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Pelvic chlamydial infection predisposes to ectopic pregnancy by 1 2 upregulating integrin B1 to promote embryo-tubal attachment

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29 Abstract

30

31 Tubal ectopic pregnancies are a leading cause of global maternal morbidity and 32 mortality. Previous infection with Chlamydia trachomatis is a major risk factor 33 for tubal embryo implantation but the biological mechanism behind this 34 association is unclear. Successful intra-uterine embryo implantation is 35 associated with increased expression of endometrial 'receptivity' integrins (cell 36 adhesion molecules). We examined integrin expression in Fallopian tubes of 37 women with previous C. trachomatis infection, in mice experimentally infected 38 with C. trachomatis, in immortalised human oviductal epithelial cells (OE-39 E6/E7) and in an *in vitro* model of human embryo attachment (trophoblast 40 spheroid-OE-E6/7 cell co-culture). Previous exposure with C. trachomatis 41 increased Fallopian tube/oviduct integrin-subunit beta-1 (ITGB1) in women and 42 mice compared to controls. C. trachomatis increased OE-E6/E7 cell ITGB1 43 expression and promoted trophoblast attachment to OE-E6/E7 cells which was 44 negated by anti-ITGB1-antibody. We demonstrate that infection with C. 45 trachomatis increases tubal ITGB1 expression, predisposing to tubal embryo 46 attachment and ectopic pregnancy.

47 Keywords: Ectopic pregnancy, *Chlamydia trachomatis*, Integrins, embryo
48 implantation; Fallopian tube

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- 50

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52 Introduction

53

54 An ectopic pregnancy is a pregnancy that implants outside the main cavity of 55 the uterus, most commonly in the Fallopian tube. It occurs in 1-2% of all pregnancies worldwide and remains the most common cause of maternal 56 57 morbidity and mortality in the first trimester of pregnancy (Jurkovic and 58 Wilkinson 2011). Chlamydia trachomatis (C. trachomatis) is the most prevalent 59 curable bacterial sexually transmitted disease worldwide, with estimated 60 incidence of greater than 100 million cases per year (WHO 2008). 61 Epidemiological studies indicate that previous pelvic *C. trachomatis* infection is 62 a major risk factor for ectopic pregnancy (Bakken et al. 2007). However, the 63 mechanism by which C. trachomatis infection leads to tubal implantation is not 64 understood and does not appear to be a direct consequence of tissue 65 destruction by the organism (J. L. V. Shaw et al. 2011). We propose that C. 66 trachomatis infection of tubal epithelial cells may alter their phenotype 67 predisposing to ectopic embryo attachment and implantation later in a woman's 68 reproductive life.

69

In the human uterus, the putative 'window of receptivity' to the embryo (that is required for successful intra-uterine implantation to occur), in the mid-luteal phase of the menstrual cycle, is accompanied by increased endometrial expression of integrin heterodimers, composed of the integrin subunits (ITG) alpha 1 (ITGA1), beta 1 (ITGB1), alpha 4 (ITGA4), alpha v (ITGAV) and beta 3 (ITGB3) (Lessey 1998). Integrins are a family of widely-expressed cell surface

76 receptors that mediate cell-cell and cell-extracellular matrix adhesion and, as 77 a result, regulate many aspects of cell behavior. Twenty-four different integrin 78 heterodimers are currently recognized in humans, each comprising a pair of 79 non-covalently associated ITGA and ITGB subunits (Barczyk et al. 2010). In 80 addition to providing a physical transmembrane link between the extracellular 81 environment and the cytoskeleton, they are capable of transducing bi-82 directional signals across the cell membrane (Hynes 2002). Unlike the uterus, all five of the ITG markers of receptivity (ITGB1, ITGB3, ITGA1, ITGA4 and 83 84 ITGAV) are constitutively expressed throughout the menstrual cycle in the 85 Fallopian tube epithelium (Brown et al. 2012). We therefore hypothesized that 86 previous infection with *C. trachomatis* may predispose to tubal implantation by 87 increasing tubal integrin expression.

88

89 To address our hypothesis, we examined integrin transcript and protein 90 expression in the Fallopian tube of women with serological evidence of previous 91 infection with C. trachomatis. We then assessed integrin expression in 92 response to C. trachomatis infection in the oviducts of mice and in human 93 immortalized oviductal epithelial cells (OE-E6/E7). Finally, due to the lack of a 94 good in vivo animal model of tubal ectopic pregnancy (in animals the abdominal 95 cavity is the most frequent extra-uterine implanation site) (Brown and Horne 96 2011), we used an *in vitro* human trophoblast spheroid (embryo surrogate) -97 Fallopian tube epithelial cell co-culture model to investigate the effect of C. 98 trachomatis exposure and functional blockage of integrin on embryo 99 attachment.

100

101 Materials and Methods

102

103 *Patient samples*

104 Ethical approval for this study was obtained from the Lothian Research Ethics 105 Committee (LREC 04/S1103/20, 05/S1103/14, 07/S1103/29), with informed, 106 written consent obtained from all study participants. Serum samples and full 107 thickness cross-sections of human Fallopian tube ampulla (total n=26) were 108 collected from women undergoing hysterectomy for benign gynaecological 109 conditions. This group of women had a regular 21-35 day menstrual cycle, were 110 non-smokers, not using contraception and had no obvious evidence of FT 111 pathology on microscopic examination (as assessed by an expert 112 histopathologist). Fallopian tubes samples were saved either into RNAlater 113 (Applied Biosystems, Warrington, UK) for RNA extraction or into neutral-114 buffered formalin (NBF) for paraffin embedding. Previous C. trachomatis 115 infection was determined by an indirect enzyme-linked immunosorbent assay 116 to serum Pgp3 antibody (Wills et al. 2009) with a cut-off value for absorbance 117 at 450 nm of ≥0.473 giving ≥96% specificity (with an observed decline in 118 seropositivity occurring following the last episode of chlamydial infection). Of the 26 women, 8 had serological evidence of previous C. trachomatis infection 119 120 and 18 had no serological evidence of previous C. trachomatis infection.

121

122 Animal studies

123 The animal studies were approved by the Moredun Research Institute Ethics124 Committee and were conducted adhering to the institution's guidelines for

animal husbandry under licence from the UK Home Office. Eight week old
female C57/BL6 mice were infected with *C. trachomatis* (Figure 2a) following a
modified protocol published by Darville *et al* (Darville et al. 1997) and described
in more detail in Supplementary Information (*Animal Studies*).

129

130 Isolation of DNA from vaginal swabs and quantitative real-time PCR

DNA was extracted from vaginal swabs using a DNeasy® Blood and Tissue Kit (Qiagen, Cat No. 69504) according to the manufacturer's instructions. Evidence of infection with *C. trachomatis* was determined by TaqMan real-time PCR using the *C. trachomatis* specific primers and probes (see Supplementary Table 1) (Darville et al. 1997). DNA extraction and qRT-PCR methods are described in detail in Supplementary Information (*Isolation of DNA from vaginal swabs and quantitative real-time PCR*).

138

139 Quantitative reverse transcription PCR for integrin mRNA expression

TaqMan real-time PCR (qRT-PCR) was performed to quantify mRNA
expression levels of human and mouse integrins using specific primers (see
Supplementary Table 1) following the protocol described in Supplementary
Information (*Quantitative reverse transcription PCR for integrin mRNA*expression).

145

146 Immunohistochemistry

147 Immunohistochemistry for ITGB1 in human Fallopian tube samples and Itgb1
148 in mouse oviducts was carried out on NBF fixed paraffin wax embedded (FPE)
149 sections following our previously described protocol (Brown et al. 2012) and

detailed in Supplementary Information (*Immunohistochemistry*). The primary
antibodies used to detect ITGB1 (both for human as well as human samples)
were rabbit-anti-ITGB1 (Santa Cruz sc-8978, diluted 1:100) or isotype matched
control (Rabbit IgG Dako X0903, diluted 1:100).

154

155 Histoscore calculation

156 Sections of immunohistochemical staining for ITGB1 were evaluated using 157 semiguantitative histoscore analysis following previously described method 158 which considers both the intensity and the percentage of cells stained in each 159 of four intensity categories (McCarty et al. 1985). Intensities were classified as 160 0 (no staining), 1 (weak staining), 2 (strong staining) and 3 (very strong 161 staining). For each stained section, a histoscore was obtained by application of 162 the following algorithm: histoscore= $\Sigma(i+1) \times Pi$, where i and Pi represent 163 intensity and percentage of cells that stain at each intensity, respectively, and 164 corresponding histoscores were then calculated.

165

166 Quantitative dual-fluorescent western blot

Quantitative dual-fluorescent western blot was performed to quantify the ITGB1 and ITGB3 proteins in human Fallopian tube lysates following our previously established protocol (Brown et al. 2012) and detailed in Supplememntary Information (*Quantitative dual-fluorescent western blot*). Primary antibodies used to detect ITGB1 were rabbit-anti-ITGB1 (Santa Cruz sc-8978, dilution 0.5 µg/ml) and for ITGB3 were rabbit anti-ITGB3 (Santa Cruz sc-14009, dilution 0.5 µg/ml).

174 Oviductal epithelial OE-E6/E7 cell culture and C. trachomatis infection

175 Immortalised human oviductal epithelial OE-E6/E7 cells (sourced from KF Lee, 176 Hong Kong) were maintained in DMEM/F12 containing 10% fetal bovine serum 177 at 37°C, 5% CO₂. OE-E6/E7 cells were seeded at 5x10⁵ cells per well of a 12-178 well dish (BD Biosciences) and cultured for 24 hours. Cells were then washed 179 with PBS and incubated overnight with serum-free DMEM/F12. The OE-E6/E7 180 cells (triplicate wells) were exposed to live C. trachomatis (serovar E) at MOI 181 values of 0.1 and 1.0 in serum-free DMEM/F12. Control cells were cultured in 182 medium alone. After 24 hours, medium was removed and the cells were treated 183 with Qiagen RLT buffer and frozen at -80°C before RNA extraction.

184

185 Trophoblastic spheroid-oviduct epithelial-cell co-culture model

186 A previously established co-culture model using human immortalized Swan71 trophoblast cells (kind gift from V. Abrahams, Yale School of Medicine, CT) 187 188 (Gipson et al. 2008) and human immortalized OE-E6/E7 oviductal epithelial 189 cells. simulate trophoblast attachment, was designed to modified 190 (Kodithuwakku et al. 2012a, Kodithuwakku et al. 2012b). Human immortalized 191 were cultured in Dulbecco's Modified Essential Medium (DMEM, Invitrogen) 192 supplemented with 10% fetal bovine serum (FBS, Invitrogen), 2mM L-193 glutamine, penicillin/streptomycin (Invitrogen) and non-essential amino acids 194 (Sigma). Swan71 cells are derived from first trimester trophoblasts and are well 195 characterised (Straszewski-Chavez et al. 2009). Both cell lines were tested for 196 mycoplasma prior to use. Swan71 cells were seeded at 2000 cells per well in a 197 96 well non-adherent round bottom tissue culture plate to encourage spheroid

198 development. During this time, confluent 12-well plates of OE-E6/E7 cells were 199 washed and maintained in serum-free conditions. For *C. trachomatis* infection 200 experiments, OE-E6/E7 cells were exposed to C. trachomatis, as described in 201 the previous section. Triplicate wells were treated for 1 hour with 0.1 or 0.01 202 µg/ml mouse anti-ITGB1 (Clone P5D2: R&D Systems) or equivalent 203 concentration of isotype-matched control IgG₁ (Sigma) prior to careful transfer 204 of sixteen Swan71 spheroids onto the OE-E6/E7 monolayers and a further 6 205 hour incubation. Non-adherent spheroids were removed by gentle washing with 206 PBS before the cells were fixed for 10 minutes in NBF, washed and stored in 207 70% ethanol. Swan71 spheroids adherence was quantified using light 208 microscopy. Percentage adherence was derived by division of the number of 209 spheroids attached by total number of spheroids.

210

211 Statistical analysis

212 Statistical analysis was performed using GraphPad PRISM, version 6.1. To 213 allow for small sample sizes, non-parametric testing was applied to analysis of 214 human and animal studies. As endometrial integrins are upregulated at the 215 window of receptivity, data were interrogated to detect a significant increase in 216 integrin transcript and protein levels using the one-tailed Mann Whitney test. 217 For *in vitro* work, normality of data was tested using Shapiro-Wilk test and 218 Kruskal-Wallis or one-way ANOVA accordingly applied, with correction for 219 multiple comparisons by Dunn's or Dunnett's tests, respectively. Differences were considered significant if P<0.05. 220

- 221 Results
- 222

ITGB1 expression is increased in the Fallopian tube of non-pregnant women
 with evidence of previous C. trachomatis infection

225 We first investigated mRNA expression levels of ITGB1, ITGB3, ITGA1, ITGA4 226 and ITGAV in Fallopian tube from women with serological evidence of previous 227 C. trachomatis infection (non-pregnant and non-smokers). We found that 228 expression of ITGB1 mRNA was higher (P<0.05) in Fallopian tube from women 229 with evidence of previous C. trachomatis infection (n=8) compared to those 230 without (n=18) (Figure 1a). ITGB1 protein expression in Fallopian tube from 231 women with previous C. trachomatis infection (n=7) correlated with ITGB1 232 mRNA levels (R=0.442, P=0.026), but changes in protein expression alone, 233 compared to a control group (n=13), did not reach significance (Figure 1b). 234 Immunohistochemistry demonstrated abundant Fallopian tube epithelium 235 ITGB1 expression in women with previous C. trachomatis infection and mild 236 stromal staining (n=8; Figure 1d, 1g). In contrast, in women without previous C. 237 trachomatis infection (n=18), only sporadic cell staining was observed (Figure 238 1c, 1f). Semiguantitative histoscore analysis revealed a significant increase 239 (P<0.0001) in ITGB1 expression in Fallopian tube epithelial cells in women with 240 previous C. trachomatis infection as compared to women without previous C. 241 trachomatis infection (Figure 1h). Although ITGB3 mRNA expression was 242 increased (P<0.05) in women with previous C. trachomatis infection 243 (Supplementary Figure 1a), ITGB3 protein levels did not show any significant 244 changes (Supplementary Figure 1b) nor did they correlate with mRNA levels.

245 Tubal expression of ITGA1, ITGA4 and ITGAV were not affected by previous

246 *C. trachomatis* infection (Supplementary Figure 1c, 1d and 1e).

247

Oviductal Itgb1 expression is increased by C. trachomatis in a mouse model ofprevious infection

250 To investigate causality between C. trachomatis infection and increased ITGB1, 251 we developed an *in vivo* mouse model of previous C. trachomatis infection 252 (Figure 2a). Female C57BL/6 mice were infected intra-vaginally with C. 253 trachomatis and confirmed to have cleared the infection by day 30 post-254 infection by gRT-PCR detection of C. trachomatis genomic DNA (n=6) (Figure 255 2b). Mice infected with C. trachomatis displayed increased expression of 256 oviductal Itgb1 mRNA compared to sham-infected controls (n=6) on day 60 257 post-infection (P<0.05) (Figure 2c). Immunohistochemistry to Itgb1 revealed 258 strongly positive epithelial cells in the oviducts isolated from mice exposed to 259 C. trachomatis (Figure 2e, 2h), with limited staining in the sham-infected mice 260 (Figure 2d, 2g). Semiguantitative histoscore analysis revealed a significant 261 increase (P<0.05) in ITGB1 expression in oviductal epithelial cells in mice 262 exposed to C. trachomatis as compared to controls (Figure 1h). Exposure to 263 C. trachomatis did not cause any significant changes in Itgb3 mRNA expression 264 levels in murine oviducts (Supplementary Figure 2).

265

266 Exposure to C. trachomatis increases ITGB1 mRNA expression in human 267 immortalised oviductal epithelial cells

ITGB1 mRNA expression in human immortalised oviductal epithelial OE-E6/E7cells was significantly increased following 24 hours of exposure to 1.0

multiplicity of infection (MOI) *C. trachomatis* compared to control (P< 0.05)
(Figure 3a). Exposure to 0.1 MOI *C. trachomatis* did not have any significant
effect on ITGB1 mRNA expression.

273

274 C. trachomatis exposure increases trophoblast spheroid attachment to 275 oviductal epithelial cells by upregulating ITGB1

276 There are no good animal models of tubal ectopic pregnancy, so to simulate 277 embryo attachment we used an in vitro trophoblastic spheroid (embryo 278 surrogate) - Fallopian tube epithelial-cell co-culture model. We demonstrated 279 that 24 hours exposure of oviductal epithelial OE-E6/E7 cells to 1.0 MOI C. 280 trachomatis significantly increased trophoblast spheroid attachment 281 (P<0.0001) (Figure 3b). However, treatment of the C. trachomatis exposed OE-282 E6/E7 cells with 0.1 µg/ml ITGB1 neutralising antibody (dose selected following 283 optimisation, data not shown) for 1 hour prior to trophoblast spheroid 284 introduction, significantly reduced the numbers of spheroids that attached to 285 the OE-E6/E7 monolayer compared with C. trachomatis exposed OE-E6/E7 286 cells (P<0.0001) and isotype control (IgG) exposed OE-E6/E7 cells (P<0.0001). 287

288

289 Discussion

290

291 It is accepted that C. trachomatis infection in women predisposes to tubal 292 ectopic pregnancy; a relationship that continues for many years after the infection has resolved and that cannot be explained by macroscopic tissue 293 294 damage as a result of inflammation (Barczyk et al. 2010, J. L. Shaw et al. 2011). 295 In this study, we provide mechanistic evidence for changes in cell adhesion 296 molecule expression that may explain this epidemiological association. Using 297 ex vivo, animal in vivo and in vitro functional models, we demonstrate that 298 previous exposure to *C. trachomatis* infection increases oviductal epithelial cell 299 expression of the adhesion molecule ITGB1, predisposing to ectopic embryo 300 attachment.

301

302 Fallopian tube from women with serological evidence of previous exposure to 303 C. trachomatis expressed higher levels of ITGB1 mRNA, with abundant 304 immunolocalisation of protein to the Fallopian tube epithelium. This 305 upregulation of mRNA and localisation of protein was replicated in our in vivo 306 model of previous C. trachomatis infection and in immortalised oviductal 307 epithelial cells. Epithelium-specific expression is important in the context of 308 ectopic pregnancy, as it is to these cells the embryo will initially attach in vivo. 309 *In utero*, integrins are upregulated at the luminal surface of the endometrium 310 during the window of implantation (Lessey et al. 1992) and interact with 311 corresponding ligands on the blastocyst trophectoderm to enable attachment 312 (Burrows et al. 1993). Through the use of our in vitro model of Fallopian tube -

313 embryo attachment, we have for the first time been able to show the effect of 314 over-expression of ITGB1 on embryo attachment. This model allows 315 investigation of causality in ectopic pregnancy which is not possible by 316 examining human biopsies of tubal implantation sites where molecular changes 317 may be an artefact of implantation and/or presence of an embryo as opposed 318 to a predisposition for ectopic implantation. In addition, in the absence of a good 319 animal model of tubal ectopic pregnancy, we have utilised an alternative in vivo 320 model, where mice are exposed to C. trachomatis and allowed to clear the 321 infection, to study the effects of *C. trachomatis* on the oviduct. The natural 322 history of untreated (or treated) pelvic chlamydial infection in women cannot be 323 observed for ethical and logistical reasons, and randomized controlled trials do 324 not provide this information because the time from the start of the infection is 325 unknown. We propose that further study using this model could significantly 326 contribute to improvements in clinical management of this prevalent infection 327 (Akande et al. 2010, Howie et al. 2011).

328

329 We acknowledge that our results demonstrate that Fallopian tube ITGB1 330 increases in response to C. trachomatis infection but do not explain how, the 331 effect endures following elimination of the infection in the face of oviductal 332 epithelial cell turnover and regeneration. This effect is also seen in ocular 333 trachoma where scarring progresses in the absence of detectable C. 334 trachomatis infection, raising uncertainty about the primary drivers of late-stage 335 trachoma (Burton et al. 2015). Persistence (where the organism adopts a 336 dormant state in the epithelial cells) occurs in a minority of C. trachomatis 337 infections and may contribute to some cases of ectopic pregnancy (Bjartling et

al. 2007). In addition, Kessler *et al* have recently demonstrated the existence
of Fallopian tube stem cells, present along the Fallopian tube epithelial surface,
with the ability to differentiate into an organoid containing both ciliated and
secretory epithelial cell types in culture (Kessler et al. 2015). It would be
interesting to discover if bacterial alterations to the genome of these cells by *C*. *trachomatis*, resulting in persistent ITGB1 upregulation, may account for the
long-term increased risk of ectopic pregnancy.

345

346 We also acknowledge that further work is required to elaborate the full 347 mechanistic pathway of Fallopian tube ITGB1 regulation by C. trachomatis. 348 However, we propose that the utilization of host cell ITGB1 that we have 349 observed in oviductal epithelial cells as a result of C. trachomatis infection, may 350 be due to a shared bacterial virulence mechanism. C. trachomatis is an obligate 351 intracellular, Gram-negative bacterium. C. trachomatis switches between an 352 extracellular, metabolically inactive, infectious form, the elementary body (EB), 353 and an intracellular replicative form, the reticulate body. Stallman and 354 Hegemann have recently shown that C. trachomatis EBs produce the adhesin 355 and invasin molecule Ctad1 (Stallmann and Hegemann 2016). This specifically 356 binds ITGB1 on epithelial cells and induces clustering of ITGB1 at the epithelial 357 cell membrane to allow EB entry into the host cell. Another Gram-negative 358 bacterium, Shigella, upregulates expression of ITGB1 in epithelial cells ITGB1, 359 in this case to stabilize intestinal epithelial cell adhesion to the extracellular 360 matrix and prevent cellular detachment (Kim et al. 2009). Shigellae utilize the 361 type III secretion system (T3SS) to introduce the effector protein OspE into the 362 cell, and OspE interacts with the host-cells integrin-linked kinase ILK, which in

363 turn upregulates ITGB1 (Kim et al. 2009). C. trachomatis also makes use of the 364 type III secretion system; a 'membrane-embedded nanomachine' that delivers virulence proteins into a host cell via a hollow needle which then hijack host cell 365 366 machinery. Chemical inhibition of T3SS dramatically reduces C. trachomatis 367 virulence (Muschiol et al. 2006). It is therefore possible that C. trachomatis 368 shares a similar bacterial virulence mechanism and that small molecule 369 inhibitors to such bacterial virulence factors might provide an effective 370 preventative therapy for ectopic pregnancy in women previously infected with 371 C. trachomatis.

372

In summary, we have shown that *C. trachomatis* upregulates oviductal epithelial ITGB1 expression which predisposes to ectopic embryo attachment. This provides an explanation for the epidemiological association between *C. trachomatis* and reproductive life-time risk of ectopic pregnancy. The pathways and mechanisms leading to long-term over-expression of ITGB1 require further study but may be a consequence of bacterial effector proteins hijacking cellular pathways to promote virulence leading to more complex disease outcomes.

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382

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385

386

387 Conflicts of Interest

388

389 AWH has received consultancy payments from Roche, Ferring and Viramal for 390 work in the field of endometriosis. AWH receives grant funding from Wellbeing 391 of Women, the UK Medical Research Council (MRC), the UK National Institute 392 for Health Research, and Ferring. HODC has clinical research support for 393 laboratory consumables and staff from Bayer AG and provides consultancy 394 advice (but with no personal remuneration) for Bayer AG, PregLem SA, 395 Gedeon Richter, Vifor Pharma UK Ltd, AbbVie Inc, Myovant Sciences GmbH. 396 397 398 **Authors Contributions** 399 AWH and HODC designed the study. JKB, SFA, SMcF, MK, CO, GSW, MOM, 400 401 SG and NW performed the experimental work. AWH, JKB, SFA, and LLC 402 analysed the results and wrote the manuscript. NW, GE, PJH, KFL, HODC and 403 WCD contributed to experimental design and critical feedback on manuscript. 404

405

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407

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412	
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526 Figure Legends

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528 Figure 1: The effect of previous *C. trachomatis* infection on Fallopian tube 529 ITGB1 expression in women. (a) Box-and-whisker plots of relative levels of 530 ITGB1 mRNA expression (measured by qRT-PCR) in Fallopian tube biopsies 531 from non-pregnant, non-smoking women who tested negative (Ct-ve; n=18) or 532 positive (Ct+ve; n=8) for previous C. trachomatis infection. The boxes represent 533 mean values ±1 standard deviation and the whiskers denote the full range of 534 the data. (*P<0.05, one-tailed Mann Whitney test). (b) Box-and-whisker plots of 535 levels of ITGB1 protein (measured by western blot analysis) from the same 536 women (where there was sufficient sample). The boxes represent mean values 537 ±1 standard deviation and the whiskers denote the full range of the data. 538 (P=0.2, one-tailed Mann Whitney test). (c) and (d) Representative images of 539 immunohistochemical localization of ITGB1 in Fallopian tube tissue from Ct-ve 540 and Ct+ve women, respectively. Bar = 50µm. (f) and (g) Higher magnification 541 of c and d respectively. Bar = $20\mu m$. (e) Negative IgG control. Bar = $50\mu m$. (h) 542 Box and whicker plots of ITGB1 histoscore in Fallopian tube biopsies from 543 women with and without previous C. trachomatis infection. The boxes represent 544 mean values ±1 standard deviation and the whiskers denote the full range of 545 the data. (**** P<0.0001, one tailed Mann Whitney test).

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Figure 2: The effect of previous C. trachomatis infection on Itgb1 552 expression in the murine oviduct. (a) Schematic representation of C. 553 554 trachomatis infection in vivo mouse model (b) C. trachomatis genome copy number (as a marker of infection) in C57/BL6 mice infected with 10⁷ IFU of C. 555 556 trachomatis Serovar E (filled circles) or vehicle alone (dashed line, 557 indistinguishable from x-axis). (C) Box-and-whisker plots of relative levels of 558 Itgb1 mRNA expression (measured by gRT-PCR) on day 60 post-infection in 559 oviducts of control (Ct-ve; n=6) and infected (Ct+ve; n=6) mice. The boxes represent mean values ±1 standard deviation and the whiskers denote the full 560 range of the data. (*P<0.05, one-tailed Mann Whitney test). (d) and (e) 561 562 Representative images of immunohistochemical localization of ltgb1 in oviducts 563 of Ct-ve and Ct+ve mice respectively. Bar = 50 μ m. (g) and (h) Higher 564 magnification of c and d respectively. Bar = 20µm. (f) Negative IgG control. Bar =50µm. (i) Box and whicker plots of ltgb1 histoscore in oviducts of C. 565 566 trachomatis infected mice as compare to controls. The boxes represent mean 567 values ±1 standard deviation and the whiskers denote the full range of the data. (* P<0.05, one tailed Mann Whitney test). 568

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Figure 3: Effect of C. trachomatis infection on immortalised human Fallopian tube epithelial OE-E6/E7 cells and an in vitro model of human embryo attachment. (a) Box and whisker plots of relative levels of ITGB1 mRNA expression (measured by gRT-PCR) in Fallopian tube epithelial OE-E6/E7 cells following exposure to *C. trachomatis* for 24 hours (MOI = multiplicity of infection). The boxes represent mean values ±1 standard deviation and the whiskers denote the full range of the data. Data are the mean of six biological replicates. (*P<0.05, Kruskal-Wallis test with Dunn's multiple comparisons post-test). (b) Trophoblast spheroid-oviductal epithelial cell attachment following 24 hours exposure to C. trachomatis +/- 1 hour pre-treatment with 0.1µg/ml anti-ITGB1 antibody. The box-and-whisker plots illustrate percentage adherence (number of spheroids attached/total number of spheroids) of SW-71 trophoblast spheroids to oviductal epithelial OE-E6/E7 cells. The boxes represent mean values ±1 standard deviation and the whiskers denote the full range of the data. Data are the mean of four biological replicates. (**** P<0.0001, one-way Anova and Dunnett's multiple comparisons post-test).

Highlights

- Integrin subunit beta 1 is increased in Fallopian tubes of women and mice with evidence of past exposure to *C. trachomatis*.
- *C. trachomatis* increases integrin subunit beta 1 in oviductal epithelial cells and promotes trophoblast attachment.
- Functional blockage of integrin subunit beta 1 abrogates the attachment of trophoblast to oviductal epithelial cells.

Research in Context

We present exciting data, derived from a combination of ex-vivo, in-vivo and in-vitro models, to explain the mechanism behind the epidemiological association of past pelvic chlamydial infection and increased risk of tubal ectopic pregnancy. Our data demonstrate that past infection with *C. trachomatis* increases integrin subunit beta 1 expression in Fallopian tubes in women and in oviducts in mice. We also show that *C. trachomatis* promotes attachment in an embryo-surrogate co-culture tubal attachment model and that this effect is negated by functional blockage of the integrin subunit beta 1.



Figure 1.



Figure 2.



Figure 3.

1 Supplemental Information

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3 Animal studies

4 Mice received 2.5 mg of medroxyprogesterone acetate (Depo-Provera) subcutaneously for 4 days to increase susceptibility to infection. Thereafter, 10⁷ 5 inclusion-forming units (IFU) of C. trachomatis human serovar E suspended in 30ul of 6 vehicle (SPG: 250 mM sucrose, 10 mM sodium phosphate, 5 mM L-glutamic acid, pH 7 8 7.2), were introduced to the vaginal vault (n=6). Control animals (n=6) received vehicle alone. Mice were sacrificed 60 days from infection. With n=6 per group, we predicted 9 that we would be able to detect a standardised difference of \geq 1.85 with power of 90% 10 11 at 5% significance level. Animals were randomly allocated between treatment and control groups, no animals were excluded from analysis and there was no investigator 12 blinding. 13

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15 Isolation of DNA from vaginal swabs and quantitative real-time PCR

Vaginal swabs were rehydrated by vigorous vortexing in 200µl of PBS prior to the 16 addition of 200µl AL buffer. The samples were vortexed again before the addition of 17 20µl proteinase K solution (supplied with kit) and incubation for 10 minutes at 70°C. 18 200µl of 100% ethanol was added to each of the samples before the mixture was 19 added directly onto a DNeasy® column. For the remaining stages of the protocol, the 20 DNA was prepared on the column as described by the manufacturer and finally eluted 21 in a total volume of 200 µl elution buffer. Quantitative real-time PCR was carried out 22 using the primers and probe specific for Ch23S (Supplementary table 1) (Darville et 23 al. 1997). The PCR consisted of 12.5 µl 2X TaqMan® Universal master mix II 24

(Invitrogen, Warrington, United Kingdom), 900 nM of each primer, 250 nM fluorescent 25 probe and 1µl gDNA, made up to a final volume of 25 µl with sterile deionised water. 26 Amplification and detection were performed using an ABI Prism 7500 sequence 27 detection system (Invitrogen), following the manufacturer's standard protocols. 28 Thermal cycling conditions were: 50°C for 2 min, 95°C for 10 min, then 45 cycles of 29 95°C for 15 sec and 60°C for 1 min. Genome copy numbers were quantified against a 30 standard curve prepared from C. abortus genomic DNA as previously described 31 (Livingstone et al. 2009). Each sample, standard and non-template control was 32 33 examined in triplicate.

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35 Quantitative reverse transcription PCR for integrin mRNA expression

RNA was extracted and treated with DNase using a RNeasy fibrous tissue mini kit 36 (Qiagen). cDNA was synthesised from 200ng of RNA using SuperScript® VILO™ 37 cDNA Synthesis Kit (Invitrogen). TagMan real-time PCR (gRT-PCR) was used to 38 quantify levels of integrin, housekeeping (UBC and GAPDH, predetermined by 39 geNorm assay, Primerdesign Ltd) and loading control (18s) transcripts. Specific 40 primers (Supplementary Table 1) were designed using the Universal Probe Library 41 42 Assay Design Center (www.roche-applied-science.com) and used in conjunction with Universal Probe Library (UPL) FAM labelled probes (Roche Applied Science, Burgess 43 Hill, UK) or purchased as validated primer-probe sets (Perfect-Probe: Primer Design, 44 UK). Reactions were performed in triplicate, using 18s to control for loading variation 45 (FAM labelled probe), under standard conditions in an ABI Prism 7900 (Invitrogen). 46 47 18s-integrin Δ Ct values obtained were normalised against mean values of 18s-UBC and 18s-GAPDH ΔCt, prior to normalisation against a cDNA positive control (Fallopian 48 tube from a post-menopausal patient). For mouse samples, integrin gene expression 49

was normalized to GAPDH expression, using the 2-ΔΔCt method, and then normalised
 against pooled Fallopian tube cDNA from the control group.

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53 *Immunohistochemistry*

5µm sections of paraffin embedded tissue (Human Falloipan tube and mouse 54 oviducts) were mounted onto microscope slides, dewaxed and rehydrated, before 55 antigen retrieval in 10mM Tris 1mM EDTA pH 9 with 5 min of pressure-cooking. Slides 56 were washed, incubated with 3% hydrogen peroxide for 30 min, then blocked in normal 57 horse serum diluted 1:12 in TBS-T20 for 30 min. Slides were incubated with primary 58 59 antibody overnight at 4°C (anti-ITGB1 Santa Cruz sc-8978, diluted 1:100) or isotype matched control (Rabbit IgG Dako X0903, diluted 1:100). They were washed in TBS-60 T20 before incubation with species specific impress kit for 30 min at room temperature 61 (Vector Laboratories, Peterborough, UK). After washing and incubation with 3, 3'-62 diaminobenzidine for 5 min, slides were counterstained with hematoxylin, dehydrated 63 and visualized by light microscopy, using an Olympus Provis microscope equipped 64 with a Kodak DCS330 camera (Olympus Optical Co., London, UK, and Kodak Ltd., 65 Herts, UK). 66

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68 Quantitative dual-fluorescent western blot

50mg wet tissue per sample of Fallopian tube was stabilized in RNALater and was
homogenized in 1ml pH 8.0 lysis buffer (50mM Tris-HCI; 150mM NaCI; 1mM EDTA;
1% Triton-X100, 1% Na-deoxycholate; EDTA-free complete mini protease inhibitors
(Roche Diagnostics, Welwyn Garden City, UK); and Halt Phosphatase Inhibitor
Cocktail (Thermo Fisher Scientific, Loughborough, UK)) using a TissueLyser bead mill

74 (Qiagen). Protein guantification was performed by Bradford Assay, adapted for the Cobas Fara centrifugal analyzer (Roche Diagnostics), and samples adjusted to 75 2mg/ml total protein in lysis buffer, before further 1:1 dilution in 2x NuPAGE LDS 76 sample buffer (Invitrogen) containing 100mM DTT (Sigma). Gel electrophoresis 77 (1DGE) was performed in 15-well NuPAGE 4-12% Bis-Tris gels (Invitrogen) using 20 78 µg of total protein/lane alongside SeeBlue® Plus2 pre-stained molecular weight 79 standards (Invitrogen). A positive control (Fallopian tube from a post-menopausal 80 patient) was included in every gel to allow intra-blot comparisons to be made. Gels 81 82 were equilibrated for 15 minutes in transfer buffer (50 mM Tris, 40 mM Glycine, 0.05% SDS), before blotting at 20V (limited to 80 mA/gel) onto polyvinylidene fluoride 83 membrane (Immobilon P: Millipore, Livingston, UK) in the presence of transfer buffer 84 + 10% methanol using a Transblot SD (Bio-Rad Laboratories, Hemel Hempstead, UK). 85 Blots were then blocked for 30 minutes in TBS-T20 (TRIS-buffered saline containing 86 0.5% Tween20, pH 7.4) + 2% Marvel (Premier Foods, St Albans, UK) and incubated 87 for 2 hours with combinations of 0.5 µg/ml rabbit anti-ITGB1 (Santa Cruz sc-8978) or 88 rabbit anti-ITGB3 (Santa Cruz sc-14009) together with 0.5 µg/ml mouse anti-GAPDH 89 and anti- β actin and/or negative control antibodies (Abcam) diluted in TBS-T20 + 2% 90 Marvel. Blots were then washed in TBS-T20 (6 x 3 minutes) and incubated for 1 hour 91 with ImmPRESS anti-rabbit Ig peroxidase Polymer Detection Kit (Vector Laboratories, 92 93 Peterborough, UK) (diluted 1/250) and 0.5 µg/ml of goat anti-Mouse DyLight-488 in TBS-T20 + 2% Marvel. Blots were then washed (6 x 3 minutes) in TBS-T20 and 94 DyLight-488 and Cy5 labelling imaged using a FLA-5100 (FUJIFILM Europe GmbH, 95 Düsseldorf, Germany). Protein band intensities were measured using ImageJ software 96 (Schneider et al. 2012). After normalizing against the mean value of GAPDH and β -97 actin, values for integrin-specific labelling were expressed relative to the positive 98

- 99 control. After imaging, blots were stained with Imperial Protein Stain (Fisher Scientific
- 100 UK, Loughborough, UK) to confirm uniform blotting efficiency.

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Supplementary Figure Legends

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105 Supplementary Figure 1: The effect of *C. trachomatis* infection on Fallopian tube expression of integrin endometrial receptivity markers in women. Box-and-whisker 106 plots illustrating relative levels of integrin mRNA expression (measured by qRT-PCR) 107 and protein levels (measured by western blot analysis) in Fallopian tube biopsies from 108 non-pregnant, non-smoking women who tested negative (Ct-ve; n=18) or positive 109 (Ct+ve; n=8) for previous C. trachomatis infection. (a) mRNA expression levels of 110 111 ITGB3. (b) protein levels (where sample sufficient) of ITGB3. (c) (d) and (e) mRNA expression levels of ITGA1, ITGA4 and ITGAV, respectively. The boxes represent 112 mean values ±1 standard deviation and the whiskers denote the full range of the data. 113 *P<0.05 (one-tailed Mann Whitney test). 114

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Supplementary Figure 2: The effect of previous C. trachomatis infection on Itgb3 116 mRNA levels in the murine oviduct. C57/BL6 mice were infected with 10⁷ IFU of C. 117 trachomatis Serovar E or vehicle alone, and levels of C. trachomatis genomic DNA 118 monitored until not detectable (day 30). Oviducts were then collected for integrin 119 expression analysis. Box-and-whisker plots of show relative Itgb3 mRNA levels on day 120 60 post-infection in oviducts of control (Ct -ve; n=6) and infected (Ct +ve; n=6) mice. 121 The boxes represent mean values ±1 standard deviation and the whiskers denote the 122 full range of the data. (P=0.1526, one-tailed Mann Whitney test). 123

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127 **Supplementary Table 1**. qRT-PCR primer and probe sequences

128	Ch23S forward	5'-CTGAAACCAGTAGCTTATAAGCGGT-3'
129	Ch23S reverse	5'-ACCTCGCCGTTTAACTTAACTCC-3'
130	Ch23S probe (FAM)	CTCATCATGCAAAAGGCACGCCG-TAMRA
131		
132	Human ITGA1 forward	5'-AATTGGCTCTAGTCACCATTGTT-'3
133	Human ITGA1 reverse	5'-CAAATGAAGCTGCTGACTGGT-'3
134	Human ITGA1 UPL probe (FAM) 14
135	Human ITGA4 forward	5'-GGAATATCCAGTTTTTACACAAAGG-'3
136	Human ITGA4 reverse	5'-AGAGAGCCAGTCCAGTAAGATGA-'3
137	Human ITGA4 UPL probe (FAM) 57
138	Human ITGAV forward	5'-GCCGTGGATTTCTTCGTG-'3
139	Human ITGAV reverse	5'-GAGGACCTGCCCTCCTTC-'3
140	Human ITGAV UPL probe (FAM	l) 64
141	Human ITGB1 forward	5'-CGATGCCATCATGCAAGT-'3
142	Human ITGB1 reverse	5'-ACACCAGCAGCCGTGTAAC-'3
143	Human ITGB1 UPL probe (FAM) 65
144	Human ITGB3 forward	5'-GGGCAGTGTCATGTTGGTAG-'3
145	Human ITGB3 reverse	5'-CAGCCCCAAAGAGGGATAAT-'3
146	Human ITGB3 UPL probe (FAM) 13
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148	Mouse ITGB1 forward	5'- CTGCTTCTAAAATTGAGATCAGGA-'3
149	Mouse ITGB1 reverse 5'-	TCCATAAGGTAGTAGAGATCAATAGGG-'3
150	Mouse ITGB1 UPL probe (FAM)) 41
151	Mouse ITGB3 forward	5'- GTGGGAGGGCAGTCCTCTA-'3
152	Mouse ITGB3 reverse	5'- CAGGATATCAGGACCCTTGG-'3
153	Mouse ITGB3 UPL probe (FAM)) 31
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155	Human 18S (VIC)	Applied Biosystems (4308329)
156	Human GAPDH (FAM)	Primer Design (HK-PP-hu-600)
157	Human UBC (FAM)	Primer Design (HK-PP-hu-600)
158		
159	Mouse GAPDH (VIC)	Applied Biosystems (4352339E)

160 Supplementary References

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Ct –ve (n=18)

Ct +ve (n=8)

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Supplementary figure 1.



Supplementary figure 2.

