma* variants have not been isolated from human clinical material or experimental
709 animal studies. Rather, there is significant evidence of MBA size variation *in vivo*.

710 **Phospholipase A and C**

711 The pathogenesis of phospholipases results from the production of membrane-destabilizing
712 compounds and degradation of the host cell membrane phospholipids (243). Endogenous
713 phospholipase A₁, A₂ and C activity has been previously identified in *U. parvum* serovar 3
714 and *U. urealyticum* serovars 4 and 8 (244-246). These phospholipases demonstrated higher
715 activity in *Ureaplasma* in their exponential growth phase; suggesting that the *Ureaplasma*
716 spp. phospholipases were membrane bound and were not being secreted (245). It was further
717 identified that phospholipase A₂ activity was three-fold higher in *U. urealyticum* serovar 8,
718 when compared to *U. urealyticum* serovar 4 and *U. parvum* serovar 3 (244). However,
719 subsequent whole genome sequencing of *U. parvum* serovar 3 could not identify any genes of
720 significant similarity to any known sequences of phospholipase A₁, A₂ or C (228). These
721 findings indicated that *Ureaplasma* may encode phospholipases that are evolutionarily
722 distinct from other phospholipase genes, or that these phospholipases may not exist within
723 *Ureaplasma* spp. Interestingly, more recent studies by the same research group revealed that
724 whole genome sequencing of the 14 *Ureaplasma* spp. serovars and four *Ureaplasma* spp.
725 clinical isolates were again unable to detect any phospholipase A₁, A₂ or C genes; however, a
726 phospholipase D domain containing protein was identified in all *Ureaplasma* spp. (129).
727 These researchers further investigated the presence/activity of these enzymes experimentally
728 and were unable to detect any significant phospholipase C or D activity in *U. parvum* serovar
729 3 and *U. urealyticum* serovar 8 (129). Further investigation into the presence and activity of
730 phospholipases within *Ureaplasma* spp. are required to elucidate if these enzymes are
731 potential virulence factors of these organisms.

732 **Immunoglobulin (Ig) A protease**

733 One of the primary defense mechanisms of the mammalian immune system is the production
734 of IgA at mucosal sites (247) and the ability of an organism to degrade IgA antibodies allows
735 the microorganism to evade this host defense mechanism. Robertson *et al.* published the first

736 evidence of an IgA protease in *U. urealyticum* that was capable of cleaving IgA₁ (248). While
737 it was subsequently determined that all 14 *Ureaplasma* serovars possess an IgA protease with
738 proteolytic activity against IgA₁ (but no proteolytic activity against IgA₂, IgG or IgM
739 antibodies) (249, 250), more recent evidence has questioned the presence of an IgA protease
740 in *Ureaplasma* spp. Initial genome sequencing studies of *U. parvum* serovar 3 were unable to
741 identify any genes with similarity to known IgA proteases (228) and more recent whole
742 genome analyses were unable to identify any IgA protease genes within the 14 *Ureaplasma*
743 serovars, nor was it found to be present in any of the *Ureaplasma* spp. clinical isolates tested
744 (129). Recently, an IgG binding protein and IgG serine protease were identified within
745 *Mycoplasma mycoides* subspecies *capri*. This study provided evidence that both *U. parvum*
746 and *U. urealyticum* contain genes that encode an IgG binding protein and an IgG serine
747 protease within their genomes (251). Based on these recent findings, further studies are
748 warranted to determine if these IgG binding/IgG protease genes are active in cleaving IgG
749 and therefore may be a previously unrecognized virulence factor of the human *Ureaplasma*
750 spp.

751 **Urease**

752 The ability of *Ureaplasma* spp. to hydrolyze urea was first identified in 1966, and the
753 production of adenosine triphosphate (ATP) *via* this mechanism appears to be unique within
754 *Ureaplasma* (125, 252). The urease enzyme is a key virulence factor of many ureolytic
755 bacteria, and the ureaplasma urease gene cluster has a similar genetic organization to that of
756 *E. coli*, *Proteus mirabilis*, *Klebsiella pneumoniae* and *K. aerogenes* (253). The urease
757 complex constitutes a major component of the ureaplasma cytoplasm (254) and Takebe *et al.*
758 demonstrated that the urease of *U. urealyticum* serovar 8 was responsible for urolithiasis in
759 humans (255). The *Ureaplasma* spp. urease has a significantly higher specific activity
760 compared to other bacterial ureases (256) and was responsible for lethal toxicity in mice

761 following intravenous injection (257). Interestingly, the *Ureaplasma* spp. are one of few
762 bacteria which encode a urease enzyme but lack the ability to assimilate ammonia into
763 glutamine or glutamate (258), potentially explaining the very high intracellular ammonia
764 concentration of these microorganisms (124).

765 Our recent studies suggest that *Ureaplasma* infection, and a subsequent increase in ammonia
766 due to urease metabolism, can alter the pH of amniotic fluid and fetal lung fluid in an ovine
767 model (190). This study also identified that the increased pH within the fetal lung was
768 associated with lung damage, even in the absence of inflammatory responses and provides the
769 first evidence that increased pH *in vivo* may be due to *Ureaplasma* infections. Other studies
770 have demonstrated that *Ureaplasma* spp. infections can result in hyperammonemia (259).
771 Clinical reports of patients who underwent lung transplantation and subsequently developed
772 hyperammonemia (abnormally high levels of ammonia within the blood) were found to be
773 infected with *Ureaplasma* spp. within their blood or bronchoalveolar lavage fluid. When
774 these patients received antibiotic treatment to eradicate the *Ureaplasma* spp., their syndromes
775 resolved and only one relapse was identified in a patient colonized with an antimicrobial
776 resistant *Ureaplasma* strain (259). Taken together, these findings suggest that the activity of
777 the *Ureaplasma* urease enzyme can result in an alkaline environment, in both fetal and adult
778 lungs, and also within amniotic fluid.

779 **HORIZONTAL GENE TRANSFER AND THE ABILITY OF *UREAPLASMA* SPP. TO**
780 **RAPIDLY ADAPT TO HOST MICROENVIRONMENTS**

781 HGT is an important mechanism used by microorganisms to acquire genetic material.
782 Although *Ureaplasma* spp. maintain minimal genomes that have undergone significant
783 degenerative evolution (228), recent evidence has identified that HGT is likely to occur
784 within these microorganisms and may be an important determinant of virulence. As

785 previously discussed, the identification of genetic hybrids (146) suggests that the *Ureaplasma*
786 spp. may be genetically promiscuous. Comparative genome sequencing studies have provided
787 further evidence of this and identified integrase-recombinase genes, transposases and phage
788 related proteins in *Ureaplasma* spp. genomes (129), which are highly indicative of HGT
789 events. Interestingly, *U. urealyticum* genomes generally contained a higher number of these
790 genes, suggesting that this species may be more capable of acquiring genes horizontally than
791 *U. parvum* (129).

792 Early attempts to define the phylogeny of *Mycoplasma* suggested that *Mycoplasma* spp. with
793 the smallest genomes have high mutation rates and undergo rapid evolution (260, 261).
794 Dando *et al.* provided evidence of the ability of the human *Ureaplasma* spp. to rapidly adapt
795 to their microenvironment in a sheep model of intrauterine infection (262). Following
796 injection of a non-clonal *U. parvum* serovar 3 isolate into the amniotic fluid of pregnant
797 sheep at 55 d, significant genetic variability within the 23S ribosomal (r) RNA gene was
798 detected between *U. parvum* isolated from the amniotic fluid and chorioamnion at the time of
799 preterm surgical delivery (125 d). While *U. parvum* isolated from amniotic fluid showed
800 100% 23S rRNA domain V sequence homology to the original strain injected, highly
801 polymorphic sequences (containing only 64 – 82% sequence homology to the inoculating
802 strain) were detected within *Ureaplasma* isolates from the chorioamnion. Furthermore,
803 chorioamnion *Ureaplasma* isolates demonstrated the presence of macrolide resistance genes,
804 which were not evident in amniotic fluid isolates. Whilst this study did not investigate the
805 presence of potential genetic transfer elements flanking these variable gene sequences, these
806 data support the concept that *Ureaplasma* spp. may undergo significant HGT *in vivo*.
807 Furthermore, this study suggests that different anatomical sites (amniotic fluid versus
808 chorioamnion) may select for different *Ureaplasma* subtypes within non-clonal populations
809 and thus influence the socio-microbiological structure of the bacterial population (262).

810 Taken together, there is increasing evidence that *Ureaplasma* spp. undergo significant genetic
811 variation, allowing them to diversify their populations, and this is likely to contribute to the
812 overall pathogenicity of *Ureaplasma* spp.

813 **TREATMENT OF *UREAPLASMA* CHORIOAMNIONITIS AND THERAPEUTIC** 814 **CONSIDERATIONS**

815 The major difficulty in treating chorioamnionitis is that a large proportion of cases are
816 clinically asymptomatic and therefore are not diagnosed until retrospective analysis of the
817 placenta and fetal membranes. This is particularly problematic for the human *Ureaplasma*
818 spp., which can cause chronic, asymptomatic intrauterine infections that modulate the host
819 immune response to prevent significant pathological events, but are still associated with
820 adverse outcomes. Whilst antibiotics are recommended for women with preterm pre-labor
821 rupture of membranes (263) to prevent ascending invasive infections from the lower genital
822 tract, the timing of administration may be too late to have beneficial effects against chronic
823 *Ureaplasma* infections that were established in early/mid gestation. It has been suggested that
824 the administration of appropriate antibiotics before 22 weeks of gestation (or before
825 inflammation and maternal-fetal damage occurs) could significantly decrease the incidence of
826 preterm birth (264). This is supported by a meta-analysis, which demonstrated that the
827 administration of macrolides and clindamycin during the second trimester of pregnancy was
828 associated with a reduced risk of preterm delivery (265). However, due to the concern of
829 antibiotic resistance, widespread antimicrobial treatment is not recommended unless there is
830 evidence of intraamniotic infection. Culture and/or PCR detection of *Ureaplasma* spp. within
831 amniotic fluid remains the gold standard for diagnosis; however, amniocentesis is an invasive
832 procedure that is not routinely performed, and it is likely that high numbers of *Ureaplasma*
833 infections during pregnancy remain undetected and therefore untreated.

834 An additional complicating factor for the treatment of *Ureaplasma* chorioamnionitis includes
835 the often polymicrobial nature of this disease, which suggests that more than one
836 antimicrobial agent may be required to successfully eradicate infection. Furthermore,
837 treatment options for pregnant women are limited due to potential teratogenic and harmful
838 effects associated with the use of some antimicrobials during pregnancy. Even fewer options
839 are available for the treatment of intrauterine *Ureaplasma* infections, as these
840 microorganisms are inherently resistant to beta-lactam and glycopeptide antibiotics (due to
841 their lack of a cell wall), as well as trimethoprim and sulphonamides (as *Ureaplasma* spp. do
842 not synthesize folic acid) (266). Antimicrobials that are potentially active against *Ureaplasma*
843 include the tetracyclines, fluoroquinolones and macrolides; however, resistance to these
844 antimicrobial classes has also been well described (267-271).

845 Erythromycin, a 14-membered lactone ring macrolide, is the most common antibiotic used
846 for the treatment of neonatal *Ureaplasma* infections and is routinely used in clinical
847 obstetrics. Large randomized controls and meta-analyses have demonstrated that
848 erythromycin administration for preterm pre-labor rupture of membranes can reduce the risk
849 of chorioamnionitis and neonatal morbidity, and delay preterm birth (272-274). However, it
850 is less clear if maternal erythromycin can eradicate existing human intrauterine infections due
851 to conflicting reports within the literature (275-277). In pregnant sheep, maternal
852 intramuscular erythromycin treatment (30 mg/kg/d for 4 days) failed to eradicate an
853 erythromycin susceptible strain of *U. parvum* from the amniotic fluid, chorioamnion and fetal
854 lung (202), presumably due to poor transplacental passage (202, 278-280). In a follow-up
855 study, it was again demonstrated that intraamniotic *Ureaplasma* infection was not eradicated
856 following: (i) single intraamniotic and repeated maternal intramuscular erythromycin, or (ii)
857 single maternal intramuscular and repeated intraamniotic erythromycin injections (281).

858 These data suggest that erythromycin may not be beneficial for the treatment of intrauterine
859 *Ureaplasma* infections.

860 Azithromycin is 15-membered semisynthetic macrolide with superior tissue penetration, a
861 prolonged half-life and broader antimicrobial coverage than erythromycin (282).

862 Azithromycin is well tolerated during pregnancy and achieves peak concentrations of $151 \pm$
863 46 ng/mL within human amniotic fluid and 2130 ± 340 ng/mL within human placentae at 6
864 hours post-injection, before rapidly declining (282). In pregnant sheep, a single intraamniotic
865 injection of azithromycin achieved therapeutic concentrations that were sustained for 48
866 hours; however there was poor maternal-fetal transfer (280). Despite this, a single maternal
867 intravenous azithromycin injection or a single maternal intravenous azithromycin injection
868 combined with an intraamniotic azithromycin injection completely eradicated an established
869 *U. parvum* infection from the amniotic fluid, chorioamnion and fetal lung in pregnant sheep
870 (283). Similarly, studies in Rhesus macaques demonstrated that maternal intravenous
871 azithromycin (25 mg/kg/d for 10 d) administered 6-8 d after intraamniotic *U. parvum*
872 inoculation successfully eradicated *Ureaplasma* from the amniotic fluid (284, 285). It should
873 be noted that in both of these sheep (283) and monkey (285) studies, histological evidence of
874 chorioamnionitis was still observed at the time of delivery, suggesting that azithromycin
875 treatment alone is not sufficient to reduce/eliminate inflammation within the fetal
876 membranes.

877 Recent research efforts have evaluated a new, broad-spectrum fluoroketolide, solithromycin,
878 in pregnant sheep and demonstrated that a single maternal dose can deliver therapeutic
879 concentrations to both the fetus and amniotic fluid (286). The transplacental transfer of
880 solithromycin was significantly higher than that reported for other macrolides, including
881 azithromycin, and a maternal intravenous infusion resulted in sustained therapeutic
882 concentrations within maternal plasma, fetal plasma and amniotic fluid for >12 hours (286).

883 *In vitro*, solithromycin has potent activity against human clinical *Ureaplasma* isolates (287,
884 288), in addition to a range of other important pathogens (289-293). Both maternal
885 intravenous solithromycin and maternal intravenous solithromycin combined with
886 intraamniotic solithromycin effectively eradicated *U. parvum* from the amniotic cavity of
887 pregnant sheep, but similar to azithromycin, failed to reduce inflammation of the
888 chorioamnion and fetal lung (283). These findings suggest that solithromycin may not
889 accumulate in high enough concentrations to exert anti-inflammatory effects and that co-
890 administration of immune modulators should be investigated. To date, solithromycin is the
891 most potent antimicrobial for the treatment of genital mycoplasmas and has several
892 pharmacokinetic advantages over older macrolides, suggesting that it may be useful for the
893 treatment of intrauterine infections. Human studies are required to further examine the
894 effectiveness and safety of solithromycin in pregnancy and chorioamnionitis.

895 **CONCLUDING REMARKS AND FUTURE RESEARCH DIRECTIONS**

896 In conclusion, the findings of both human and animal studies have now demonstrated that
897 infection with *Ureaplasma* spp. alone are able to cause chorioamnionitis, demonstrating a
898 true causal role for these microorganisms in disease. Furthermore, the ability of *Ureaplasma*
899 spp. to vary the expression and size of their major surface-exposed antigen, the MBA,
900 indicates that these pathogens have evolved specific virulence mechanisms to avoid immune
901 detection by the host. Despite the lack of genetic manipulation studies, both animal and
902 human research has now shown the involvement of the MBA in modulating the host response
903 to chorioamnionitis, and our most recent study has demonstrated that recombinant MBA
904 proteins of different sizes elicit different immune responses, potentially as a consequence of
905 altered NF-kappa B activation. We predict that this highly variable surface antigen expression
906 facilitates immune evasion, enabling these microorganisms to cause chronic *in utero*
907 infections, and further research is required to elucidate the mechanisms of antigenic variation

908 in *Ureaplasma* spp. This may also assist in understanding the progression of disease during
909 *Ureaplasma* infections and provide unique insights into the host-microbe interactions that
910 occur *in vivo*. Furthermore, the development of genetic tools to create isogenic deletion
911 mutants would enable researchers to assign definitive roles to proposed ureaplasma virulence
912 factors.

913 Due to the difficulties associated with identifying and diagnosing *Ureaplasma* infections and
914 chorioamnionitis, additional research should be undertaken to identify biomarkers for the
915 rapid diagnosis of *Ureaplasma* in order to detect subclinical infections and clinically silent
916 chorioamnionitis. Due to the unique metabolism of the *Ureaplasma* spp., ‘omics’ profiling of
917 *Ureaplasma*-infected amniotic fluid may identify unique molecular signatures that could be
918 used for diagnostic purposes, in combination with conventional *Ureaplasma* culture/PCR
919 identification. This is a critical area of research that may lead to the improved identification
920 and treatment of *in utero* inflammation, which will ultimately lead to improved maternal and
921 neonatal outcomes. We also propose that amniotic fluid collected from pregnant women
922 undergoing amniocentesis should be routinely tested for *Ureaplasma* spp., even in the
923 absence of clinical signs/symptoms of chorioamnionitis. Additionally, further studies are
924 required to identify effective and targeted therapies that eradicate intrauterine *Ureaplasma*
925 spp. infections and reduce inflammation. Continued research investigating the
926 pharmacokinetics and anti-*Ureaplasma* activity of new generation drugs, potentially in
927 combination with immunomodulatory agents, may lead to the development of more effective
928 treatment options for *Ureaplasma* chorioamnionitis.

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1984 Emma L. Sweeney received her Ph.D in 2015, from Queensland University of Technology
1985 (QUT), Australia. Her project investigated the presence and diversity of microorganisms,
1986 particularly the human *Ureaplasma* species, in adverse pregnancy outcomes with a focus on
1987 *Ureaplasma* pathogenesis in histological chorioamnionitis. Emma was subsequently
1988 appointed a postdoctoral research fellow at QUT, investigating the oral neonatal microbiome
1989 and how oral bacterial communities are regulated by reactive oxygen species that are
1990 produced when human breastmilk and neonatal saliva combine. Emma has worked on the
1991 topic of *Ureaplasma* spp. for six years and hopes to continue research into the role of these
1992 minimalistic pathogens in human and animal infections, and the host-microbe interactions
1993 that facilitate disease.

1994 **Samantha J. Dando:**

1995 Samantha J. Dando received her PhD in microbiology in 2012 from Queensland University of
1996 Technology, Australia, where she studied the pathogenesis of intrauterine *Ureaplasma*
1997 infections in an experimental ovine model. She has published seminal papers in this field,
1998 which have significantly improved our understanding of chronic, intraamniotic ureaplasma

1999 infections. Samantha subsequently undertook postdoctoral research at Griffith University,
2000 where she investigated the novel mechanisms by which *Burkholderia pseudomallei* can
2001 directly invade the central nervous system *via* the olfactory and trigeminal nerves within the
2002 nasal cavity. In her current position at Monash Biomedicine Discovery Institute, Monash
2003 University, Samantha's research focuses on characterizing myeloid cell populations within
2004 various sub-compartments of the eye and brain, and how these cells respond to systemic
2005 inflammatory mediators. Samantha also continues to be active in *Ureaplasma* research, and is
2006 interested in the ability of these microorganisms to undergo antigenic variation and modulate
2007 the host immune response.

2008 **Suhas G. Kallapur:**

2009 Suhas G. Kallapur received his Bachelor in medicine (MBBS) and a doctorate in medicine
2010 (MD) degree from the Bombay University, India. He then completed a residency in Pediatrics
2011 at the Wayne State University, Michigan USA followed by a fellowship in Neonatal-Perinatal
2012 medicine at Cincinnati Children's Hospital Ohio, USA. He is currently a tenured-Professor of
2013 Pediatrics at Cincinnati Children's Hospital, University of Cincinnati and is a practicing
2014 Neonatologist. Dr. Kallapur leads a laboratory, funded by NIH, March of Dimes, and
2015 Burroughs Wellcome trust, whose main thrust since 2000 is to understand the pathogenesis of
2016 infection or inflammation-mediated preterm birth. This condition is an important contributor
2017 to prematurity, which is a leading cause of infant mortality and morbidity world-wide.
2018 *Ureaplasma* species most commonly cause perinatal infections, and Dr. Kallapur has
2019 collaborated with co-authors and others to create sheep and Rhesus macaque models of
2020 intrauterine infection and inflammation.

2021 **Christine L. Knox:**

2022 Christine L. Knox obtained her PhD in 1998 from the Queensland University of Technology
2023 (QUT), where she pioneered the study at QUT of the *Ureaplasma* species and their role in
2024 adverse pregnancy outcomes. As an Associate Professor she now leads the Reproductive
2025 Health Research Group at QUT and was the principal PhD supervisor for Samantha Dando
2026 and Emma Sweeney, the joint co-authors of this review. Funding from the National Institute
2027 of Health and the National Health and Medical Research Council, Australia has enabled this
2028 group to further investigate the pathogenesis of *Ureaplasma* spp. in pregnant women
2029 delivering late preterm and at term, and in an ovine model of intraamniotic infection.
2030 Christine Knox is an appointed member of the 'International Subcommittee for the
2031 Taxonomy of *Mollicutes*' and in 2016 she was the Chair of the local organizing committee of
2032 the 21st Congress of the International Organization for Mycoplasmaology.

2033

2034 **FIGURE LEGENDS**

2035 **Figure 1: Comparison of key events involved in normal parturition and inflammation-**
2036 **induced parturition.**

2037 Normal parturition is initiated by the increased placental synthesis of CRH at term, which
2038 causes the production of cortisol. Cortisol induces the production of prostaglandin E2 and
2039 prostaglandin F_{2α}, and works in a positive feedback loop to further stimulate placental CRH
2040 production. Prostaglandins induce the production of matrix metalloproteases, which facilitate
2041 membrane rupture and cervical remodeling. In concert, activation of the fetal HPA axis leads
2042 to a functional progesterone withdrawal and production of contraction-associated proteins,
2043 which cause myometrial activation and uterine contractility. During chorioamnionitis,
2044 inflammatory cytokines and chemokines produced in response to microbial invasion of the
2045 chorioamnion and/or amniotic fluid stimulate prostaglandin production and neutrophil
2046 infiltration, leading to the synthesis of matrix metalloproteases and subsequent membrane
2047 weakening. Recognition of pathogen associated molecular patterns by pattern recognition
2048 receptors (such as TLRs) is critical for the initiation of inflammation-induced parturition.
2049 CAPs = contraction-associated proteins; CRH = corticotropin releasing hormone; HPA =
2050 hypothalamic-pituitary-adrenal; MMPs = matrix metalloproteases; NF-κB = nuclear factor-
2051 kappa B; PGDH = prostaglandin dehydrogenase; PGs = prostaglandins; PGS2 =
2052 prostaglandin-endoperoxide synthase-2; TLRs = Toll-like receptors. The direction of the
2053 black arrows represents either an increase or decrease in expression.

2054 **Figure 2: Differences in the presence of chorioamnionitis in *Ureaplasma* spp.-infected**
2055 **women.**

2056 Hematoxylin and eosin stained chorioamnion tissue demonstrates that some women whose
2057 placentae are colonized with *Ureaplasma* spp. have no evidence of chorioamnionitis (panels

2058 A & B), whilst other women have mild/moderate (panels C & D) or severe (panels E & F)
2059 evidence of inflammation (demonstrated by neutrophil influx, arrows) within their
2060 chorioamnion, despite high numbers of *Ureaplasma* spp. present within the tissue. Images are
2061 shown at x200 (A, C, E) and x400 (B, D, F) total magnification; boxed areas in A, C and E
2062 are shown in B, D and F respectively.

Author	Gestational age (GA) in weeks	Specimen	n =	Incidence of <i>Ureaplasma</i> spp. infection	Incidence of polymicrobial infections	<i>Ureaplasma</i> spp. with chorioamnionitis	<i>Ureaplasma</i> spp. without chorioamnionitis	Reference
Viscardi <i>et al.</i> (2008)	< 33	S/CSF	313	74/313 (23.6%)	- ^a	30/46 (65.0%)	16/46 (35.0%)	(206)
Hassanein <i>et al.</i> (2012)	< 35	CB	30	13/30 (43.3%)	no polymicrobial infections	7/13 (53.8%)	6/13 (46.2%)	(294)
Gray <i>et al.</i> (1992)	< 28	AF	2461	8/2461 (0.4%)	- ^b	8/8 (100.0%)	0/8 (0.0%)	(295)
Yoon <i>et al.</i> (1998)	≤ 36	AF	120	25/120 (20.8%)	11/120 (9.0%)	5/25 (20.0%)	-	(44)
Yoon <i>et al.</i> (2003)	≤ 35	AF	252	23/252 (9.1%)	- ^c	-	-	(296)
Park <i>et al.</i> (2013)	< 34	AF	56	35/56 (62.5%)	7/56 (12.5%)	26/47 (55.31%) [#]	0/3 (0.0%)	(120)
Kacerovsky <i>et al.</i> (2014)	24 – 36	AF	124	26/124 (21.0%)	5/124 (4.0%) ^d	-	-	(297)
Romero <i>et al.</i> (2015)	≤ 35	AF	59	6/24 (25.0%)	10/24 (41.7%)	3/6 (50.0%)	2/6 (33.3%) [#]	(298)
Stepan <i>et al.</i> (2016)	24 - 34	AF	122	33/122 (27.0%)	8/122 (6.6%)	29/33 (87.9%)	4/33 (12.1%)	(299)
Musilova <i>et al.</i> (2015)	24 – 36	AF	166	40/166 (24.1%)	19/166 (11.4%)	26/40 (65.0%)	14/40 (35.0%)	(300)

Stepan <i>et al.</i> (2016)	24 – 36	AF	386	103/386 (26.7%)	32/386 (8.3%)	70/103 (68.0%) [#]	16/103 (15.5%) [#]	(301)
Berger <i>et al.</i> (2009)	≤ 33	AF/PL	114	32/114 (28.1%)	- ^a	11/25 (44.0%) [#]	14/25 (66.0%) [#]	(302)
Hillier <i>et al.</i> (1988)	< 37	PL	112	32/112 (28.6%)	- ^c	19/29 (65.5%) [#]	10/65 (15.4%) [#]	(1)
Stein <i>et al.</i> (1994)	Any GA	PL	182	21/182 (11.5%)	- ^e	11/16 [#]	5/16 [#]	(303)
Van Marter <i>et al.</i> (2002)	< 36	PL	206	58/155 (37.4%)	- ^e	51/77 (66.2%)	7/78 (9.0%)	(304)
Miralles <i>et al.</i> (2005)	< 33	PL	14	5/14 (35.7%)	5/14 (35.7%)	4/5 (80.0%)	1/5 (20.0%)	(305)
Egawa <i>et al.</i> (2007)	< 32	PL	83	4 (4.8%)	5/83 (6.0%) ^b	4/4 (100.0%)	0/4 (0.0%)	(119)
Olomu <i>et al.</i> (2009)	< 28	PL	866	52/866 (6.0%)	21/52 (40.4%)	34/52 (65.4%)	18/52 (34.6%)	(306)
Kasper <i>et al.</i> (2010)	< 34	AF	118	32/118 (27.1%)	- ^a	5/19 (26.3%) [#]	14/19 (73.7%) [#]	(186)
Namba <i>et al.</i> (2010)	≤ 32	PL	151	63/151 (41.7%)	13/151 (8.6%)	52/63 (82.5%)	11/63 (17.5%)	(118)
Roberts <i>et al.</i> (2012)	> 37	PL	195	2/195 (1.0%)	1/195 (0.5%)	0/2 (0.0%)	2/2 (100.0%)	(4)
Kundsin <i>et al.</i>	Various	PL	801	156/801 (19.5%)	18/801 (2.2%) ^b	32/53 (60.4%) [#]	21/53 (39.6%)	(307)

(1984)								
Sweeney <i>et al.</i> (2016)	> 32	PL	535	42/535 (7.9%)	4/57 (7.0%)	26/38 (68.4%)	12/38 (31.6%)	(46)
Cox <i>et al.</i> (2016)	< 37	PL	57	13/57 (22.8%)	-	9/24 (37.5%)	4/33 (12.1%)	(117)

Table 1. The incidence of *Ureaplasma* spp. infection, polymicrobial infections and chorioamnionitis in women delivering preterm, late preterm or at term. The incidence of chorioamnionitis in *Ureaplasma* spp.-infected women is frequently high, indicating that these microbes are associated with chorioamnionitis. AF = amniotic fluid; CB = cord blood; GA = gestational age; PL = placenta; S = serum.

^a Only *Ureaplasma* spp. were tested for within study

^b Only genital mycoplasmas (*Ureaplasma* spp. and *Mycoplasma hominis*) were tested for within this study

^c Study states that >1 organism may have been isolated, but prevalence of polymicrobial infections not stated

^d Only *Ureaplasma* spp., *Mycoplasma hominis* and *Chlamydia trachomatis* tested for within this study

^e No comment on polymicrobial infections

[#] not all placentae in study were tested

Box 1: Development, structure and function of the chorioamnion.

The amnion develops from the ectoderm of the embryo 8 days after conception and surrounds the developing embryo to form an amniotic sac, which contains amniotic fluid. As the amniotic sac expands due to fetal growth and the production of amniotic fluid, the amnion makes contact with the chorion, which lines the decidua of the uterine wall, to form the chorioamnion at 10-12 weeks of gestation (308). The avascular chorioamniotic membranes persist until term in healthy pregnancies and perform critical barrier and container functions (309). The amnion comprises five layers: (i) a cuboidal epithelium which is in contact with the amniotic fluid; (ii) an acellular basement membrane; (iii) a compact layer; (iv) a mesenchymal cell layer and (v) a spongy layer, which is in contact with the chorion (310). The amniotic epithelial cells and mesenchymal cells possess stem cell and immunomodulatory properties, and have shown promising results for use in regenerative medicine (311). The chorion comprises four layers: (i) a cellular, fibroblast layer; (ii) a reticular layer; (iii) a pseudo-basement membrane and (iv) a trophoblast layer (310).

Box 2: Diagnosis of chorioamnionitis.

The diagnosis of chorioamnionitis is currently based on clinical signs coupled with histological and microbiological analysis of the placenta after delivery of the newborn. Histologic grading of the placenta is considered the gold standard for the diagnosis of chorioamnionitis; however, this retrospective diagnosis is not useful in informing patient management throughout pregnancy, especially in the absence of clinical signs. Several studies have investigated the diagnostic value of amniotic fluid and maternal serum biomarkers for the detection of chorioamnionitis in pregnant women undergoing amniocentesis. Elevated inflammatory markers such as interleukin (IL)-6, IL-8, matrix metalloproteinase (MMP)-8, MMP-9 and monocyte chemotactic proteins within amniotic fluid are positive predictors of intra-amniotic inflammation and/or clinical chorioamnionitis (297, 312-317); however, these markers may have poor positive predictive values for the detection of sub-clinical, histologic chorioamnionitis and may be variably expressed within the amniotic fluid and fetal membranes during chorioamnionitis (318-320). Recently, Liu *et al.* (321) reported that surface-enhanced laser desorption/ionization time-of-flight mass spectrometry (SELDI-TOF-MS) for the detection of human neutrophil defensins (HNP) -1 and HNP-2, calgranulins A and calgranulins C within amniotic fluid was highly accurate for the diagnosis of sub-clinical chorioamnionitis, but further studies with larger patient cohorts are required to validate these findings. Non-inflammatory markers such as amniotic fluid lactate dehydrogenase and glucose were also recently investigated for the detection of histologic chorioamnionitis (322), but the diagnostic accuracy of these assays was low, suggesting that additional amniotic fluid biomarkers should be investigated for the diagnosis of chorioamnionitis.

