

LONDON  
SCHOOL of  
HYGIENE  
& TROPICAL  
MEDICINE



Roberts, CH; Molina, S; Makalo, P; Joof, H; Harding-Esch, EM; Burr, SE; Mabey, DC; Bailey, RL; Burton, MJ; Holland, MJ (2014) Conjunctival Scarring in Trachoma Is Associated with the HLA-C Ligand of KIR and Is Exacerbated by Heterozygosity at KIR2DL2/KIR2DL3. PLoS neglected tropical diseases, 8 (3). e2744. ISSN 1935-2727 DOI: <https://doi.org/10.1371/journal.pntd.0002744>

Downloaded from: <http://researchonline.lshtm.ac.uk/1621387/>

DOI: [10.1371/journal.pntd.0002744](https://doi.org/10.1371/journal.pntd.0002744)

#### Usage Guidelines

Please refer to usage guidelines at <http://researchonline.lshtm.ac.uk/policies.html> or alternatively contact [researchonline@lshtm.ac.uk](mailto:researchonline@lshtm.ac.uk).

Available under license: <http://creativecommons.org/licenses/by/2.5/>

# Conjunctival Scarring in Trachoma Is Associated with the HLA-C Ligand of KIR and Is Exacerbated by Heterozygosity at KIR2DL2/KIR2DL3

Chrissy h. Roberts<sup>1\*</sup>, Sandra Molina<sup>1</sup>, Pateh Makalo<sup>2</sup>, Hassan Joof<sup>2</sup>, Emma M. Harding-Esch<sup>1</sup>, Sarah E. Burr<sup>1,2</sup>, David C. W. Mabey<sup>1</sup>, Robin L. Bailey<sup>1</sup>, Matthew J. Burton<sup>3</sup>, Martin J. Holland<sup>1,2</sup>

**1** Clinical Research Department, London School of Hygiene and Tropical Medicine, London, United Kingdom, **2** Medical Research Council Unit, The Gambia, Atlantic Boulevard, Fajara, The Gambia, **3** International Centre for Eye Health, London School of Hygiene and Tropical Medicine, London, United Kingdom

## Abstract

**Background:** *Chlamydia trachomatis* is globally the predominant infectious cause of blindness and one of the most common bacterial causes of sexually transmitted infection. Infections of the conjunctiva cause the blinding disease trachoma, an immuno-pathological disease that is characterised by chronic conjunctival inflammation and fibrosis. The polymorphic Killer-cell Immunoglobulin-like Receptors (KIR) are found on Natural Killer cells and have co-evolved with the Human Leucocyte Antigen (HLA) class I system. Certain genetic constellations of KIR and HLA class I polymorphisms are associated with a number of diseases in which modulation of the innate responses to viral and intracellular bacterial pathogens is central.

**Methodology:** A sample of 134 Gambian pedigrees selected to contain at least one individual with conjunctival scarring in the F<sub>1</sub> generation was used. Individuals (n=830) were genotyped for HLA class I and KIR gene families. Family Based Association Tests and Case Pseudo-control tests were used to extend tests for transmission disequilibrium to take full advantage of the family design, genetic model and phenotype.

**Principle findings:** We found that the odds of trachomatous scarring increased with the number of genome copies of HLA-C2 (C1/C2 OR = 2.29<sub>BH</sub> P-value = 0.006; C2/C2 OR = 3.97<sub>BH</sub> P-value = 0.0004) and further increased when both *KIR2DL2* and *KIR2DL3* (C2/C2 OR = 5.95<sub>BH</sub> P-value = 0.006) were present.

**Conclusions:** To explain the observations in the context of chlamydial infection and trachoma we propose a two-stage model of response and disease that balances the cytolytic response of KIR expressing NK cells with the ability to secrete interferon gamma, a combination that may cause pathology. The data presented indicate that HLA-C genotypes are important determinants of conjunctival scarring in trachoma and that *KIR2DL2/KIR2DL3* heterozygosity further increases risk of conjunctival scarring in individuals carrying HLA-C2.

**Citation:** Roberts Ch, Molina S, Makalo P, Joof H, Harding-Esch EM, et al. (2014) Conjunctival Scarring in Trachoma Is Associated with the HLA-C Ligand of KIR and Is Exacerbated by Heterozygosity at KIR2DL2/KIR2DL3. *PLoS Negl Trop Dis* 8(3): e2744. doi:10.1371/journal.pntd.0002744

**Editor:** Fasil Tekola Ayele, National Institutes of Health, United States of America

**Received:** October 7, 2013; **Accepted:** January 30, 2014; **Published:** March 20, 2014

**Copyright:** © 2014 Roberts et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Funding:** This study was funded by grants from the Wellcome Trust (079246/Z/06/Z and GR079246MA). The funders had no part in the study design; in the collection, analysis, and interpretation of data; in the writing of the report; and in the decision to submit the paper for publication.

**Competing Interests:** The authors have declared that no competing interests exist.

\* E-mail: chrissy.roberts@lshtm.ac.uk

## Introduction

*Chlamydia trachomatis* (*Ct*) is an obligate intracellular bacterium [1] which causes significant morbidity as the causative factor of around 106 million new sexually transmitted infections per annum [2]. As the cause of trachoma, the same bacterium is the most common infectious cause of blindness [3]. *Ct* serovars exhibit highly specific tissue tropism, with serovars A–C being limited to the mucosal epithelium of the ocular conjunctiva. The remaining serovars are sexually transmitted, but whilst serovars D–K are limited to the mucosal epithelia of the genitourinary tract and rectum, the strains L1–L3 are able to invade other tissues including the lymph nodes. Ocular infection in trachoma is spread among young persons through exposure to secretions from

the infected eye via direct physical contact, on fomites or by eye-seeking flies [4]. Repeated and prolonged cycles of infection and inflammation have been identified as the main factors that lead to the progressive formation of fibrotic scars on the tarsal conjunctiva, which ultimately becomes deformed. This can cause entropion and trachomatous trichiasis (TT), a condition where the eyelashes turn inwards and irreversibly damage the cornea by scratching the globe of the eye. If left unchecked, TT causes corneal opacity, visual impairment and blindness.

Active trachoma is frequently found in the absence of detectable *Ct* infection and both tissue damage and scarring are thought to be the result of a chronic immuno-pathological reaction [5]. Human conjunctival transcriptome studies in trachoma suggest that in addition to T cell and innate responses of epithelial cells, the

## Author Summary

*Chlamydia trachomatis* is a pathogen that causes sexually transmitted infections (STIs) and the blinding disease trachoma. Natural Killer (NK) cells are part of the host immune system's first line of defence against infection. NK cell functions are genetically encoded and differences between individuals mean that some people are better able to respond to infections than others. We found that in certain combinations, specific variants of the gene *HLA-C* (Human Leucocyte Antigen, C) and of a complex set of genes called the Killer-cell Immunoglobulin-like Receptors (KIR) were associated with a six-fold increase in the relative risk of scarring tissue damage resulting from ocular *C. trachomatis* infection (trachoma). This combination of genetic variants may reduce the host's ability to effectively resolve infections and result in a harmful immune response that ultimately leads to tissue damage and scarring. KIR<sup>+</sup> NK cells are potential cellular mediators of the damaging immune response. Previous studies have identified that the same HLA-KIR genetic constellation that associates with trachoma is actually protective against infectious diseases such as malaria and tuberculosis. The high frequency of the trachoma-associated constellation in African populations may therefore be explained by the evolutionary benefits of protection from the complications of severe disease.

activation and cytotoxic responses of natural killer (NK) cells is an important determinant of the severity of active trachoma [6,7]. NK cells are a rich source of multiple chemokines and cytokines, including interferon gamma (IFN $\gamma$ ), a cytokine that is central to the control of chlamydial intracellular development and growth. IFN $\gamma$  also has anti-fibrotic properties that can counteract the effects of TGF- $\beta$  and inhibit fibroblast proliferation and collagen synthesis [8], but when inappropriately expressed may cause immunopathology. NK cells in mucosal-associated lymphoid tissues are known to be important in the maintenance of epithelial cell integrity via production of the cytokine IL-22 [9]. NK cells therefore have the potential to fulfil multiple roles that encompass tissue homeostasis, tissue re-modelling and immunity.

Early studies in murine chlamydial model infections found that NK cell depletion exacerbated disease, delayed clearance and limited the development of specific T cell responses [10,11]. Subsequent studies have confirmed that in response to chlamydial stimulation, NK cells are promoters of T cell immunity and a major source of IFN $\gamma$  [10,12] but their role as lytic effector cells is less clear. Although *Ct* infected cell lines are lysed *in vitro*, NK cells purified from the peripheral blood of individuals with current chlamydial infection had diminished lytic activity (and reduced IFN $\gamma$ ) compared with uninfected controls [13]. Population diversity in the highly polymorphic genes that encode the variable NK receptors and their ligands [14] along with functional heterogeneity in the NK cell repertoire may account for these findings [15].

Trachoma is a complex inflammatory fibrotic disease in which host polymorphism in immune response genes plays a significant role [16–18]. The conjunctival epithelial surface is compromised in trachoma [5] as a result of the host response to the causative bacterium, which occupies an intracellular niche. Therefore the mechanisms used by NK cells in the control of other intracellular infections such as Hepatitis B [19], Hepatitis C [20] and HIV [21–23] might also be effective against intracellular *Ct*.

NK cells become activated when they are released from inhibition that is normally bound by interaction of specific HLA

class I ligands with inhibitory Killer-cell Immunoglobulin-like Receptors (KIRs) [24]. The ligands of several inhibitory KIR have been described including HLA-A3 and HLA-A11 alleles, which are ligands of the KIR3DL2 receptor [25,26] and the HLA-Bw4 public epitope which is the ligand of KIR3DL1 [27,28]. *HLA-C* alleles can be classified (according to a functional dimorphism at amino acid position 80) as carrying one of two KIR binding epitopes, which are known as HLA-C1 and HLA-C2 [29]. The HLA-C2 group of alleles (*HLA-C\*02/04/05/06...*) are ligands of the inhibitory receptor KIR2DL1 [30–32] and its activating counterpart KIR2DS1 [33]. The HLA-C1 group alleles (*HLA-Cw\*01/03/07/08...*) are ligands of both KIR2DL2 and KIR2DL3 [30–32], however, the latter KIR are both able to cross-react (with differing avidities) with a small number of HLA-C2 and HLA-B allotypes [34]. Although germ-line encoded, the KIR gene system is highly polymorphic and exhibits extensive diversity both between individuals and between populations [35–38]. KIRs exhibit haplotype diversity such that different individuals possess variable gene contents. Since KIR and HLA are also found on different chromosomes, individuals can possess a KIR for which they have no cognate ligand, or vice versa. The extensive polymorphism in the KIR system culminates in a repertoire of NK cells within an individual that is more or less sensitive to release from inhibition under appropriate physiological conditions [39]. The strength of the signals mediated by interactions between specific HLA and KIR alleles is also highly variable [29,40,41] and this further limits overall NK cell responsiveness [42]. In part the responsiveness might be predicted by the presence of type 'A' and type 'B' KIR haplotypes. Type A haplotypes carry genes encoding predominantly inhibitory KIRs. B haplotypes contain some or all of the same genes found on A haplotypes, but additionally may carry the inhibitory *KIR2DL2* and *KIR2DL5* genes and numerous activating KIRs [36]. KIR haplotypes can be separated into two variable regions, defined by their orientation towards the centromeric (Cen) or telomeric (Tel) regions of the chromosome [43]. The KIR A and B haplotypes are present in all populations studied to date and are thought to be maintained by the balancing selection pressures of infection, immunopathology and healthy reproduction [44–47]. In recent human history, a wide range of infectious diseases may have reduced the balancing effects in African populations, leading to more directional selection and a unique pattern of HLA and KIR diversity in this region [38,47]. We therefore assessed the extent to which host genotypes at the HLA and KIR loci were associated with trachomatous scarring in a trachoma endemic population from The Gambia.

## Methods

### Ethics statement

The study was conducted in accordance with the tenets of the Declaration of Helsinki. The Ethics Committee of the Gambian Government/Medical Research Council Unit, and the ethics committee of the London School of Hygiene and Tropical Medicine approved the study (MRC SCC1177). Individual written informed consent was obtained from all adult participants. Written informed consent was obtained from a parent/guardian on behalf of those subjects aged <18 years who wished to take part in the study. All samples were anonymised.

### Study population, sampling and ascertainment

We selected a family study design and identified probands at a relatively early age for clinical signs of conjunctival scarring. This maximised statistical power whilst controlling for population stratification through the use of related control samples. The

**Table 1.** Clinical and Demographic features of the sample.

Group	Age in years (Median [min - max])	Scarring (C) Grade (n [%])				No FPC Grading
		C0	C1	C2	C3	
<b>F<sub>1</sub> Generation</b>						
Total (n = 570)	08 [0.1–40]	386 (67.8)	48 (8.4)	112 (19.6)	20 (3.5)	4 (0.7)
Male (n = 296)	08 [0.1–28]	188 (63.6)	25 (8.4)	71 (24.0)	12 (4.0)	0 (0.0)
Female (n = 274)	08 [0.1–40]	198 (72.2)	23 (8.4)	41 (15.0)	8 (2.9)	4 (1.5)
Proband (n = 134)	05 [0.3–22]	12 (9.0)	12 (9.0)	93 (69.4)	16 (11.9)	1 (0.7)
Siblings (n = 436)	10 [0.1–40]	374 (85.7)	36 (8.3)	19 (4.4)	4 (0.9)	3 (0.7)
<b>P<sub>0</sub> Generation</b>						
Total (n = 260)	39 [18–72]	121 (46.6)	65 (25.0)	69 (26.5)	4 (1.5)	1 (0.4)
Female (n = 132)	34 [18–65]	77 (58.2)	22 (16.7)	31 (23.5)	1 (0.8)	1 (0.8)
Male (n = 128)	45 [23–72]	44 (34.5)	43 (33.6)	38 (29.7)	3 (2.3)	0 (0.0)
<b>Families</b>	Minimum	1 <sup>st</sup> Quantile	Median	3 <sup>rd</sup> Quantile	Maximum	
Number persons F <sub>1</sub>	1	3	4	5	11	

doi:10.1371/journal.pntd.0002744.t001

study population came from multiple regions of The Gambia and included multiplex families of mixed ethnic background. Families were ascertained through the identification of probands in which there were signs of trachomatous scarring at an early age (age  $\leq 30$  years). This approach maximised the extent to which genetic rather than environmental factors could be expected to have contributed significantly to the probands' phenotypes. We recruited first-degree relations of the probands. In most cases this meant that we sampled both biological parents of the probands and all their (self-described) full siblings. Samples for DNA analysis were collected from buccal mucosae using sterile cyto-brushes (Part Number F-440151, SLS, Nottingham, UK). After collection, brushes were returned to their original packaging and stored dry at room temperature for up to 6 months [48] before DNA extraction was performed using a salting out procedure.

### Sample size and power calculation

An average of 4 offspring per family was assumed with a population prevalence of scarring in those  $< 30$  years of age in The Gambia of  $\sim 2\%$  [49]. The Pedigree Based Association Test (PBAT) v3.6 program [50] was used to calculate the power of the study to detect with 95% confidence ( $\alpha < 0.05$ ) a genetic association with odds ratios 1.5, 2 and 3 when the hypothetical disease allele had a frequency between 0.01 and 0.50. Figure S1 shows the estimated power of this study to detect genetic associations with trachomatous scarring at a range of allele frequencies and effect magnitudes, given the sample size. We had  $> 90\%$  power to detect an effect size greater than an odds ratio (OR) = 3 when the allele frequency was  $\geq 0.05$  and similar power to detect an effect size of OR = 2 when the allele frequency was  $\geq 0.19$ .

### Trachoma phenotypes

Trachoma was graded in the field using the WHO simplified grading system by field supervisors certified for trachoma grading with regular performance checks as described by the PRET clinical trial manual of operations [51]. Left and right tarsal conjunctivae of all subjects were photographed as described by Derrick *et al.* [52]. Photographs were subsequently reviewed by two ophthalmologists with experience of grading trachoma and a final grade agreed. Subjects were assigned to the 'scarred' group if there were any signs of

trachomatous scarring, in either eye. Individuals where phenotypes could not be confirmed for reasons of poor quality photography (n = 5) did not contribute to the statistical tests of association.

### Genotyping and pedigree tests for Mendelian inheritance

KIR genotyping for the presence or absence of 17 KIR genes was performed by PCR using the set of sequence specific primers described by Vilches *et al.* [53]. The genotyping method was validated by participation in the UCLA Immunogenetics Center KIR exchange programme (<http://www.hla.ucla.edu/cellDna.htm>). Medium resolution *HLA-A*, *-B* and *-C* genotyping was performed using LABtype sequence specific oligonucleotide probes (OneLambda, Canoga Park, CA, USA) on a Luminex platform (Luminexcorp, Austin, TX, USA). Medium resolution HLA typing data generates strings of possible allele combinations. Information from the HLA genotypes of family members was used to reduce the length of the strings of possible allele pairs and to eliminate alleles that were not compatible with Mendelian inheritance within a given pedigree. Strings were further shortened where possible to include only common and well-defined alleles [54]. In order to maximise statistical power, highly sequence similar HLA alleles were combined in to groups (table S1) before FBAT. KIR ligands of HLA (*HLA-A\*03/11/Bw4*, *HLA-B-Bw4*, *HLA-C1/C2*) were inferred from the full HLA genotypes of individual specimens rather than the reduced strings. The *HLA-C\*16:01* (HLA-C1) and *HLA-C\*16:02* (HLA-C2) alleles were frequently ambiguous and where this was the case alleles were assigned to *HLA-C\*16:01* because the *HLA-C\*16:02* allele has not been observed in other West African populations whilst *HLA-C\*16:01* is very common (data from allelefrequencies.net). HLA types were used to identify cases of parental mis-assignment and inconsistent parent-offspring genotypes. KIR phenotypes (presence/absence) were tested for Mendelian inconsistencies. *KIR2DL5*, *KIR2DS3* and *KIR2DS5* were not included in the association tests as they can segregate to both Cen-B and Tel-B regions and confound haplotype assignments.

### Statistical analysis

KIR gene frequencies were compared to those of other world populations using data from allelefrequencies.net and PCA using

**Table 2.** HLA Class I allele frequencies and FBAT tests of association.

Locus	Allele Name*	Allele frequency (P <sub>0</sub> )	# informative families (n)	S-E(S)	Var(S)	Z	P	Corrected P
HLA-A	A*02:01	0.067	37	-4.66	10.767	-1.42	0.155552	1
	A*23:01	0.164	67	-0.56	24.675	-0.113	0.910241	1
	A*26:01	0.063	32	-2.74	8.366	-0.947	0.343476	1
	A*30:02	0.065	28	-0.54	8.752	-0.183	0.855165	1
	A*33:01	0.138	62	2.557	18.996	0.587	0.557473	1
	A*68:01	0.05	21	2.95	7.209	1.099	0.27191	1
	A*68:02	0.052	27	3.18	8.352	1.1	0.271184	1
HLA-B	B*07:02	0.067	33	2.66	10.335	0.827	0.407994	1
	B*08:01	0.069	41	-12.18	11.786	-3.548	0.000388	0.01
	B*35:01	0.133	51	6.77	17.467	1.62	0.105266	1
	B*15:03	0.071	35	-0.14	12.033	-0.04	0.967807	1
	B*53:01	0.123	48	9.62	16.341	2.38	0.017324	0.49
	B*58:01	0.075	40	2.28	12.467	0.646	0.518451	1
	B*78:01	0.056	29	-0.53	8.268	-0.184	0.853761	1
HLA-C	C*02:02	0.114	53	-0.29	16.851	-0.071	0.943679	1
	C*03:04	0.083	45	-11.888	13.791	-3.201	0.001369	0.04
	C*04:01	0.186	66	11.629	23.828	2.382	0.017205	0.49
	C*06:02	0.089	33	5.52	10.042	1.742	0.081515	1
	C*07:01	0.114	55	-2.403	17.979	-0.567	0.570849	1
	C*16:01/02	0.12	52	-7	14.981	-1.809	0.070526	1
	C*17:01	0.054	27	2.834	7.569	1.03	0.302871	1
HLA-A3/11	No KIR epitope	0.772	81	-2.41	31.893	-0.427	0.669564	1
	Bw4_80I	0.183	69	-0.06	26.511	-0.012	0.990703	1
HLA-Bw4/Bw6	Bw6	0.625	108	-3.907	42.358	-0.6	0.548333	1
	Bw4_80I	0.318	101	3.867	41.641	0.599	0.549034	1
	Bw4_80T	0.056	28	0.04	10.116	0.013	0.989966	1
HLA-C1C2	C2	0.499	99	23.08	40.6	3.622	0.000292	0.008

\*Named alleles may indicate the first allele identifier in a longer string of related alleles, but these have been shortened for ease of reading. Full details can be found in table S1.

doi:10.1371/journal.pntd.0002744.t002

R. Family based tests of HLA association were carried out using FBAT v.2.0.3 [55] performing a series of bi-allelic tests (i.e. association of an index allele against all other alleles) under an additive genetic model and the null hypothesis of no linkage and no association of any factor of the HLA system with trachomatous scarring. This approach is robust to effects of population structure [55,56] and is applicable to a data set with samples originating in mixed ethnic backgrounds. We tested for associations between scarring and all HLA alleles with a sample frequency greater than 0.05 with an offset value of 0.02 (population prevalence of scarring in persons  $\leq 30$  years of age) to allow the unaffected siblings to contribute to the test statistic. All FBAT p-values were adjusted using a conservative Bonferroni correction. Significant associations were tested again using a case/pseudo-control conditional logistic regression (CLR) [57], which generated estimates of odds ratios and associated p-values. To test for independence between the disease-associated alleles, we included all alleles that had a corrected  $p < 0.05$  in a multivariate CLR model. To establish whether significant HLA associations were restricted to F<sub>1</sub> subjects with specific KIR genotypes we tested the full data set under a genotype model [58,59], using CLR, in different subsets of the F<sub>1</sub>

data where the population was limited by the KIR genotype. Because of the high linkage disequilibrium between factors of the KIR system, these tests were not considered to be independent and test statistics were corrected using the Benjamini-Hochberg method.

## Results

### Sample population

We sampled 830 individuals from 134 pedigrees and 146 nuclear families in which scarring trachoma had been identified in the first filial (F<sub>1</sub>) generation. The self-described ethnic background of the parental (P<sub>0</sub>) population (n = 260) was approximately 40% Mandinka, 23% Fula, 15% Jola, 15% Wolof, 5% Bambara and 2% other minority ethnic groups. There were 570 persons in the F<sub>1</sub> generation, where the gender distribution was 52% (n = 296) male and 48% (n = 274) female. The median number of offspring per pedigree was 4 (range 1–11). Eight families had one missing parent. There were 180 (~32%) cases of trachomatous scarring in the F<sub>1</sub> generation and of these, 72 (40%) were female and 108 (60%) were male. Three hundred and eighty six (~67.8%) F<sub>1</sub>

	A/B Genotype	CEN genotype	TEL Genotype	3DL3	2DS2	2DL2	2DL3	2DL5	2DS3	2DS5	2DP1	2DL1	3DP1	3DP1V	2DL4	3DL1	3DS1	2DS1	2DS4*001	2DS4d22	3DL2	n	Genotype frequency
1	AA	AA	AA																			52	0.2000
2	AA	AA	AA																			45	0.1731
3	Bx	Bx	AA																			19	0.0731
4	AA	AA	AA																			12	0.0462
5	Bx	*	*																			8	0.0308
6	Bx	Bx	AA																			7	0.0269
7	Bx	Bx	AA																			6	0.0231
8	Bx	Bx	AA																			6	0.0231
9	Bx	Bx	AA																			6	0.0231
10	Bx	Bx	AA																			5	0.0192
11	Bx	Bx	AA																			5	0.0192
12	Bx	Bx	AA																			5	0.0192
13	Bx	Bx	AA																			5	0.0192
14	Bx	Bx	Bx																			4	0.0154
15	Bx	Bx	AA																			4	0.0154
16	Bx	*	Bx																			4	0.0154
17	Bx	Bx	Bx																			3	0.0115
18	Bx	Bx	Bx																			3	0.0115
19	Bx	Bx	AA																			3	0.0115
20	Bx	Bx	Bx																			3	0.0115
21	Bx	Bx	AA																			3	0.0115
22	Bx	Bx	Bx																			2	0.0077
23	Bx	*	*																			2	0.0077
24	Bx	Bx	*																			2	0.0077
25	Bx	Bx	AA																			2	0.0077
26	Bx	Bx	*																			2	0.0077
27	Bx	*	*																			2	0.0077
28	Bx	Bx	*																			2	0.0077
29	Bx	Bx	AA																			2	0.0077
30	Bx	Bx	Bx																			2	0.0077
31	Bx	Bx	Bx																			1	0.0038
32	Bx	Bx	Bx																			1	0.0038
33	Bx	Bx	Bx																			1	0.0038
34	Bx	*	Bx																			1	0.0038
35	Bx	Bx	Bx																			1	0.0038
36	Bx	Bx	*																			1	0.0038
37	Bx	Bx	*																			1	0.0038
38	Bx	*	*																			1	0.0038
39	Bx	Bx	*																			1	0.0038
40	Bx	Bx	*																			1	0.0038
41	Bx	Bx	*																			1	0.0038
42	Bx	Bx	AA																			1	0.0038
43	Bx	Bx	*																			1	0.0038
44	Bx	Bx	Bx																			1	0.0038
45	Bx	Bx	Bx																			1	0.0038
46	Bx	Bx	Bx																			1	0.0038
47	Bx	Bx	Bx																			1	0.0038
48	Bx	*	*																			1	0.0038
49	Bx	Bx	*																			1	0.0038
50	Bx	Bx	*																			1	0.0038
51	Bx	Bx	AA																			1	0.0038
52	Bx	Bx	*																			1	0.0038
53	Bx	Bx	AA																			1	0.0038
54	Bx	Bx	Bx																			1	0.0038
55	Bx	*	Bx																			1	0.0038
56	Bx	Bx	Bx																			1	0.0038
57	Bx	Bx	Bx																			1	0.0038
58	Bx	Bx	Bx																			1	0.0038
59	Bx	Bx	Bx																			1	0.0038
60	Bx	*	*																			1	0.0038
61	Bx	Bx	AA																			1	0.0038
62	Bx	Bx	*																			1	0.0038
63	Bx	Bx	*																			1	0.0038
64	Bx	Bx	Bx																			1	0.0038
<b>Gene Frequencies</b>				1.000	0.396	0.500	0.885	0.488	0.242	0.262	0.977	0.977	0.992	0.073	1.000	0.996	0.085	0.115	0.827	0.542	1.000	260	

\* Could not be determined due to uncertainty in location of 2DL5A8 and 2DS35S

**Figure 1. KIR genotypes and observed frequencies in the P<sub>0</sub> population (n = 260).**  
doi:10.1371/journal.pntd.0002744.g001

individuals were unaffected and phenotypic status could not be confirmed for 4 (<1%). Table 1 gives a detailed description of the phenotype distribution in the families. Detailed examination of photographs revealed that 12 probands did not have sufficient signs of trachomatous scarring. One proband could not be graded. In all the families where there was no photography confirmed scarred proband, at least one sibling was identified who was under 30 years of age and had signs of scarring. HLA genotyping identified paternal misassignment in 63 F<sub>1</sub> individuals (11%) who were reassigned to an unknown father but were otherwise retained for analysis.

### HLA and KIR genotypes

Table 2 shows the Family Based Association Test (FBAT) estimates of the HLA allele and KIR epitope frequencies in the sample population. Figure 1 describes the 64 unique KIR genotypes that were observed in the P<sub>0</sub> generation. Thirty-eight

additional KIR genotypes were revealed by re-assortment of the parental haplotypes in the F<sub>1</sub> generation (Figure 2). All observed genotypes were assigned as either the ‘AA’ or ‘Bx’ genotypes (where Bx includes both AB and BB genotypes) for the full KIR region and where possible, for each of the Cen and Tel regions. A number of unusual genotypes were identified in this population, most notably, 10.4% of P<sub>0</sub> individuals (n = 27/260) possessed *KIR2DL2* but not *KIR2DS2*.

### Linkage disequilibrium

Pairwise linkage disequilibrium data (LD) for the KIR genes were calculated (figure S2). Contrary to data from other studied human populations [58,60,61] and consistent with other findings within Africa [47], we observed reduced LD between KIR genes. We did not identify any pairs of KIR genes that were in perfect LD (r<sup>2</sup> = 1 : only two of the four possible haplotypes observed), although a number of KIR genes were found to be in complete LD

	A/B Genotype	CEN genotype	TEL Genotype	3DL3	2DS2	2DL2	2DL3	2DL5	2DS3	2DS5	2DP1	2DL1	3DP1	3DP1V	2DL4	3DL1	3DS1	2DS1	2DS4*001	2DS4d22	3DL2	
65	AA	AA	AA																			
66	AA	AA	AA																			
67	Bx	AA	Bx																			
68	Bx	*	Bx																			
69	Bx	*	*																			
70	Bx	*	Bx																			
71	Bx	*	Bx																			
72	Bx	Bx	AA																			
73	Bx	Bx	*																			
74	Bx	Bx	AA																			
75	Bx	Bx	*																			
76	Bx	Bx	*																			
77	Bx	Bx	*																			
78	Bx	Bx	Bx																			
79	Bx	Bx	*																			
80	Bx	Bx	*																			
81	Bx	Bx	*																			
82	Bx	Bx	AA																			
83	Bx	Bx	AA																			
84	Bx	Bx	AA																			
85	Bx	Bx	AA																			
86	Bx	Bx	AA																			
87	Bx	Bx	Bx																			
88	Bx	Bx	Bx																			
89	Bx	Bx	Bx																			
90	Bx	Bx	*																			
91	Bx	Bx	*																			
92	Bx	Bx	*																			
93	Bx	Bx	Bx																			
94	Bx	Bx	Bx																			
95	Bx	Bx	Bx																			
96	Bx	Bx	Bx																			
97	Bx	Bx	Bx																			
98	Bx	Bx	Bx																			
99	Bx	Bx	Bx																			
100	Bx	Bx	*																			
101	Bx	Bx	Bx																			
102	Bx	Bx	Bx																			

\* Could not be determined due to uncertainty in location of 2DL5AB and 2DS355

**Figure 2. KIR genotypes and that were uniquely identified in the F<sub>1</sub> population.**  
doi:10.1371/journal.pntd.0002744.g002

(D' = 1 : only three of the four possible haplotypes observed). The extent of LD was insufficient for high confidence imputation of missing KIR genotypes for use in FBAT [58].

**Association tests**

Any HLA alleles and KIR epitopes with estimated frequencies above 0.05 were included in the FBAT. Three sets of HLA alleles were significantly associated with trachomatous scarring (Table 2). These were *HLA-B\*08:01* (Z = -3.548, p = 0.0004, corrected p = 0.01), *HLA-C\*03:04* (Z = -3.201, p = 0.0014, corrected p = 0.04) and the KIR epitope HLA-C1/C2 (Z = 3.622, p = 0.0003, corrected p = 0.008). Only HLA-C1/C2 remained significant (HLA-C2, OR = 1.684 p = 0.0033) in a multivariate case/pseudo-control, additive model that included all three factors

(Table 3), indicating that the HLA-C1/C2 epitope was the only significant independent factor of the HLA system that was associated with trachomatous scarring. In line with previous study designs and analyses we divided the data into several subsets [58,59]. We identified that in the majority of subsets, as with the unselected sample, the relative risk of scarring increased with the number of genomic copies of the HLA-C2 epitope in an additive manner (Table 4). The association of the HLA-C2 homozygote genotype with trachomatous scarring was restricted to the subsets of offspring who were *KIR2DL2<sup>+</sup>* and *KIR2DL3<sup>+</sup>* (Cen-AB) (OR = 5.95, p = 0.0025, BH corrected p = 0.006) and to those who were *KIR3DL1<sup>+</sup>* *KIR3DS1<sup>-</sup>* and *KIR2DS1<sup>-</sup>* (Tel-AA) (HLA-C2 homozygote OR = 4.89, p = 0.00006, BH corrected p = 0.0004). Elevated odds ratios were observed in sensitivity analyses (Table 4) in F<sub>1</sub> samples where the case definition was restricted to those with moderate or severe (WHO FPC grade C2 or C3) rather than evidence of any (C1, C2 or C3) scarring.

**Table 3. Significant results of case/pseudo-control CLR analysis of total family data set.**

	Allele	Odds Ratio	P Value
Multivariate CLR TEST	<i>HLA-B*08:01/...*</i>	0.694	0.7000
	<i>HLA-C*03:04/...**</i>	0.500	0.1500
	<i>HLA-C</i> EPITOPE C2	1.684	0.0033

Likelihood ratio test = 23.1 on 3 df, p = 0.0000379 n = 580, number of informative events = 152.

doi:10.1371/journal.pntd.0002744.t003

**Comparison of Gambian KIR gene frequencies to other human populations**

We used Principle Components Analysis (PCA) to compare the KIR gene frequencies observed in the P<sub>0</sub> generation of the Gambian trachoma families to those observed in other populations where data was available (allele frequencies.net database, (Figure 3)). The proportions of the total variance explained by the first three principle components were 0.42 (σ = 2.05), 0.28 (σ = 1.69) and 0.11 (σ = 1.03). The P<sub>0</sub> specimens clustered with other populations of African descent, which could be recognised by the observation of

**Table 4.** Subset analysis of HLA-C1C2 genotype associations with scarring.

Offspring Genotype	Genotype test HLA-C1/C2	BH Corrected P	Genotype test HLA-C2/C2	BH Corrected P	n	Number of events
Unselected	OR=2.29 p=0.0026	0.0061	OR=3.97 p=0.000051	0.0004	636	159
<i>KIR2DL2</i> <sup>-</sup> <i>KIR2DL3</i> <sup>+</sup> (Cen-AA)	OR=1.94 p=0.08	0.120	OR=2.00 p=0.15	0.191	296	74
<i>KIR2DL2</i> <sup>+</sup> <i>KIR2DL3</i> <sup>+</sup> (Cen-AB)	OR=2.33 p=0.057	0.100	OR=5.95 p=0.0025	0.006	240	60
<i>KIR2DL2</i> <sup>+</sup> <i>KIR2DL3</i> <sup>-</sup> (Cen-BB)	OR=1.5 p=0.73	0.786	OR=6.00 p=0.13	0.182	76	19
<i>KIR3DL1</i> <sup>+</sup> <i>KIR3DS1</i> <sup>-</sup> <i>KIR2DS1</i> <sup>-</sup> (Tel-AA)	OR=2.86 p=0.0013	0.006	OR=4.89 p=0.00006	0.0004	524	131
<i>KIR3DS1</i> <sup>+</sup> and/or <i>KIR2DS1</i> <sup>+</sup> (Tel-Bx)	OR=0.52 p=0.29	0.338	OR=0.90 p=0.89	0.890	88	22
Affected cases defined by more severe scarring (WHO FPC score C2 or C3) & <i>KIR2DL2</i> <sup>+</sup> <i>KIR2DL3</i> <sup>+</sup> (Cen-AB)	OR=2.07 p=0.026	0.052	OR=3.57 p=0.0017	0.006	444	111

doi:10.1371/journal.pntd.0002744.t004

high frequencies of the genes defining the Cen-B (*KIR2DS2*, *KIR2DL2*) and Tel-A (*KIR3DL1* and *KIR2DS4*) haplotypes.

## Discussion

We identified three factors of the HLA system (HLA-C1/C2, *HLA-B*\*08:01 and *HLA-C*\*03:04) that associated with trachomatous scarring. However, the protective associations of *HLA-B*\*08:01 and *HLA-C*\*03:04 observed by univariate analysis were not independent of the HLA-C1/C2 association under a multivariate model. This dependence can be explained by the presence of a common *HLA-B*\*08~*C*\*03 haplotype, which we estimate to have a frequency of around 5.7% in the Gambian trachoma families. In Senegalese Mandinka, this haplotype has an estimated population frequency of 5.5% [62] whilst in African-Americans the frequency is estimated to be as high as 22% [63]. The associations that were observed between *HLA-B*\*08 and *HLA-C*\*03 (an HLA-C1 group allele) appear to be proxies for the association of the HLA-C1/C2 epitope, which reached statistical significance in univariate analysis because of their high population frequencies and the relatively large contribution they therefore made to the HLA-C epitope data.

We observed patterns of transmission disequilibrium in our sample of families that suggest HLA and KIR genotypes associate with high magnitude increases in the relative risk of scarring in trachomatous disease. Through sensitivity analysis (Table 4) we demonstrated the robustness of the analysis and consistency of the results when the cases were defined by more stringently defined phenotypes relating to severity of scarring.

### HLA-C2 epitopes potentially impair NK cell responses and facilitate chronic Ct infection

The chlamydial protease, CPAF has been reported to interfere with the surface presentation of HLA class I molecules [14,64–66], but recently this has been called in to question by Chen et al. [67]. Kägebein et al. [68] then demonstrated that *Ct* infection does not lead to alteration in normal MHC Class-I expression, maturation or surface presentation. This implies that *Ct* infected cells are unlikely to be targets for missing-self reactions mediated by NK cells which selectively monitor down-regulation or loss of self-type MHC class I on target cells. Instead it is more likely that cytotoxic NK responses

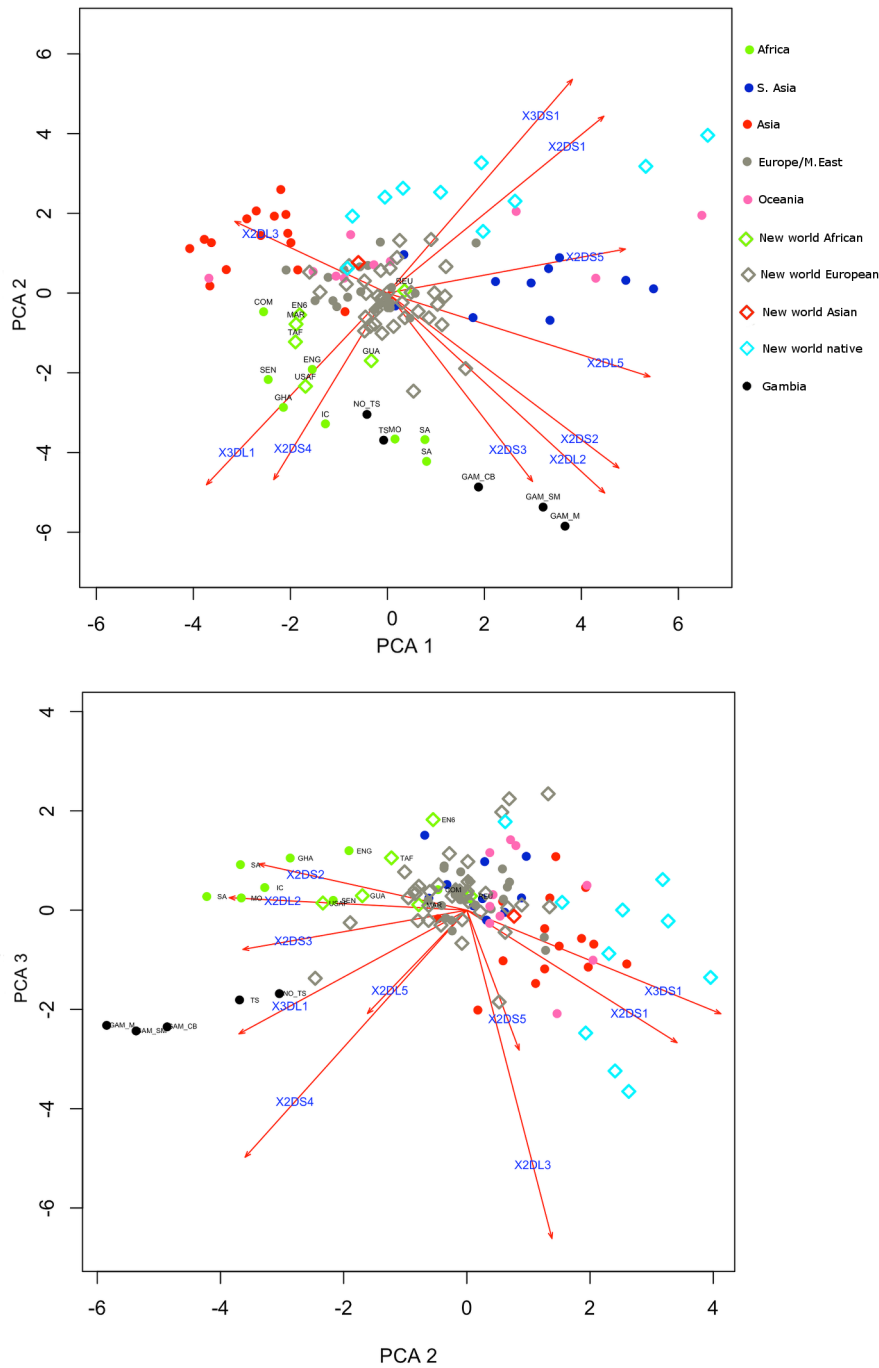
in chlamydial infections are controlled by dynamic changes in the expression levels of activating NK receptors. These changes may occur as a result of infection and other environmental triggers [69,70] and might overwhelm the inhibitory effects of the more strictly expression-regulated [69] NK inhibitory pathways.

HLA-C1:*KIR2DL3* inhibited NK cells have weaker inhibitory signals than other HLA-C inhibited cells [29] and may have a lower threshold for activation. Khakoo *et al.* [40] reported that the HLA-C1/C1 *KIR2DL3/2DL3* genotype constellation increased probability of clearance of early stage Hepatitis C Virus (HCV) infections. Ahlenstiel *et al.* [42] provided evidence that HLA-C1 homozygotes might be better able to challenge early infections by showing that the proportion of the total NK cell repertoire that is educated and inhibited by HLA-C is ~50% greater in this group than that in HLA-C2 homozygotes [42]. The same study showed that HLA-C1 inhibited NK cells are better able to mount rapid, intense responses to infection through degranulation and IFN $\gamma$  secretion [42]. In *Ct* infections, HLA-C1/C1 individuals may be able to limit chronicity by controlling the early stages of *Ct* infections with an NK response that is easily activated, and involves a more substantial component of the NK repertoire than in HLA-C2/C2 individuals. This may also be true of HLA-C2<sup>+</sup> individuals who possess only weakly responsive *KIR2DL1* alleles, such as those alleles that are found on the commonest B haplotypes in Caucasian populations [41]. However, in the Ga-Adangbe population of Ghana, there was a great diversity B haplotypes, none of which were found at high frequency and many of which carried non-attenuated *KIR2DL1* alleles [38]. Any assumption about how the presence of Cen-B might indicate reduced cellular inhibition in Gambians should therefore be made with some caution.

### A role for within-person inhibitory KIR diversity in influencing immunopathology

The role of KIR in mediating NK cytotoxic responses is well studied, but it is now clear that KIR expressing NK cells are also a major source of IFN $\gamma$  [71]. The ability of NK cells to produce IFN $\gamma$  in response to microbial stimuli is related to the density of NCAM-1 (CD56) expressed on their surface, their KIR genotype and the degree of stimulus by accessory cells. An indication of the strength of regulation imposed by the KIR genotype can be estimated as a ratio, known as the 'DIM factor', between the response of the CD56<sup>dim</sup>

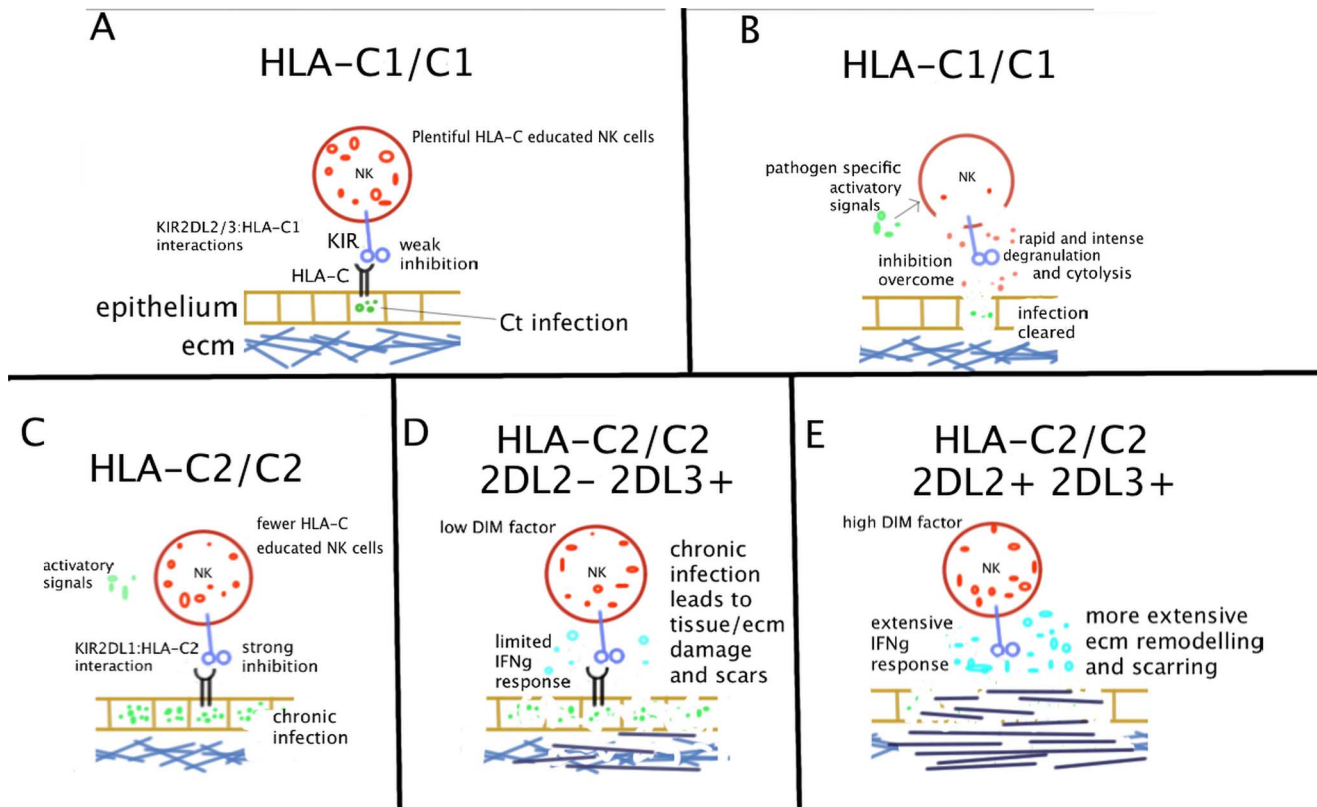




**Figure 3. Principle Components Analysis of Gambian KIR frequencies and other world populations.** African populations are characterised by high frequencies of the Cen-B (*KIR2DS2*–*KIR2DL2*, *KIR2DL2*) and Tel-A (*KIR3DS1*–*KIR2DS4*) haplotypes. Gambian samples, including the P<sub>0</sub> specimens and malaria cases cluster together and have some of the highest observed frequencies of Cen-B and Tel-A. The proportions of the total variance explained by the first three principal components were respectively 0.42, 0.28 and 0.11. Footnote to figure 3. NO\_TS : Parents from Gambian trachoma families, unaffected, TS : Parents from Gambian trachoma families, affected, GAM\_SM : Gambian severe malaria cases, GAM\_M : Gambian uncomplicated Malaria cases, GCB : Gambian cord bloods, COM : Comoros, ENG : Equatorial New Guinea, GHA : Ghana, IC : Ivory Coast, MO : Morocco, SEN : Senegal, SA : South Africa, EN6 : England – West Midlands Afro-Caribbean, GUA : Guadaloupe, MAR : Martinique, REU : Reunion, TAF (Trinidad Africans), USAF : USA Californian African Americans.  
doi:10.1371/journal.pntd.0002744.g003

(KIR-HLA dependent) and CD56<sup>bright</sup> (KIR-HLA independent) IFN $\gamma$  responding populations [71]. The majority of human NK cells in the periphery are CD56<sup>dim</sup>, express KIR and are susceptible to inhibition through KIR-HLA interaction. KIR genotype directly influences the DIM factor, but the exact genotypic conformation

that defines this has yet to be elucidated. It has been proposed that the NK cell IFN $\gamma$  response will be higher in individuals with more KIR educated NK cells, a situation found when there is a greater diversity of within-person inhibitory KIR genes. Experimentally, IFN $\gamma$  production in CD56<sup>dim</sup> NK cells showed least inhibition (and



**Figure 4. Model of NK cell mediated scarring in trachoma.** (A) An HLA-C1/C1 NK cell interacts with HLA class I molecules on a *Ct* infected epithelial cell via interactions between *KIR2DL2/L3* and HLA-C1. HLA-C educated NK cells represent a greater proportion of the total NK repertoire in HLA-C1 homozygotes, compared to those who carry HLA-C2 (B) The inhibitory signals are overcome by loss of the inhibitory HLA-C molecule and/or by activatory signals, which may be from intracellular or extracellular pathogen derived moieties. The NK cytotoxic response is triggered and the target cell is lysed, which culminates in effective resolution of the infection. (C) An HLA-C2/C2 NK cell interacts with MHC class I molecules on *Ct* infected epithelial cell via interactions between *KIR2DL1* and HLA-C2. A smaller proportion of the NK cell repertoire is HLA-C educated in this setting. Cytotoxic and  $\text{IFN}\gamma$  responses are less likely to be triggered and responses are less intense than in HLA-C1/C1 individuals. Chronic infection is established (D) *KIR2DL2*<sup>-</sup>, *KIR2DL3*<sup>+</sup> individuals have a low DIM factor and NK cell release of  $\text{IFN}\gamma$  is more limited. Chronic infection leads to some damage to epithelium and extracellular matrix (ECM) but anti-fibrotic properties of  $\text{IFN}\gamma$  are maintained. (E) *KIR2DL2/KIR2DL3* heterozygous individuals have a high DIM factor and NK cells release larger quantities of  $\text{IFN}\gamma$ . Chronic infection is coupled with pathologically high levels of  $\text{IFN}\gamma$ . HLA-C1/C2 genotypes confer intermediate risks that do not significantly differ from the homozygous individuals. Relative risk of scarring was increased in *KIR2DL2* homozygotes, but this was not significant. doi:10.1371/journal.pntd.0002744.g004

the highest DIM factor) in KIR AB heterozygotes [71]. In HLA-C2 homozygotes, we observed a significant *KIR2DL2/L3* heterozygote (Cen-AB) disadvantage (Table 4) and an increased relative risk in those with the Tel-AA genotype. The number of persons with Tel-B genotypes was very low in this study, which reflects the low diversity in the Tel region that was reported in another West African population [38]. The high phenotypic frequency of *KIR3DL1* (Tel-A) in this Gambian population (~99.6%) indicates that most individuals with the Cen-AB genotype possess at least one Tel-A haplotype. The Cen-AB, Tel-A<sup>+</sup> genotype represents a full complement of the known MHC specific inhibitory KIRs (*KIR2DL1*, *KIR2DL2*, *KIR2DL3*, *KIR3DL1* and *KIR3DL2*) and this genotype might define a high DIM factor [71]. NK cell clones with a Cen-AB genotype would therefore be relatively resistant to inhibition (DIM factor >1) and would retain the potential for high  $\text{IFN}\gamma$  production.

#### Common tropical infectious diseases drive selection of high frequencies of trachoma risk genotype constellations

The KIR system exhibits extensive diversity in African populations [47,72,73] possibly driven by a high burden of life

threatening infectious diseases, that have exerted strong (diversifying) selective pressures on each population [46,47,74]. The high prevalence of *Ct* STIs in some African populations has been implicated as a contributory factor to the high incidences of infection related infertility that are observed in Africa [75]. It is therefore surprising that *Ct* disease associated KIR and HLA genotypes are enriched in Africa. One explanation is that opposing selection pressures from other infectious diseases negate selection by *Ct*. Our sample was selected based on disease phenotype and we found KIR gene frequencies similar to other African populations (Figure 3). The Gambian samples are clearly separated from those in other geographical regions by high frequencies of the genes that define the Cen-B and Tel-A haplotypes (Figure 3) [72]. The frequency of HLA-C2 epitopes is reported to be higher in African populations than in other populations [46,76,77] and the HLA-C epitope frequencies that we observed are similar to those previously described [77]. Yindom *et al.* [78] reported that the proportion of persons with the constellation HLA-C1 and *KIR2DL2/KIR2DS2* (Cen-B) is higher in cases of malaria than in population matched, cord-blood controls [78]. In a study of a South-East Asian population, Hirayasu *et al.* [79] reported that natural selection may have

reduced the frequency of the HLA-C1 and *KIR2DL3* (Cen-A) because this genotype associates with cases of cerebral malaria. Both studies identify HLA-C1 in association with malarial disease, but they implicate different KIR Cen haplotypes. In the Gambian trachoma families, we observed that many Cen-B haplotypes lacked *KIR2DS2*, whilst maintaining *KIR2DL2*. This genotype has previously been identified in an African population [73] and its presence could be explained if *KIR2DS2*, rather than *KIR2DL2*, were mediating the Cen-B risk effect. The combined evidence of several TB studies shows that KIR Cen-A [80–82] and Tel-B [82,83] haplotypes associate with TB cases. We therefore suggest that the HLA-C2 homozygous, Cen-AB, Tel-A<sup>+</sup> population are more resistant to the complications of both malaria and TB, but more susceptible to trachomatous scarring and that trachomatous scarring (and possibly reduced fertility) is the penalty of increased survival.

### A dual role for KIR-HLA restricted NK cells in trachoma and its implications for chlamydial vaccine development

We identified KIR-HLA interactions as an important contributory factor to risk of scarring. The HLA-C2 homozygous, *KIR2DL2*<sup>+</sup>, *KIR2DL3*<sup>+</sup> genotype associates with high relative risk of scarring. We suggest a model that may explain the data in which HLA-C2 may favour chronic infection, whilst *KIR2DL2/L3* heterozygosity favours chronic inflammation (Figure 4). In some aspects this is similar to the model put forward by Hollenbach *et al.* to explain the observation of HLA-C1/C1, *KIR2DL2/L3* heterozygote risk in Crohn's disease [84], which like trachoma is characterised by chronic inflammation and fibrotic immunopathology. It is possible that the high burden of trachomatous scarring, TT and infection related infertility in observed in Africa can be explained in part by unusually high frequencies of HLA-C2 and *KIR2DL2/L3* heterozygosity and the effects of NK cell responsiveness. The therapeutic consequences of such a theory would impact on vaccine immune-therapies and we would expect that current efforts in the development of chlamydial vaccines, adjuvants and immunisation schedules would additionally monitor the boosting or modulating effects on the NK cell compartment. As early as the 1990 it was shown that vaccination with influenza virus was able to elicit NK cell responses [85]. More recent work has demonstrated that many vaccination regimes against viruses boost not only adaptive T and B cell response but also lead to repetitive expansions of NK cells [86–88]. Some immunologists have termed these “memory-like NK cell responses” and have now begun to consider the role of these responses in vaccine induced immunity [89]. The effectiveness of NK cells as targets of vaccine immuno-therapy has been described in oncology

[90]. Efforts are now required to investigate the role of NK cells in immunity following vaccination with a wider spectrum of bacterial vectors and in natural immunity to infectious diseases such as trachoma.

### Supporting Information

**Figure S1 PBAT estimates of power in this study to detect genetic associations with trachomatous scarring at a range of allele frequencies and effect magnitudes.** (TIF)

**Figure S2 Evidence for (a) complete [ $D' = 1$ ] but (b) not perfect [ $R^2 = 1$ ] linkage disequilibrium between pairs of KIR genes.** LD was insufficiently strong to be used to reconstruct missing genotype data in the family study. In (a) dark grey indicates strong evidence of linkage, light grey is uninformative and white indicates strong evidence of recombination.  $D'$  values below 1 are shown. In (b) white indicates  $R^2 = 0$ , shades of grey indicate  $0 < R^2 < 1$  and black indicates  $R^2 = 1$ .  $R$  squared values below 1 are shown. 2DS4d22 indicates alleles of *KIR2DS4* carrying a 22 bp deletion. 3DP1V indicates alleles of *KIR3DP1* carrying exon 2. (TIF)

**Table S1 HLA Allele strings used in FBAT and associated frequencies.** For the purposes of grouping for FBAT and in order to maximise statistical power, individual HLA genotypes were assigned to the ‘identifier’ groups if they possessed any or all of the alleles shown in the full genotype string. (DOCX)

### Acknowledgments

The authors wish to thank Omar Camera and Omar Ceasay for their work in the field. Dr. Elizabeth Trachtenberg and Dr. Kathleen Houchens for confirmatory genotyping. Prof. Mary Carrington, Prof. Eleanor Riley, Dr. Paul Norman, Dr. Jill Hollenbach, Dr. Taane Clark, Dr. James Traherne, Dr. Becca Asquith and Marina Collins for technical advice, discussions and critical reading. Thanks also to the members of the Partnership for the Rapid Elimination of Trachoma (PRET) team, MRC laboratories The Gambia and to the families and individuals who consented to participate in this study.

### Author Contributions

Conceived and designed the experiments: ChR DCWM MJH. Performed the experiments: SM ChR. Analyzed the data: ChR. Wrote the paper: ChR MJH. Assessed the phenotypes: RLB MJB. Performed the field work: PM HJ MJH ChR SEB EMHE.

### References

- Abdelrahman YM, Belland RJ (2005) The chlamydial developmental cycle. *FEMS Microbiol Rev* 29: 949–959. doi:10.1016/j.femsre.2005.03.002.
- Rowley J, Toskin I, Ndowa F (2008) Global Incidence and Prevalence of Selected Curable Sexually Transmitted Infections, 2008. World Health Organisation.
- Resnikoff S, Pascolini D, Etya D, Kocur I, Pararajasegaram R, et al. (2004) Policy and Practice Global data on visual impairment in the year 2002. 0128 31.
- Harding-Esch EM, Edwards T, Mkocha H, Munoz B, Holland MJ, et al. (2010) Trachoma prevalence and associated risk factors in the gambia and Tanzania: baseline results of a cluster randomised controlled trial. *PLoS Negl Trop Dis* 4: e861. doi:10.1371/journal.pntd.0000861.
- Hu VH, Holland MJ, Burton MJ (2013) Trachoma: protective and pathogenic ocular immune responses to Chlamydia trachomatis. *PLoS Negl Trop Dis* 7: e2020. doi:10.1371/journal.pntd.0002020.
- Hu VH, Weiss HA, Ramadhani AM, Tolbert SB, Massac P, et al. (2012) Innate immune responses and modified extracellular matrix regulation characterize bacterial infection and cellular/connective tissue changes in scarring trachoma. *Infect Immun* 80: 121–130. doi:10.1128/IAI.05965-11.
- Natividad A, Freeman TC, Jeffries D, Burton MJ, Mabey DCW, et al. (2010) Human conjunctival transcriptome analysis reveals the prominence of innate defense in Chlamydia trachomatis infection. *Infect Immun* 78: 4895–4911. doi:10.1128/IAI.00844-10.
- Gurujeyalakshmi G, Giri SN (1995) Molecular mechanisms of antifibrotic effect of interferon gamma in bleomycin-mouse model of lung fibrosis: downregulation of TGF-beta and procollagen I and III gene expression. *Exp Lung Res* 21: 791–808. doi:10.3109/01902149509050842.
- Cella M, Fuchs A, Vermi W, Facchetti F, Otero K, et al. (2009) A human natural killer cell subset provides an innate source of IL-22 for mucosal immunity. *Nature* 457: 722–725. doi:10.1038/nature07537.
- Nagarajan UM, Sikes J, Prantner D, Andrews CW, Frazer L, et al. (2011) MyD88 deficiency leads to decreased NK cell gamma interferon production and T cell recruitment during Chlamydia muridarum genital tract infection, but a predominant Th1 response and enhanced monocytic inflammation are associated with infection resolution. *Infect Immun* 79: 486–498. doi:10.1128/IAI.00843-10.
- Tseng CT, Rank RG (1998) Role of NK cells in early host response to chlamydial genital infection. *Infect Immun* 66: 5867–5875.

12. Gall A, Horowitz A, Joof H, Natividad A, Tetteh K, et al. (2011) Systemic effector and regulatory immune responses to chlamydial antigens in trachomatous trichiasis. *Front Microbiol* 2: 10. doi:10.3389/fmicb.2011.00010.
13. Holland MJ, Bailey RL, Conway DJ, Culley F, Miranpuri G, et al. (1996) T helper type-1 (Th1)/Th2 profiles of peripheral blood mononuclear cells (PBMC); responses to antigens of Chlamydia trachomatis in subjects with severe trachomatous scarring. *Clin Exp Immunol* 105: 429–435.
14. Ibanja JA, Aiyar A, Quayle AJ, Schust DJ (2012) Modulation of MICA on the surface of Chlamydia trachomatis-infected endocervical epithelial cells promotes NK cell-mediated killing. *FEMS Immunol Med Microbiol* 65: 32–42. doi:10.1111/j.1574-695X.2012.00930.x.
15. Valiante NM, Uhrberg M, Shilling HG, Lienert-Weidenbach K, Arnett KL, et al. (1997) Functionally and structurally distinct NK cell receptor repertoires in the peripheral blood of two human donors. *Immunity* 7: 739–751.
16. Natividad A, Wilson J, Koch O, Holland MJ, Rockett K, et al. (2005) Risk of trachomatous scarring and trichiasis in Gambians varies with SNP haplotypes at the interferon-gamma and interleukin-10 loci. *Genes Immun* 6: 332–340. doi:10.1038/sj.gene.6364182.
17. Natividad A, Holland MJ, Rockett KA, Forton J, Faal N, et al. (2008) Susceptibility to sequelae of human ocular chlamydial infection associated with allelic variation in IL10 cis-regulation. *October*: 323–329. doi:10.1093/hmg/ddm310.
18. Natividad A, Hanchard N, Holland MJ, Mahdi OSM, Diakite M, et al. (2007) Genetic variation at the TNF locus and the risk of severe sequelae of ocular Chlamydia trachomatis infection in Gambians. *Genes Immun* 8: 288–295. doi:10.1038/sj.gene.6364384.
19. Lu Z, Zhang B, Chen S, Gai Z, Feng Z, et al. (2008) Association of KIR genotypes and haplotypes with susceptibility to chronic hepatitis B virus infection in Chinese Han population. *Cell Mol Immunol* 5: 457–463. doi:10.1038/cmi.2008.57.
20. Khakoo SI, Thio CL, Martin MP, Brooks CR, Gao X, et al. (2004) HLA and NK cell inhibitory receptor genes in resolving hepatitis C virus infection. *Science* 305: 872–874. doi:10.1126/science.1097670.
21. Flores-Villanueva PO, Yunis EJ, Delgado JC, Vittinghoff E, Buchbinder S, et al. (2001) Control of HIV-1 viremia and protection from AIDS are associated with HLA-Bw4 homozygosity. *Proc Natl Acad Sci U S A* 98: 5140–5145. doi:10.1073/pnas.071548198.
22. Martin MP, Qi Y, Gao X, Yamada E, Martin JN, et al. (2007) Innate partnership of HLA-B and KIR3DL1 subtypes against HIV-1. *Nat Genet* 39: 733–740. doi:10.1038/ng2035.
23. Martin MP, Gao X, Lee J-H, Nelson GW, Detels R, et al. (2002) Epistatic interaction between KIR3DS1 and HLA-B delays the progression to AIDS. *Nat Genet* 31: 429–434. doi:10.1038/ng934.
24. Moretta A, Vitale M, Bottino C, Orengo AM, Morelli L, et al. (1993) P58 molecules as putative receptors for major histocompatibility complex (MHC) class I molecules in human natural killer (NK) cells. Anti-p58 antibodies reconstitute lysis of MHC class I-protected cells in NK clones displaying different specificities. *J Exp Med* 178: 597–604.
25. Döhning C, Colonna M, Döhning C (1996) Human natural killer cell inhibitory receptors bind to HLA class I molecules. *Eur J Immunol* 26: 365–369. doi:10.1002/eji.1830260215.
26. Pende D, Biassoni R, Cantoni C, Verdiani S, Falco M, et al. (1996) The natural killer cell receptor specific for HLA-A allotypes: a novel member of the p58/p70 family of inhibitory receptors that is characterized by three immunoglobulin-like domains and is expressed as a 140-kD disulphide-linked dimer. *J Exp Med* 184: 505–518.
27. Colonna M, Samaridis J (1995) Cloning of Immunoglobulin-Superfamily Members Associated with HLA-C and HLA-B Recognition by Human Natural Killer Cells. *Science* (80-) 268: 405–408.
28. Gumperz JE, Litwin V, Phillips JH, Lanier LL, Parham P (1995) The Bw4 public epitope of HLA-B molecules confers reactivity with natural killer cell clones that express NKB1, a putative HLA receptor. *J Exp Med* 181: 1133–1144.
29. Winter CC, Gumperz JE, Parham P, Long EO, Wagtmann N (1998) Direct binding and functional transfer of NK cell inhibitory receptors reveal novel patterns of HLA-C allotype recognition. *J Immunol* 161: 571–577.
30. Colonna M, Borsellino G, Falco M, Ferrara GB, Strominger JL (1993) HLA-C is the inhibitory ligand that determines dominant resistance to lysis by NK1- and NK2-specific natural killer cells. *Proc Natl Acad Sci U S A* 90: 12000–12004.
31. Colonna M, Brooks EG, Falco M, Ferrara GB, Strominger JL (1993) Generation of allospecific natural killer cells by stimulation across a polymorphism of HLA-C. *Science* (80-) 260: 1121–1124.
32. Ciccone E, Pende D, Vitale M, Nanni L, Di Donato C, et al. (1994) Self class I molecules protect normal cells from lysis mediated by autologous natural killer cells. *Eur J Immunol* 24: 1003–1006.
33. Stewart CA, Laugier-Anfossi F, Vely F, Saulquin X, Riedmuller J, et al. (2005) Recognition of peptide-MHC class I complexes by activating killer immunoglobulin-like receptors. *Proc Natl Acad Sci U S A* 102: 13224–13229.
34. Moesta AK, Norman PJ, Yawata M, Yawata N, Gleimer M, et al. (2008) Synergistic polymorphism at two positions distal to the ligand-binding site makes KIR2DL2 a stronger receptor for HLA-C than KIR2DL3. *J Immunol* 180: 3969–3979.
35. Uhrberg M, Parham P, Wernet P (2002) Definition of gene content for nine common group B haplotypes of the Caucasoïd population: KIR haplotypes contain between seven and eleven KIR genes. *Immunogenetics* 54: 221–229. doi:10.1007/s00251-002-0463-7.
36. Uhrberg M, Valiante NM, Shum BP, Shilling HG, Lienert-Weidenbach K, et al. (1997) Human diversity in killer cell inhibitory receptor genes. *Immunity* 7: 753–763.
37. Wilson MJ, Torkar M, Haude A, Milne S, Jones T, et al. (2000) Plasticity in the organization and sequences of human KIR/ILT gene families. *Proc Natl Acad Sci U S A* 97: 4778–4783.
38. Norman PJ, Hollenbach JA, Nemat-Gorgani N, Guethlein LA, Hilton HG, et al. (2013) Co-evolution of human leukocyte antigen (HLA) class I ligands with killer-cell immunoglobulin-like receptors (KIR) in a genetically diverse population of sub-Saharan Africans. *PLoS Genet* 9: e1003938. doi:10.1371/journal.pgen.1003938.
39. Moretta A, Sivori S, Vitale M, Pende D, Morelli L, et al. (1995) Existence of both inhibitory (p58) and activatory (p50) receptors for HLA-C molecules in human natural killer cells. *J Exp Med* 182: 875–884.
40. Khakoo SI, Thio CL, Martin MP, Collin R, Gao X, et al. (2008) HLA and NK Cell Inhibitory Receptor Genes in Resolving Hepatitis C Virus Infection. *Science* (80-) 872. doi:10.1126/science.1097670.
41. Bari R, Bell T, Leung W-H, Vong QP, Chan WK, et al. (2009) Significant functional heterogeneity among KIR2DL1 alleles and a pivotal role of arginine 245. *Blood* 114: 5182–5190. doi:10.1182/blood-2009-07-231977.
42. Ahlenstiel G, Martin MP, Gao X, Carrington M, Rehermann B (2008) Distinct KIR/HLA compound genotypes affect the kinetics of human antiviral natural killer cell responses. *J Clin Invest* 118: 1017–1026. doi:10.1172/JCI32400 [doi].
43. Hsu KC, Chida S, Geraghty DE, Dupont B (2002) The killer cell immunoglobulin-like receptor (KIR) genomic region: gene-order, haplotypes and allelic polymorphism. *Immunol Rev* 190: 40–52.
44. Gendzekhadze K, Norman PJ, Abi-Rached L, Layrisse Z, Parham P (2006) High KIR diversity in Amerindians is maintained using few gene-content haplotypes. *Immunogenetics* 58: 474–480. doi:10.1007/s00251-006-0108-3.
45. Gendzekhadze K, Norman PJ, Abi-Rached L, Graef T, Moesta AK, et al. (2009) Co-evolution of KIR2DL3 with HLA-C in a human population retaining minimal essential diversity of KIR and HLA class I ligands. *Proc Natl Acad Sci U S A* 106: 18692–18697. doi:10.1073/pnas.0906051106.
46. Parham P, Moffett A (2013) Variable NK cell receptors and their MHC class I ligands in immunity, reproduction and human evolution. *Nat Rev Immunol* 13: 133–144. doi:10.1038/nri3370.
47. Norman PJ, Abi-Rached L, Gendzekhadze K, Korbel D, Gleimer M, et al. (2007) Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. *Nat Genet* 39: 1092–1099. doi:10.1038/ng2111.
48. Saftlas AF, Waldschmidt M, Logsdon-sackett N, Triche E, Field E (2004) Optimizing buccal cell DNA yields in mothers and infants for human leukocyte antigen genotyping. *Am J Epidemiol* 160: 77–84. doi:10.1093/aje/kwh171.
49. Dolin PJ, Faal H, Johnson GJ, Ajewole J, Mohamed A, et al. (1998) Trachoma in the Gambia. *Br J Ophthalmol* 82: 930–933. doi:10.1136/bjo.82.8.930.
50. Van Steen K, Lange C (2005) PBAT: a comprehensive software package for genome-wide association analysis of complex family-based studies. *Hum Genomics* 2: 67–69.
51. Stare D, Harding-Esch E, Munoz B, Bailey R, Mabey D, et al. (2011) Design and baseline data of a randomized trial to evaluate coverage and frequency of mass treatment with azithromycin: the Partnership for Rapid Elimination of Trachoma (PRET) in Tanzania and The Gambia. *Ophthalmic Epidemiol* 18: 20–29. doi:10.3109/09286586.2010.545500.
52. Derrick T, Roberts C h., Rajasekhar M, Burr SE, Joof H, et al. (2013) Conjunctival MicroRNA Expression in Inflammatory Trachomatous Scarring. *PLoS Negl Trop Dis* 7: e2117. doi:10.1371/journal.pntd.0002117.
53. Vilches C, Castano J, Gomez-Lozano N, Estefania E, Castan J, et al. (2007) Facilitation of KIR genotyping by a PCR-SSP method that amplifies short DNA fragments. *Tissue Antigens* 70: 415–422. doi:10.1111/j.1399-0039.2007.00923.x.
54. Cano P, Klitz W, Mack SJ, Maier M, Marsh SGE, et al. (2007) Common and well-documented HLA alleles: report of the Ad-Hoc committee of the American Society for Histocompatibility and Immunogenetics. *Hum Immunol* 68: 392–417.
55. Horvath S, Xu X, Laird NM (2001) The family based association test method: strategies for studying general genotype-phenotype associations. *Eur J Hum Genet* 9: 301–306. doi:10.1038/sj.ejhg.5200625.
56. Laird NM, Horvath S, Xu X (2000) Implementing a unified approach to family-based tests of association. *Genet Epidemiol* 19 Suppl 1: S36–42. doi:10.1002/1098-2272(2000)19:1+<:AID-GEPI6>3.0.CO;2-M.
57. Cordell HJ, Barratt BJ, Clayton DG (2004) Case/pseudocontrol analysis in genetic association studies: A unified framework for detection of genotype and haplotype associations, gene-gene and gene-environment interactions, and parent-of-origin effects. *Genet Epidemiol* 26: 167–185. doi:10.1002/gepi.10307.
58. Besson C, Roctyng S, Williams F, Orsi L, Amiel C, et al. (2007) Association of killer cell immunoglobulin-like receptor genes with Hodgkin's lymphoma in a familial study. *PLoS One* 2: e406. doi:10.1371/journal.pone.0000406.
59. Malik S, Abel L, Tooker H, Poon A, Simkin L, et al. (2005) Alleles of the NRAMP1 gene are risk factors for pediatric tuberculosis disease. *Proc Natl Acad Sci U S A* 102: 12183–12188.
60. Middleton D, Meenagh A, Gourraud PA (2007) KIR haplotype content at the allele level in 77 Northern Irish families. *Immunogenetics* 59: 145–158. doi:10.1007/s00251-006-0181-7.

61. Martin MP, Single RM, Wilson MJ, Trowsdale J, Carrington M (2008) KIR haplotypes defined by segregation analysis in 59 Centre d'Etude Polymorphisme Humain (CEPH) families. *Immunogenetics* 60: 767–774. doi:10.1007/s00251-008-0334-y.
62. Sanchez-Mazas A, Steiner Q-G, Grundschober C, Tiercy J-M (2000) The molecular determination of HLA-Cw alleles in the Mandenka (West Africa) reveals a close genetic relationship between Africans and Europeans. *Tissue Antigens* 56: 303–312. doi:10.1034/j.1399-0039.2000.560402.x.
63. Maiers M, Gragert L, Klitz W (2007) High-resolution HLA alleles and haplotypes in the United States population. *Hum Immunol* 68: 779–788. doi:10.1016/j.humimm.2007.04.005.
64. Ibana JA, Schust DJ, Sugimoto J, Nagamatsu T, Greene SJ, et al. (2011) Chlamydia trachomatis immune evasion via downregulation of MHC class I surface expression involves direct and indirect mechanisms. *Infect Dis Obstet Gynecol* 2011: 420905. doi:10.1155/2011/420905.
65. Zhong G, Liu L, Fan T, Fan P, Ji H (2000) Degradation of transcription factor RFX5 during the inhibition of both constitutive and interferon gamma-inducible major histocompatibility complex class I expression in chlamydia-infected cells. *J Exp Med* 191: 1525–1534.
66. Zhong G, Fan P, Ji H, Dong F, Huang Y (2001) Identification of a chlamydial protease-like activity factor responsible for the degradation of host transcription factors. *J Exp Med* 193: 935–942.
67. Chen AL, Johnson KA, Lee JK, Sütterlin C, Tan M (2012) CPAF: a Chlamydial protease in search of an authentic substrate. *PLoS Pathog* 8: e1002842. doi:10.1371/journal.ppat.1002842.
68. Kägebein D, Gutjahr M, Große C, Vogel AB, Rödel J, et al. (2013) Chlamydia-infected epithelial cells and fibroblasts retain the ability to express surface-presented MHC class I molecules. *Infect Immun*: 1–31. doi:10.1128/IAI.01473-13.
69. Horowitz A, Strauss-Albee DM, Leipold M, Kubo J, Nemat-Gorgani N, et al. (2013) Genetic and environmental determinants of human NK cell diversity revealed by mass cytometry. *Sci Transl Med* 5: 208ra145. doi:10.1126/scitranslmed.3006702.
70. Leavy O (2013) Natural killer cells: a virtual pick and mix. *Nat Rev Immunol* 13: 844–845. doi:10.1038/nri3566.
71. Korb DS, Norman PJ, Newman KC, Horowitz A, Gendzekhadze K, et al. (2009) Killer Ig-like receptor (KIR) genotype predicts the capacity of human KIR-positive CD56dim NK cells to respond to pathogen-associated signals. *J Immunol* 182: 6426–6434. doi:10.4049/jimmunol.0804224.
72. Hollenbach JA, Necedal I, Ladner MB, Single RM, Trachtenberg EA (2012) Killer cell immunoglobulin-like receptor (KIR) gene content variation in the HGDP-CEPH populations. *Immunogenetics* 64: 719–737. doi:10.1007/s00251-012-0629-x.
73. Norman PJ, Carrington C V, Byng M, Maxwell LD, Curran MD, et al. (2002) Natural killer cell immunoglobulin-like receptor (KIR) locus profiles in African and South Asian populations. *Genes Immun* 3: 86–95.
74. Qutob N, Balloux F, Raj T, Liu H, Marion de Procé S, et al. (2012) Signatures of historical demography and pathogen richness on MHC class I genes. *Immunogenetics* 64: 165–175. doi:10.1007/s00251-011-0576-y.
75. Cates W, Farley T, Rowe P (1985) Worldwide Patterns Of Infertility: Is Africa Different? *Lancet* 5800: 596–598.
76. Parham P, Norman PJ, Abi-Rached L, Guethlein LA (2012) Human-specific evolution of killer cell immunoglobulin-like receptor recognition of major histocompatibility complex class I molecules. *Philos Trans R Soc Lond B Biol Sci* 367: 800–811. doi:10.1098/rstb.2011.0266.
77. Single RM, Martin MP, Gao X, Meyer D, Yeager M, et al. (2007) Global diversity and evidence for coevolution of KIR and HLA. *Nat Genet* 39: 1114–1119. doi:10.1038/ng2077.
78. Yindom L-M, Forbes R, Aka P, Janha O, Jeffries D, et al. (2012) Killer-cell immunoglobulin-like receptors and malaria caused by *Plasmodium falciparum* in The Gambia. *Tissue Antigens* 79: 104–113. doi:10.1111/j.1399-0039.2011.01818.x.
79. Hirayasu K, Ohashi J, Kashiwase K, Hananantachai H, Naka I, et al. (2012) Significant association of KIR2DL3-HLA-C1 combination with cerebral malaria and implications for co-evolution of KIR and HLA. *PLoS Pathog* 8: e1002565. doi:10.1371/journal.ppat.1002565.
80. Mendez A, Granda H, Meenagh A, Contreras S, Zavaleta R, et al. (2006) Study of KIR genes in tuberculosis patients. *Tissue Antigens* 68: 386–389. doi:TAN685 [pii] 10.1111/j.1399-0039.2006.00685.x [doi].
81. Mahfouz R, Halas H, Hoteit R, Saadeh M, Shamseddeen W, et al. (2011) Study of KIR genes in Lebanese patients with tuberculosis. *Int J Tuberc Lung Dis* 15: 1688–1691. doi:10.5588/ijtld.11.0138.
82. Pydi SS, Sunder SR, Venkatasubramanian S, Kovvali S, Jonnalagada S, et al. (2013) Killer cell immunoglobulin like receptor gene association with tuberculosis. *Hum Immunol* 74: 85–92. doi:10.1016/j.humimm.2012.10.006.
83. Lu C, Shen Y-J, Deng Y-F, Wang C-Y, Fan G, et al. (2012) Association of killer cell immunoglobulin-like receptors with pulmonary tuberculosis in Chinese Han. *Genet Mol Res* 11: 1370–1378. doi:10.4238/2012.May.15.7.
84. Hollenbach J a, Ladner MB, Saeteurn K, Taylor KD, Mei L, et al. (2009) Susceptibility to Crohn's disease is mediated by KIR2DL2/KIR2DL3 heterozygosity and the HLA-C ligand. *Immunogenetics* 61: 663–671. doi:10.1007/s00251-009-0396-5.
85. Schapiro JM, Segev Y, Rannon L, Alkan M, Rager-Zisman B (1990) Natural killer (NK) cell response after vaccination of volunteers with killed influenza vaccine. *J Med Virol* 30: 196–200.
86. Horowitz A, Hafalla JCR, King E, Lusingu J, Dekker D, et al. (2012) Antigen-specific IL-2 secretion correlates with NK cell responses after immunization of Tanzanian children with the RTS,S/AS01 malaria vaccine. *J Immunol* 188: 5054–5062. doi:10.4049/jimmunol.1102710.
87. Horowitz A, Behrens RH, Okell L, Fooks AR, Riley EM (2010) NK cells as effectors of acquired immune responses: effector CD4+ T cell-dependent activation of NK cells following vaccination. *J Immunol* 185: 2808–2818. doi:10.4049/jimmunol.1000844.
88. Hall IJ, Clare S, Dougan G (2010) NK cells influence both innate and adaptive immune responses after mucosal immunization with antigen and mucosal adjuvant. *J Immunol* 184: 4327–4337. doi:10.4049/jimmunol.0903357.
89. Rölle A, Pollmann J, Cerwenka A (2013) Memory of infections: an emerging role for natural killer cells. *PLoS Pathog* 9: e1003548. doi:10.1371/journal.ppat.1003548.
90. Woo CY, Clay TM, Lysterly HK, Morse MA, Osada T (2006) Role of natural killer cell function in dendritic cell-based vaccines. *Expert Rev Vaccines* 5: 55–65. doi:10.1586/14760584.5.1.55.