Intrauterine *Candida albicans* infection elicits severe inflammation in fetal sheep

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Abstract

Background—Preventing preterm birth and subsequent adverse neonatal sequelae is among the greatest clinical challenges of our time. Recent studies suggest a role for *Candida* spp. in preterm birth and fetal injury, as a result of their colonization of either the vagina and/or the amniotic cavity. We hypothesised that intraamniotic *C. albicans* would cause a vigorous, acute fetal inflammatory response.

Methods—Sheep carrying singleton pregnancies received single intraamniotic (IA) injections of either saline (control) or 10^7 CFU *C. albicans* 1 or 2 d prior to surgical delivery and euthanasia at 124 ± 2 d gestation.

Results—Colonization of the amniotic cavity by *C. albicans* resulted in a modest inflammatory response at 1 d and florid inflammation at 2 d, characterised by fetal thrombocytopenia, lymphopenia and significant increases of inflammatory cytokines/chemokines in the fetal membranes skin, lung and the amniotic fluid.

Conclusion—Acute colonization of the amniotic cavity by *C. albicans* causes severe intrauterine inflammation and fetal injury. *C. albicans* is a potent fetal pathogen which can contribute to adverse pregnancy outcomes.

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Introduction

Preterm birth remains a leading cause of neonatal mortality and morbidity worldwide. Although the causes of preterm birth are multi-factorial, infection of the amniotic cavity and subsequent intrauterine inflammation are both strongly associated with preterm delivery and adverse neonatal outcomes (including respiratory, gastrointestinal and neurological injuries), most notably in deliveries occurring at 32 weeks completed gestation [1–3]. Culture and molecular-based analyses have identified bacterial genera including *Ureaplasma*, *Fusobacterium, Streptococcus, Bacteroides* and *Gardnerella* spp. as the microorganisms most commonly isolated from preterm deliveries [1,4,5]. Recent studies suggest that many of the intrauterine infections associated with preterm labour are polymicrobial in nature [5,6].

Historically, the role of *Candida* spp. in preterm birth and neonatal injury has been somewhat unclear. However, recent molecular data suggest that *Candida albicans* may colonise the amniotic cavity more frequently than initially suggested by culture-based analyses, and cases of congenital candidiasis have been reported in the literature [7–12]. Rode and colleagues have suggested a possible association between serial amniocenteses and candida chorioamnionitis [13]. More recently, Bean *et al*. published the resolution of two cases of intraamniotic *Candida albicans* infection with maternal and intraamniotic fluconazole. Key conclusions of this case report were that intraamniotic *Candida albicans* infection has devastating implications for the fetus and that prompt diagnosis and treatment of infection is essential for pregnancy wellbeing [14].

Candida spp., (most commonly *C. albicans*) are believed to asymptomatically colonise the vagina of 20% of healthy women (more frequently during pregnancy), and invasive candidiasis can be a primary cause of death and neurological injury in extremely low birth-weight infants (<1000 g) [5,15–17]. Although a causal association for bacterial infection in early preterm labour is well established, the role of *Candida* spp. in uterine infection and preterm delivery is more controversial [5,16]. A large multi-centre study of pregnancy outcomes and *Candida* spp. colonization in 13,914 women concluded that colonization with *Candida* spp. was not associated with low birth weight or preterm delivery [18]. In direct contrast, a retrospective study of 38,151 infants, identified a 34–64% reduction in preterm birth in a subset (8.1%) born to mothers that received Clotrimazole (anti-*Candida* spp.) treatment during pregnancy [19]. In addition, more recent smaller intervention studies reported either a significant reduction or a trend to reduction in preterm birth in groups receiving treatment for asymptomatic vaginal candidiasis [16,20]. Of particular interest is research suggesting an apparent association between indwelling contraceptives and cervical cerclage with *Candida* spp. infection of the amniotic cavity [5].

We have previously utilised pregnant sheep to investigate the effects of *E.coli* lipopolysaccharides (LPS)[21], antenatal corticosteroids [22], interleukin (IL)-1 [23] and live *Ureaplasma* spp. [24] on the fetal lung [25], gut[26] and skin[27] and modulation of the fetal immune system [28]. In light of emerging clinical data, animal studies are now needed to clarify the impact of acute intraamniotic *C. albicans* infection. To that end, we tested the pathogenicity of acute intrauterine *C. albicans* infection in a sheep model of human

pregnancy. We hypothesised that intraamniotic *C. albicans* would cause a vigorous, acute fetal inflammatory response.

Materials and Methods

Animals

All procedures involving animals were performed at The University of Western Australia (Perth, Western Australia) following review and approval by the animal care and use committees of The University of Western Australia and Cincinnati Children's Hospital (Cincinnati, OH.). Twenty nine date-mated Australian merino ewes with singleton pregnancies were randomised to receive either: **i)** a single ultrasound-guided intraamniotic injection of 2 mL saline (n=13); or **ii)** a single ultrasound-guided intraamniotic injection of 10^7 CFU *C. albicans* (Western Australian clinical isolate) in 2 mL saline with delivery after 1 d (1 d Candida group; n=8) or 2 d (2 d Candida group; n=8). Successful placement of intraamniotic injections were confirmed with electrolyte (Cl^-) analysis of amniotic fluid using a Siemens Rapidlab 1265 Analyser (Siemens, Munich, Germany). No fetal losses occurred in the 1 d Candida, 2 d Candida or Saline control groups.

Fetuses were surgically delivered at 124 ± 2 d GA, and euthanized with intravenous pentobarbitone (100 mg/kg). Fetal lung fluid and tissues for protein and mRNA expression analyses were collected at autopsy and snap frozen in liquid nitrogen. To eliminate a potential sampling bias, fetal skin was selectively collected from the fetal groins. A minimum of five, randomly selected animals were analysed from each group. Fetal lung tissues for histological analysis were inflation fixed in 10% neutral buffered formalin for 24 h before paraffin embedding. Fetal skin tissues for histological analysis were cryopreserved in OCT.

Candida albicans culture for intraamniotic injection

A single Western Australian clinical isolate of *C. albicans* was cultured on Difco Sabaraud-Dextrose agar (Becton Dickinson & Co., Franklin Lakes, NJ.) at 37°C for 48 h and single colonies were inoculated into sterile $1 \times$ phosphate buffered saline (Sigma-Aldrich, St. Loius, MO.). *C. albicans* colony morphology was confirmed by growth on Brilliance Candida Agar (Oxoid). Inoculums were quantified using a plate dilution series as per standard microbiological methods and recorded as CFU/mL. Quantified inoculums (10^7 CFU in 2 mL $1 \times$ phosphate buffered saline) were stored at −80°C prior to use.

Nucleic acid extraction

To develop a standard curve for quantitation of *C. albicans* in fetal tissues, total RNA was extracted from 250 μL of *C. albicans* (the same Western Australian clinical isolate used *in vivo* in this study) using the Versant Sample Preparation kit 1.0 (Siemens, Munich, Germany) on a Kingfisher automated extraction platform (Thermo Scientific, Rockford, IL.) as per manufacturer's instructions. Total RNA was extracted from liquid nitrogen-homogenised fetal tissues using TRIzol as previously reported[21]. Extracted RNA was treated with Turbo-DNase (Life Technologies, Carlsbad, CA.) to remove any residual DNA and

subsequently quantified on a Qubit fluorometer (Life Technologies) using a broad-range RNA quantitation kit. RNA yields from fetal tissues were normalised to 100 ng/μL.

Candida albicans detection/quantitation

RNA extracted from fetal lung, skin, chorioamnion and spleen was screened using a real-time PCR assay targeting the RNase P RNA gene of *C. albicans* [29]. RNA-based reactions were performed using an EXPRESS One-Step SuperScript qRT-PCR Kit (Life Technologies) with 0.5 μM each primer, 0.2 μM probe, 400 ng template RNA and water to a final volume of 20 μL. To enable quantitation of *C. albicans* within each sample, a standard curve of pure *C. albicans* (study isolate) RNA was included in each assay at a final concentration of 40, 4 and 0.4 ng per 20 uL reaction. Reaction cycling conditions were as follows: 15 min reverse transcription at 50°C and an initial denaturation at 95°C for 20 s, followed by 40 cycles of 95°C for 3 s and 60°C for 30 s. All reactions were performed in 96 well plates on a ViiA7 real-time PCR thermocycler (Life Technologies). The presence of viable *C. albicans* in amniotic fluid samples was determined using a Sabaraud-Dextrose agar plate dilution series as described above. Three single colonies from positive plates were subsequently inoculated onto Candida Brilliance agar (Oxoid, Basingstoke, UK) for confirmation of isolate identification.

Relative quantification of mRNA expression

Ovine-specific PCR primers and hydrolysis probes for IL-1β, IL-6, IL-8, TNF-α, MCP-1 and MCP-2 (Life Technologies) were used to perform quantitative PCR reactions on RNA from fetal lung, skin, and chorioamnion tissue. Reactions were performed using an EXPRESS One-Step SuperScript qRT-PCR Kit (Life Technologies) with 400 ng template RNA in a total volume of 20 μL. Reaction cycling conditions were as described above. Cq values were normalised to 18s rRNA and expressed as fold changes relative to pooled control values. Reaction efficiencies were within limits proposed in the MIQE guidelines [30].

Enzyme-linked immunosorbent assays

Quantification of IL-1β and IL-8 protein concentrations in AF was performed as previously described [31]. AF samples were diluted 1:5 in assay buffer. Quantification of IL-6 protein concentration in ovine AF was performed using an identical protocol with the following modifications: Plate wells were coated overnight at 4°C with 5 μg/mL capture antibody (MCA1659; ABD Serotech, Kidlington, UK). Recombinant sheep IL-6 protein standards (Protein Express, Cincinnati, OH.) and AF samples, diluted 1:2 in assay buffer, were incubated overnight at 4°C. The detection antibody (AHP424; ABD Serotech) was diluted 1:750 in assay buffer. All samples and standards were assayed in duplicate. Cortisol measurements were performed with a Cortisol EIA kit (Oxford Biomedical Research, Rochester Hills, MI.) on 1:10 diluted fetal arterial cord blood plasma according to the manufacturer's instructions.

Haematology

Complete blood counts (CBC) and differential analyses were performed with an automated Coulter counter customised for sheep blood.

Histology

5 μm-thick sections from formalin fixed lung (right upper lobe) tissues embedded in paraffin blocks or 10 μm-thick sections from cryopreserved skin tissues embedded in OCT were stained with haematoxylin and eosin. For lung tissues, five random fields were scored for inflammatory cell infiltration and airway consolidation as follows: 0: Normal; 1: Airway inflammatory cells, no consolidation; 2: Airway inflammatory cells + microconsolidation focii (1–2/5 Low Power Field); 3: Airway inflammatory cells + microconsolidation focii (3/5 Low Power Field); and 4: Extensive airway inflammatory cells and consolidation. Immunohistochemical staining of fetal lung for CD3 (A0452, Dako, Glostrup, Denmark, working concentration 1:100) and *C. albicans* (B65411R, Meridian Life Science, Inc. Memphis, TN., working concentration 1:50) was performed as previously published[32]. CD3 counts in fetal lung were obtained by counting positively stained cells in five randomly selected, non-overlapping fields at $20 \times$ objective magnification.

Statistical analyses

All values are expressed as mean ± standard deviation (SD). All analyses were performed using IBM SPSS Statistics for Windows, software version 20.0 (IBM Corp. Armonk, NY.). Data were assessed for normality with Shapiro-Wilk tests and histograms. Parametric data were screened for outliers with Dixon's Q-parameter and differences tested for significance with one-way ANOVA employing an α-value of 0.05. Multiple post-hoc comparisons were performed using Tukey's test. Apparent differences in non-parametric data were tested for significance with Kruskal-Wallis one-way ANOVA employing an α-value of 0.05. Multiple post-hoc comparisons were performed using Rank Sum Tests with an α-value corrected for *n* multiple comparisons.

Results

Intrauterine infection with 10^7 CFU *C. albicans* resulted in florid intrauterine inflammation at 2 d post-infection. Limited histological changes in skin and lung, and relatively modest increases in cytokine/chemokine expression were detected in fetal tissues collected 1 d post-infection.

Detection of viable *Candida albicans*

Amniotic fluid from all 1 d and 2 d *C. albicans* exposed animals but none of the controls were positive for viable *C. albicans* growth (data not shown). qPCR analysis demonstrated increased *C. albicans* RNA in fetal lung (3.8 ± 3 ng), chorioamnion (78 ± 32 ng) and skin (50 ± 48 ng) taken from animals exposed to *C. albicans* for 2 d, relative to fetal lung (0.2 ng ± 0.1 ng), chorioamnion (14 ± 10 ng) and skin (6.0 ± 5.0 ng) exposed to *C. albicans* for 1 d (Figure 1a). The highest levels of *C. albicans* RNA were detected in chorioamnion tissue after a 2 d exposure ($p < 0.010$ vs. 2 d fetal lung). No *C. albicans* RNA was detected in the fetal spleen after either 1 d or 2 d *C. albicans* exposure or in any saline control animal.

Cytokine/chemokine protein concentration in fetal plasma, amniotic fluid and fetal lung fluid

No changes in IL-1β, IL-6 or IL-8 protein concentration were detected in fetal plasma from animals exposed to *C. albicans* for either 1 d or 2 d, relative to control (data not shown). Analysis of IL-1β, IL-6 and IL-8 protein concentrations in the AF demonstrated significant increases in the concentration of: **i)** IL-1β in 2 d *C.albicans* exposed animals relative to 1 d *C. albicans* exposed animals (p=0.001) and control (p=0.002); and **ii)** IL-8 in 2 d *C. albicans* exposed animals relative to 1 d *C. albicans* exposed animals (p=0.044) and control (p=0.046). No change in IL-6 concentration was detected (Figure 1b). Analysis of IL-1β, IL-6 and IL-8 protein concentration in fetal lung fluid demonstrated significant increases in the concentration of: **i)** IL-1β in 2 d *C. albicans* exposed animals relative to control (680 ± 900 pg/mL vs. 157 ± 10 pg/mL; p=0.048); and **ii)** IL-8 in 2 d *C. albicans* exposed animals, relative to control (20 ± 18.5 ng/mL vs. 1.4 ± 2.0 ng/mL p=0.002). No change in fetal lung fluid IL-6 concentration was detected (data not shown).

Elevated circulating fetal cortisol

Concentrations of cortisol in fetal arterial plasma demonstrated variable, but significant increases in concentration at 2 d post-infection relative to 1 d post-infection (p=0.007) and control (p=0.002) (Figure 2).

Haematological analyses

Complete/differential fetal blood counts demonstrated marked thrombocytopenia and leukopenia after 2 d intrauterine *C. albicans* infection (Table 1); circulating platelets (p=0.026) and white blood cells (p=0.006) were significantly reduced relative to control. Lymphocytes at 2 d post-infection were significantly reduced relative to counts at 1 d post-infection (p=0.015) and an apparent reduction relative to control counts closely approached significance (p=0.08).

Elevated cytokine/chemokine mRNA expression in the fetal lung, skin and membranes

Analysis of cytokine/chemokine expression in the fetal lung, skin and membranes identified a pattern of significant mRNA up-regulation at 2 d post-*C. albicans* infection, relative to both control and 1 d post-*C. albicans* infection tissues. Significant increases in IL-1β (p=0.007), IL-6 (p=0.007), IL-8 (p=0.010), TNF-α (p=0.003) and MCP-1 (p=0.003) mRNA expression were identified in the fetal lung at 2 d post-infection, relative to control (Figure 3a). In the fetal skin, significant mRNA increases were observed in the expression of IL-6 at 2 d (p=0.004), TNF-α at 2 d (p=0.019), IL-8 at 1 d (p=0.000) and 2 d (p=0.000), and MCP-2 at 1 d (p=0.031) and 2 d (p=0.000) post-*C. albicans* infection, relative to control (Figure 3b). In fetal membranes, a significant increase was only observed in IL-8 mRNA expression (p=0.020) at 2 d post-*C. albicans* infection, relative to control (Figure 3c).

Histological analysis of the fetal lung and skin

Seven of eight fetal lung samples from the 2 d Candida group assessed for inflammation and consolidation were graded 2 (n=4) or 3 (n=3) (Figure 4a), consistent with robust inflammation of the fetal lung. A marked increase in *C. albicans* staining intensity and

distribution was apparent in lung tissues taken from 2 d *C. albicans*-exposed animals, relative to 1 d *C. albicans*-exposed and saline control animals (Figure 4a insert). CD3-positive cells were significantly increased (33.0 ± 8.0 vs. 12.0 ± 4.0 cells/low power field, *p*=0.006) in the fetal lung of animals exposed to *C. albicans* for 2 d, relative to control (Figure 4b). Haemotoxylin and eosin staining of transverse fetal skin sections demonstrated numerous foci of basophilic infiltration of the *stratum corneum* at 2 d post-infection (Figure 5a). Immunofluorescent analysis of IL-8 expression in the fetal skin demonstrated distinct increases in signal intensity and distribution in 1 d and 2 d *C. albicans* exposed tissues, relative to control (Figure 5b).

Discussion

Comparatively little animal data are available to describe the inflammatory response to acute *C. albicans* colonization of the amniotic cavity [33–35]. We present novel data demonstrating: **i)** the colonization of the amniotic environment by *C. albicans* following intra-amniotic infection; and **ii)** that intrauterine infection with *C.albicans* rapidly progresses to an active infection involving multiple fetal surfaces yielding florid intrauterine inflammation and depletion of circulating fetal immunocytes and platelets. These findings add weight to recent clinical reports concluding that the prompt diagnosis and treatment of intraamniotic *C. albicans* infection is critical to pregnancy wellbeing [14].

Infection of the amniotic cavity with *C. albicans* was characterised by a quasi-latent period of at least 1 d post-infection. Although significant increases in IL-6, IL-8 and MCP-2 mRNA transcript expression were identified in the fetal skin and IL-8 protein concentration in the AF at 1 d post-infection, no changes were identified in lung or chorioamnion mRNA expression, fetal arterial plasma cortisol levels or fetal white blood cell counts. At 2 d post-infection, significant increases in mRNA expression were detected in the fetal skin and lung, with a limited (IL-8 only) response detected in the chorioamnion.

Cytokine/chemokine mRNA expression in the fetal skin and lung, and cytokine protein concentrations in the fetal lung fluid correlated with increased *C. albicans* RNA levels at 2 d. Interestingly, the vigorous inflammatory response identified in the fetal lung in the 2d post-infection group was disproportionate to the comparatively low level of *C. albicans* RNA detected. Conversely, the inflammatory response detected in the chorioamnion was comparatively mild (given the high levels of *C. albicans* RNA isolated from this tissue) at both 1 d and 2 d. These data suggest a differential sensitivity between tissues (lung, skin and chorioamnion) to inflammatory stimulation by *C. albicans.* Surprisingly, no *C. albicans* RNA was detected in the fetal spleen in either the 1 d or 2 d post-infection groups. Although we did not extensively culture from aseptically harvested fetal organs, these molecular data indicate that *C. albicans* does not gain access to the fetal circulation by 2 d despite significant colonization of the fetal lung and skin. This observation also suggests that the systemic changes (alterations in leukocyte counts and fetal arterial plasma) identified in this study are due to inflammatory signalling derived from amniotic fluid-exposed skin/amnion and lung. Using chronically instrumented preterm lambs, we have previously demonstrated the importance of the fetal lung to acute systemic inflammation[32]. Those findings are supported by data in the present study, which also suggest that fetal lung inflammation is a

key mediator of a systemic fetal response. Additionally, our data also suggest that inflammation of the fetal skin/chorioamnion, in the absence of fetal lung inflammation, is sufficient to increase cytokine (IL-8) concentrations in the AF. Although not investigated in the present study, it would be of great interest to assess the inflammatory and structural changes deriving from colonization of the fourth AF-exposed fetal surface, the gastro-intestinal tract, by *C. albicans*.

Our data also contrast with earlier LPS-based studies in this model, wherein intraamniotic injection of 10 mg LPS resulted in broad increases in mRNA expression in both the fetal lung and chorioamnion at 1 d post-injection[36]. The isolation of fetal inflammatory response to the skin at 1 d post *C. albicans* infection may derive from the complete exposure of the fetal skin to the AF and *C. albicans'* preference this epithelial surface [37]. It may also reflect a temporal difference in inflammatory response between skin and chorioamnion in the sheep . Interestingly, the magnitude and scope of inflammatory response elicited by 2 d infection with *C. albicans* was much greater than that identified in previous studies in fetal sheep involving *E. coli* lipopolysaccharides or *Ureaplasma* spp. over a similar time frame [27,38,39].

The marked increase in fetal cortisol identified in the 2 d post-infection group is consistent with a robust fetal inflammatory response [40] and is similar in relative size to that demonstrated by Challis and colleagues in chronically catheterised fetal sheep immediately prior to parturition[41]; chorioamnionitis and elevated levels of IL-1β and IL-6 have also been demonstrated to increase fetal cortisol production, inducing fetal lung maturation and reduced birth weight [40,42].

Thrombocytopenia is a salient feature of congenital and neonatal candidiasis [43,44]; an especially striking feature of 2 d *C. albicans* infection in the present study was a marked reduction in fetal platelets. In contrast to our 2 d findings, however, congenital candidiasis is associated with a marked increase in total white blood cells [8,9,45]. This difference may relate to species or gestation-dependent responses to *C. albicans* infection or be a function of the acute (2 d) nature of our experimental model.

Limitations of this study include the acute time frame over which the impact of *C. albicans* infection was assessed and that the infection was established by intraamniotic injection as opposed to ascending vaginal infection and penetration of the fetal membranes, the hypothesised route of the majority of intrauterine infection in humans [2]. Further studies, potentially employing a low-titre inoculum and sub-chorionic infection to mimic ascending infection via a focal breach in the fetal membranes [46], are warranted to advance our understanding of the pathogenic role played by *C. albicans* in pregnancy.

Conclusions

An increasing number of clinical studies now suggest a role for *Candida* spp. in preterm birth and fetal injury. Our data support the recently published findings of Bean and colleagues [14] and further suggest a likely role for *C. albicans* in preterm birth and chorioamnionitis. Importantly, our data demonstrate that an untreated acute infection of the

amniotic cavity with *C. albicans* can cause a devastating, florid fetal inflammatory response that is consistent with adverse neonatal outcomes. Additional animal and clinical studies are warranted to further assess the role of *Candida* spp. in preterm birth and fetal injury, the potential benefits of *Candida* spp. screening and the best means of administering prophylaxis and treatment in pregnancy.

Acknowledgments

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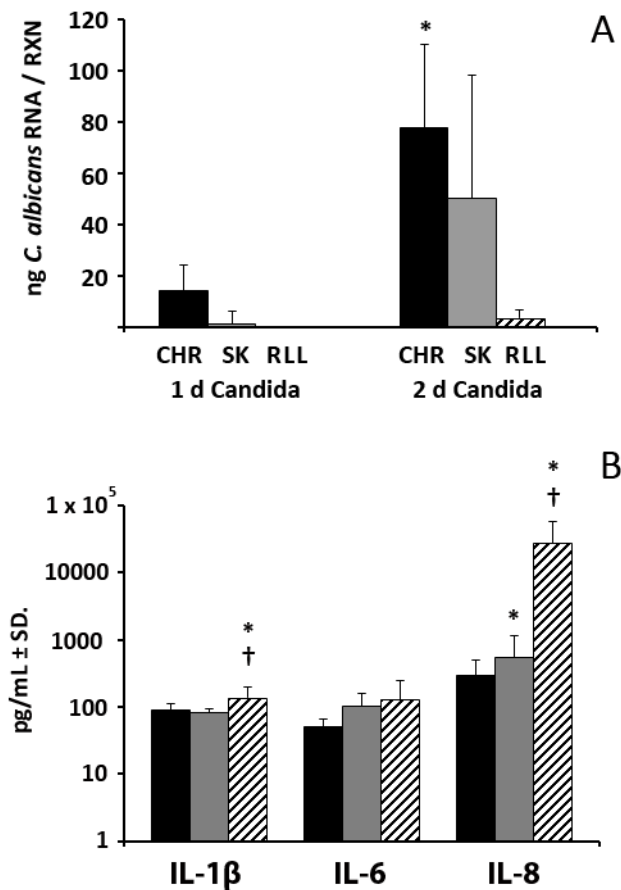
Figure 1.
Panel A: *C. albicans* RNA in fetal tissues in 1 d and 2 d post-infection groups. (1 d Candida n=5; 2 d Candida n=5). CHR, chorioamnion; SK, skin; RLL, right lower lobe of lung. *, significant difference ($p < 0.010$) vs. RUL. **Panel B:** Concentration of IL-1β (Black bars, Control n=10; Grey bars, 1 d Candida n=8; Hatched bars, 2 d Candida n=8) and IL-8 (Black bars, Control n=6; Grey bars, 1 d Candida n=6; Hatched bars, 2 d Candida n=6), but not IL-6 (Black bars, Control n=6; Grey bars, 1 d Candida n=6; Hatched bars, 2 d Candida n=6;) is increased in AF in response to IAI with *C. albicans*. * $p<0.05$ vs. control; † $p<0.05$ vs. 1 d *Candida albicans* exposure.
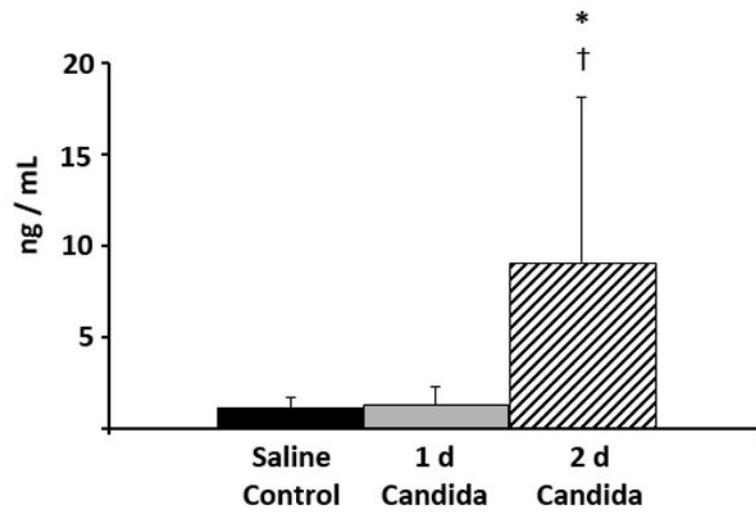
Figure 2.
Concentration of fetal arterial plasma cortisol (Control n=13; 1 d Candida n=8; 2 d Candida n=8) is increased in response to 2 d *C. albicans* exposure, vs. control. * $p<0.05$ vs. control; † $p<0.05$ vs. 1 d *C. albicans* exposure.
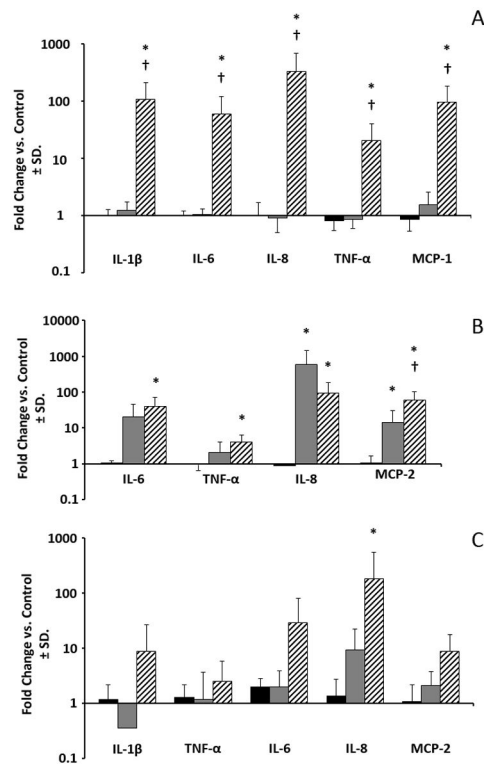
Figure 3.
Panel A: Expression of cytokine/chemokine mRNA is increased in the fetal lung in response to 2 d *C. albicans* exposure. Black bars, Control n=13; Grey bars, 1 d Candida n=8; Hatched bars, 2 d Candida n=8. * *p*<0.05 vs. control; † *p*<0.05 vs. 1 d *C. albicans* exposure. **Panel B:** Expression of cytokine/chemokine mRNA is variably increased in the fetal skin in response to 1 d and 2 d *C. albicans* exposure. Black bars, control n=6; Grey bars, 1 d Candida n=5; Hatched bars, 2 d Candida n=6. * *p*<0.05 vs. control; † *p*<0.05 vs. 1 d *C. albicans* exposure. **Panel C:** Only IL-8 is significantly increased in the chorioamnion in response to 1 d and 2 d *C. albicans* exposure. Black bars, Control n=6; Grey bars, 1 d Candida n=6; Hatched bars, 2 d Candida n=5) * *p*<0.05 vs. control.
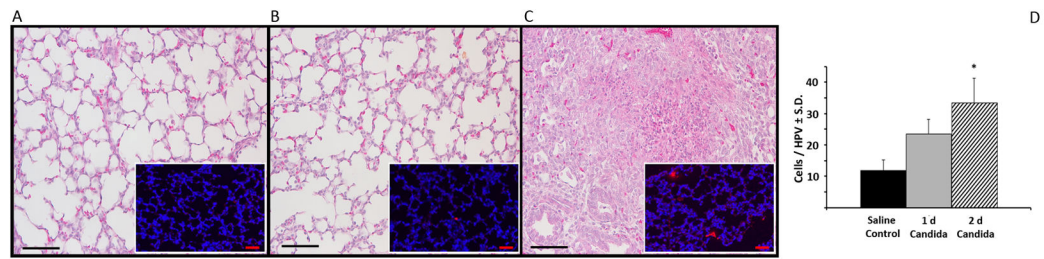
Figure 4.
Infiltration and consolidation of the fetal lung in response to 2 d *C. albicans* exposure
(Control n=13; 1 d Candida n=8; 2 d Candida n=8). **Panel A:** Control; **Panel B:** 1 d *C. albicans* exposure; and **Panel C:** 2 d *C. albicans* exposure. Inserts: Immunofluorescent staining for cell nuclei (DAPI; blue) and *C. albicans* (Alexa 594; red). All scale bars represent 50 μm. **Panel D:** Analysis of Infiltration of fetal lung by CD3-positive cells in response to colonization with *C. albicans*. (Control n=6; 1 d Candida n=5; 2 d Candida n=5) * *p*<0.05 vs. control. HPV, high power view.
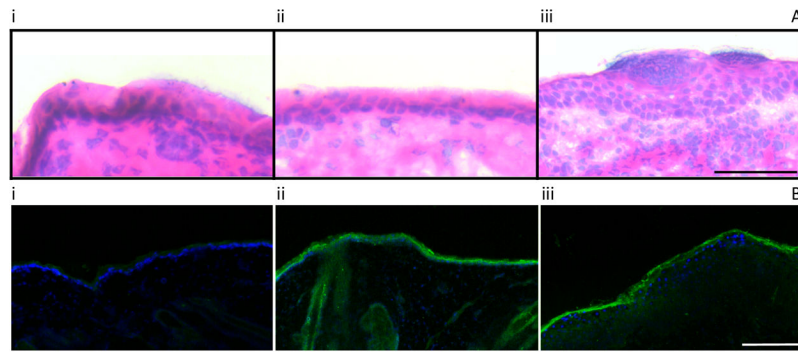
Figure 5.

Panel A: Infiltration of the fetal skin in response to *C. albicans* exposure. (Control n=5; 1 d Candida n=5; 2 d Candida n=5). i: Control; ii: 1 d *C. albicans* exposure; and iii: 2 d *C. albicans* exposure. Scale bar represents 50 μm. **Panel B:** Relative to control, immunofluorescent staining for IL-8 (Alexa 488; green) is increased in the fetal dermis and epidermis after 1 d and 2 d *C. albicans* exposure. i: Control n=5 ii: 1 d Candida n=5; iii: 2 d Candida n=5. Cell nuclei are stained blue with DAPI. Scale bar represents 200 μm.

Table 1

Group, birth-weight and differential blood count summary data for control (n=13), 1 d (n=8) and 2 d (n=8) Candida post-infection groups.

	n	Fetal Weight Kg	Platelet 10^9/L	Total WBC 10^{11}/L	Monocytes 10^9/L	Lymphocytes 10^9/L
Saline	13	2.8 ± 0.3	616 ± 157	2.83 ± 1.3	0.1 ± 0.1	1.90 ± 1.0
1 d Candida	8	3.1 ± 0.4	576 ± 63	3.50 ± 1.0	0.2 ± 0.01	2.30 ± 1.0
2 d Candida	8	2.9 ± 0.2	$\mathbf{437 \pm 170}^*$	$\mathbf{1.50 \pm 1.1}^*$	0.2 ± 0.10	$0.90 \pm 0.80^{\dagger}$

*
$p<0.05$ vs. control;

$\dagger$
$p<0.05$ vs. 1 d Candida post-infection group.