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PREFACE

The wide variation in the incidence and severity of infectious diseases among individuals in the same population and between populations may be (largely) due to variation in socioeconomic circumstances, human behaviour and variation in microbial virulence. However, host susceptibility and severity of infectious diseases in humans can also be linked to polymorphisms in the human genome. This 14th Kurhaus Workshop on Infectious Diseases explores several important examples of genetic polymorphisms that have recently been linked to host susceptibility and infection. Although much remains to be discovered in this field the evidence presented at this Workshop clearly pointed toward the future impact of genomic information in the management of infectious diseases in individuals as well as in public health.

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The role of mannose-binding lectin in health and disease

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ABSTRACT

Mannose-binding lectin (MBL) is an important element of the innate immune defence system. The protein binds to the sugars present on many microbial surfaces and subsequently activates the complement system through a family of specific proteases called the MASPs (MBL-associated serine proteases). Studies of MBL binding to selected Gram-negative organisms suggest that the lipopolysaccharide (LPS) structure is of primary importance. For a range of clinically relevant organisms MBL binding leads to activation and cleavage of C4 and C3, suggesting that this is a major pathway for opsonophagocytosis. MBL deficiency, resulting from three mutations in exon 1 and polymorphisms in the promoter region of the gene, is associated with both increased susceptibility to infections and autoimmune disease. Recent evidence indicates that the protein also modulates disease severity, possibly by influencing cytokine production.

INTRODUCTION

Mannose-binding lectin (MBL) is a pattern recognition molecule of the innate immune system.1 It belongs to a family of proteins called the collectins,2-4 in which lectin (carbohydrate recognition) domains are found in association with collagenous structures. In man these proteins include serum MBL, lung surfactant protein A (SP-A) and lung surfactant protein D (SP-D). Each of these proteins plays an important role in innate immune defence, but MBL is of particular interest because it is able to activate the complement system in an antibody- and C1-independent manner.

MBL STRUCTURE

MBL has a bouquet-like structure with many similarities to C1q. However, unlike C1q it can exist as dimers, trimers, tetramers or hexamers. All higher-order oligomers of MBL are based on subunits comprising three identical peptide chains of 32 kDa. Each chain is characterised by a lectin domain, an α-helical coiled-coil hydrophobic neck region, a collagenous region and a cysteine-rich N-terminal region.5,6 Three such chains interact to give a collagenous triple helix,7 but separate at the neck region to give three independent carbohydrate recognition domains.

MBL is a C-type (calcium-dependent) lectin that is able to interact with the 3- and 4-hydroxyl groups of various sugars, including N-acetyl-D-glucosamine, mannose, N-acetyl-mannosamine, fucose and glucose.8 The repeating arrays or patterns of sugar groups expressed on microbial surfaces make ideal targets for MBL binding, since the three sugar-binding sites of one subunit provide a flat platform with a constant distance between the individual binding sites (45 Å for human MBL).9 Because the Kd of each separate MBL-sugar interaction is relatively low (10⁻⁷ M)10 such simultaneous multiple binding is critical in order to achieve a high avidity.

MBL FUNCTION

The activation of complement by MBL represents a pathway which is independent of both the classical and alternative pathways, but which has similarities to the classical pathway. In the circulation MBL is found in association with
four structurally related pro-enzymes. These are the MBL-associated serine proteases (MASPs) 1, 2 and 3 and a truncated version of MASP-2 called MAP. In serum there is a 20-fold excess of MASP-1 over MBL and some evidence that the enzyme cleaves C3 directly. MASP-2, which is present at much lower concentrations than MASP-1, appears to be the more important in complement activation. The available data suggest that MBL – MASP-2 complexes become activated when bound to appropriate sugar arrays on microbial surfaces. The enzyme specificity of MASP-2 is apparently identical to that of Cl esterase and results in the sequential cleavage of C4 and C2. The C4b fragments generated bind covalently either to the MBL itself or to the nearby microbial surface and act as a focus for C2 binding/activation. The resultant C4b2a complex has C3 convertase activity and cleaves C3 in a similar manner to the C3 convertases of both the classical and alternative pathways of complement activation (see figure 1).

**MBL GENETICS AND POLYMORPHISMS**

Within the human collecting gene cluster mapped to 10q there is a single functional MBL gene comprising four exons. Exon 1 encodes the signal peptide, a cysteine-rich region and part of the glycine-rich collagen-like region. Exon 2 encodes the remainder of the collagenous region, whilst exon 3 encodes for the C-terminal carbohydrate recognition domain. The fourth exon encodes the C-terminal carbohydrate recognition domain. Upstream of the MBL gene are a number of regulatory, promoter elements which are believed to enhance MBL transcription approximately threefold during acute-phase responses.

MBL deficiency results predominantly from three single-point gene mutations in codons 52, 54 and 57 of exon 1 of the MBL gene. These are commonly referred to as the D, B and C variants, with A indicating wild type. The B variant mutation occurs in approximately 26% of Caucasians, whereas the C variant mutation is characteristic of sub-Saharan African populations in whom it may reach frequencies of 50 to 60%. Both the B and C mutations result in the substitution of a dicarboxylic acid for an axial glycine, and this impairs correct oligomerisation. In addition to the above structural gene mutations, several polymorphisms exist within the promoter region of the MBL gene. These polymorphisms are the H/L, X/Y and P/Q loci at positions -550, -221 and +4 of the MBL gene. The alleles expressed at these loci are in linkage disequilibrium and four promoter haplotypes (LXP, LYP, LYQ and HYP) are commonly found. Of these the HYP haplotype is associated with high MBL levels, whereas the LXP haplotype is found in association with low levels of the protein. The HXP haplotype has never been unequivocally identified.

The three structural gene mutations are also in linkage disequilibrium with the promoter polymorphisms and every individual expresses two of the following seven possible haplotypes – HYP, LYQ, LYQ, LXQ and HYPD. The frequencies of these haplotypes differ markedly between different population groups. Our observations on the distribution of the B and C alleles in African and non-African populations led us to suggest that the two mutations probably arose independently after the migration of hominids out of Africa some 100,000 to 150,000 years ago. It is of interest that none of these haplotypes has been proposed, including cClqR/calreticulin, ClqRp and Crt. However, it is unclear whether MBL acts as a direct opsonin for micro-organisms or simply enhances other well-established pathways of complement and/or immunoglobulin receptor-mediated phagocytosis.

![Figure 1](image-url)

**Figure 1**

*Mannose-binding lectin (MBL) complexed with the pro-enzyme MASP-2 is shown binding to a sugar array on the surface of a micro-organism*

The MASP-2 becomes activated and is able to cleave sequentially both C4 and C2. A complex of the major fragments of these components, C4b2a, is a functionally-active C3-cleaving enzyme (or C3-convertase) and is able to generate large amounts of C3b, an important opsonin.

The C3b generated by the MBL – MASP pathway is fed into the positive feedback amplification loop of complement activation and results in the deposition of large amounts of opsonic C3b on the microbial surface.

There is some evidence to suggest that MBL is able to interact directly with cell surface receptors and promote opsonophagocytosis and other immune processes. Several putative MBL-binding proteins/receptors have been proposed, including cClqR/calreticulin, ClqRp and Crt. However, it is unclear whether MBL acts as a direct opsonin for micro-organisms or simply enhances other well-established pathways of complement and/or immunoglobulin receptor-mediated phagocytosis.
of the three structural gene mutations were introduced into Australia at the time of first settlement (c. 50,000 years ago) whereas the B mutation was introduced into North America at the time of the last glaciation (c. 20,000 years ago). This suggests that the B mutation may have arisen between 20,000 and 50,000 years ago on the LYP promoter background.

**MBL BINDING TO MICRO-ORGANISMS**

We have used flow cytometry to study MBL binding to a range of clinically relevant pathogens isolated from immunocompromised children and found large differences. Some organisms such as *Candida albicans*, β-haemolytic Group A *Streptococci* and *Staphylococcus aureus* have consistently exhibited high binding, whereas others such as *Clostridium* sp., *Pseudomonas aeruginosa*, *Staphylococcus epidermidis*, β-haemolytic *Streptococci* Group B and *Streptococcus pneumoniae* appear not to bind the protein. In between are other organisms with more variable patterns of binding, such as *Klebsiella* species and *Escherichia coli*. In our present state of knowledge such heterogeneity is not readily explained, and it has prompted us to explore in more detail the determinants of MBL binding to bacteria.

To this end we have studied the effect of LPS structure on MBL attachment to both *Salmonella enterica* serovar Typhimurium and to the human pathogens *Neisseria gonorrhoeae* and *N. meningitidis* (serogroups B and C).

In particular, we have examined the relative importance of LPS structure and capsule in determining MBL binding to the serogroup-B meningococcus. It was observed that the absence of sialic acid from the LOS of *Neisseria meningitidis* serogroup B, serogroup C and *Neisseria gonorrhoeae* permitted MBL to bind to each of these organisms. In contrast, MBL appeared to bind very poorly or not at all to organisms with sialylated LOS. In the case of *Salmonella* species, organisms of the rough chemotype (not expressing the O-antigen) showed MBL binding whereas organisms with the smooth chemotype and expressing the O-antigen exhibited little or no MBL binding. These results suggest that LPS structure exerts a major influence on MBL attachment to bacteria.

**THE ROLE OF MBL IN DISEASE**

The immunological significance of MBL deficiency was initially established in children, but there are now numerous studies indicating a role for the lectin in later life and supporting the notion that it should be considered as an ante-antibody, a humoral factor playing a critical role in immune defence before the production of antibodies.

There is increasing evidence that MBL – disease associations are very complex. At present the topic may be considered under the following separate headings: (a) MBL and disease susceptibility, (b) MBL and disease severity and (c) inappropriate activation of the MBL – MASP pathway.

**MBL AND DISEASE SUSCEPTIBILITY**

Several studies have shown that deficiency of MBL is associated with an increased overall susceptibility to infectious disease. In terms of community health this may go some way towards explaining why some individuals suffer more infections than others. However, in a hospital setting it also appears that MBL deficiency has an important influence on the occurrence and duration of febrile neutropenic episodes in children with malignancy. In addition to such increased generalised susceptibility, other studies have identified an increased susceptibility to infection by specific pathogens in MBL-deficient individuals, including human immunodeficiency virus, *Plasmodium falciparum*, *Cryptosporidium parvum* and *N. meningitidis*. However, in the case of intracellular parasites (e.g. *Leishmania*) it appears that MBL deficiency may actually protect against disease. It is suggested that since such parasites exploit C3b opsonisation to facilitate uptake by the C3 receptors of macrophages and thereby gain entry to those cells, any reduction in the complement-activating function of the host may help reduce the probability of infection.

The most convincing evidence to date of such a mechanism is a study of patients with visceral leishmaniasis in Brazil. The median MBL level of these patients was significantly higher than that of healthy individuals and MBL mutations were significantly more common in the healthy controls.

In addition to the above reports of associations with infectious disease, there have been several investigations of possible associations between MBL deficiency and susceptibility to autoimmune disease. There is strong evidence of such an association in the case of systemic lupus erythematosus (SLE). Cohorts of British, Hong Kong Chinese, American Black and Spanish SLE patients have all shown evidence of an increased frequency of mutant MBL alleles or deficiency of the serum protein. The interpretation of these findings has usually reiterated the hypothesis proposed in relation to components of the classical complement pathway, namely that an impairment of the mechanisms involved in the removal of immune complexes may predispose to the development of autoimmune disease.
MBL AND DISEASE SEVERITY

In addition to the mounting evidence that MBL deficiency influences susceptibility to disease there have been several reports suggesting that the protein can also modulate disease severity. In the field of autoimmunity there is evidence of such a modulatory role for MBL, and recent studies from two centres have indicated that MBL variant alleles are associated with both severity and early onset of disease in patients with rheumatoid arthritis. \(^{10-11}\) The mechanism by which MBL exerts such effects is unclear but our recent studies on Neisseria meningitidis \(^{12}\) suggest that one possible pathway may be through cytokine modulation. When *N. meningitidis* organisms were incubated with increasing concentrations of MBL and added to whole blood from an MBL-deficient donor, the release of the cytokines TNF-α, IL-1β and IL-6 from monocytes was enhanced at lower MBL concentrations (<4 µg/ml) but reduced at higher concentrations (>4 µg/ml). Further work is required to establish whether this complex modulation of proinflammatory cytokine release occurs with other infectious organisms.

INAPPROPRIATE ACTIVATION OF THE LECTIN PATHWAY

Pathology associated with unregulated or inappropriate activation of the classical and alternative pathways of complement has been well documented over many years and it is to be expected that similar reports involving the MBL – MASP pathway will appear. At the time of writing there have been a small number of such studies in the fields of renal disease and reperfusion injury.

In one of the first studies in this area Endo and colleagues reported that MBL – MASP activation contributed to the glomerular damage observed in a significant number of patients with IgA nephropathy. \(^{13}\) However, in another study of renal biopsies from several patients with different forms of glomerulonephritis, Lhotta and co-workers claimed that the MBL deposition observed was of minor importance. \(^{14}\) Subsequent studies have described MBL deposition in the glomeruli of a patient with poststreptococcal glomerulonephritis \(^{15}\) and in ten patients with Henoch-Schönlein purpura nephritis. \(^{16}\) Much further work is required to evaluate the role of the MBL – MASP system in these disorders.

Recently MBL depletion and anti-human MBL monoclonal antibodies have been used to establish a role for the MBL – MASP pathway in initiating the complement activation which occurs following hypoxia-reoxygenation of human endothelial cells. \(^{17}\) In a separate study from the same group the MBL – MASP pathway was shown to be activated in rats following myocardial ischaemia reperfusion, suggesting that it is implicated in the subsequent tissue injury. \(^{18}\) Blockade of the lectin pathway with inhibitory monoclonal antibodies protected the heart from ischaemia reperfusion, and suggests that this therapeutic approach should be explored in human patients.

REFERENCES


Discussion following lecture by M.W. Turner

Verbrugh: This topic is now open for discussion. I would first like to discuss the binding of mannose-binding lectin (MBL) to the surfaces of micro-organisms, one of the first observations that you talked about. There was quite some heterogeneity in binding between species of micro-organisms and within species. You did not say much about that, except that there was some focal site of binding, but is there anything else that you or anybody else in this room may add on that phenomenon? Because that seems to be important for MBL’s mode of action.

Turner: Well, we have looked at both Neisseria meningitidis B and C and a range of isogenic mutants of salmonella. The bulk of the work that has been published has been done in those organisms. There is a consistent story that the presence of sialic acid strongly inhibits the binding of MBL. But there are problems with some organisms regarding the expression of sugars. Sometimes there will be a terminal sugar accessible that ought to bind MBL and yet we do not see any binding. So I must say that there is still an awful lot of work to be done. We cannot simplistically take the sugar structure that has been published for a particular organism and say with any certainty, without doing the experiments, that MBL will bind or not. The fact is that sugars are not fixed in space. They are waving around and there are all sorts of stereo configurations that need to be taken into account. It is more complicated than simple linear sequences would suggest. Not a very satisfactory answer, but I am afraid that is the way it is.

Verbrugh: Because microbes are also rather dynamic structures where cell walls are broken down and synthesised, and you do show some binding at certain sites of the cell surface, but not at other sites, that may have to do with the structuring of the cell wall at the time in that organism.

Turner: I should also say, by the way, that the flow cytometry is not that sensitive, because when we came to do the immuno gold staining, we found that the sialylated parent organism of Neisseria meningitidis serogroup B did show some foci of binding but in much lower numbers and with the serogroup C, the 8026 mutant, which we can exogenously sialylate. We have data showing that a little bit of binding does occur. So obviously, whatever one says about the flow-cytometry results, one has to bear in mind that there is a sensitivity issue there and that one can push that a little bit further by using better techniques.

Van Strijp: One thing that would be far more sensitive is looking at it functionally. Is there complement activation, yes or no? Is there a correlation between the binding assay and complement activation in all of these organisms that you showed?

Turner: That is a good question. First of all, two things we always do are to worry a bit about the possibility that the binding we see may be going in the opposite direction and that there is some lectin on the surface of the organism recognising a sugar on the MBL, because it is a sugar-bearing molecule itself. So we always do an EDTA chelation experiment to show that the binding is a calcium-dependent one. And we always do an inhibition with an inositol glucosamine or mannose and show that that competes. So we have two controls in all these systems to help us confirm that it really is a C-type lectin interaction. Whenever we looked for C4 binding, which we can do with purified C4, we always found an absolute correlation. If it binds MBL, we can go on. We have got data to show those strains which bind MBL, bind C4, and there is a strong correlation between the levels of binding, so the answer is, yes, there is a correlation. We have yet to see an exception to that.
Van Strijp: There are people stating that the old-fashioned alternative pathway may no longer exist and that most of it is mediated by MBL. Do you think that is true?

Turner: The thing about the alternative pathway, the real important point about it, is the amplification loop, which certainly exists. I think the only point at issue is whether there is circulating this small amount of precleaved C3 which will pick up factor B. Even Peter Lackman, who was very positive about that concept in the 1980s, was very happy to think that it might well be MBL causing some of that entrée into the system. I do not have a strong view on that, but I think the fact is that both MBL-associated serine proteases (MASP) and MBL have been shown in quite primitive organisms, and even in urochordates all the MASP proteins are present. So it is an ancient system, there is no doubt about it. Whether or not there is a separate mechanism whereby organisms can become coated by alternative pathway components without MBL playing a role, I do not know.

Degener: In your experiments you have probably worked with MBLs in a solution with a bacterial inoculum, but in the human body, or in the animal experiment, where does the binding take place then? Is that at the level of mucous membranes or is there anything more needed before the binding to MBLs takes place, for instance adherence of bacteria to a membrane?

Turner: We can say that the protein is essentially an intravascular protein most of the time, but in the presence of inflammation it certainly gets extravascular. It is present in the synovial fluids of rheumatoid arthritis patients for example, it is present in jejunal secretions of AIDS patients with cryptosporidial diarrhoea. We made Western blots of such aspirates and proved MBL to be there. So it gets to some mucosal surfaces when there is inflammation, but I do not think it would normally be present at such sites. Two other members of the same family, the collectin family, are lung surfactant protein A and protein D. Many like to think of them as innate immune equivalents of IgA on mucosal surfaces. The other area where there has been some work suggesting it might get into mucosal surfaces is with cystic fibrosis, because again you would not expect it to play any role at all in that disease. But there are data to suggest that it does get into alveolar fluids.

De Vries: You said that there might be some discussion about the suggested selective advantage for the mutations. And you had two possible explanations. One was the decreased complement-mediated immunopathology and the other was the decreased invasion of intracellular parasites. Those are quite testable hypotheses. Is there any data on the subject?

Turner: Well, on the question of the parasites there was a paper in Infection and Immunity last year from Alan Ezekowitz collaborating with a group in Brazil. MBL binding to Leishmania has been directly demonstrated to the promastigotes. But population studies in Brazilians with and without Leishmania support the concept that having the mutation protects against leishmaniasis. There is a small population study with that disease which does support it.

De Vries: That is the outcome. But is there any evidence in that study or in any other related study that the mutation decreases the invasion by Leishmania parasites for instance of macrophages?

Turner: Not that I am aware of.

De Vries: And about the complement-mediated immunopathology?

Turner: There is no direct data there, but there is with C6 deficiencies some very good work from South Africa. In the Cape C6 deficiency is very common among the coloured population. These people are more susceptible to Neisserial infections, but they are far less likely to die of those infections. Many years ago Ross and Denton suggested that this is a possible explanation of the fact that they are not activating the complement system through to the end of the lytic pathway, and therefore not releasing the mediators which are so damaging, and that this might be an advantage for them in their particular environment. So it is by analogy with that C6 deficiency story that this suggestion has been put forward. Obviously, MBL should be regarded as a complement component, there is no question about that. So it is not an outrageous extrapolation to think of it in the same sort of way, but there is no more direct supportive data.

Vandenbroucke: The mutation changes the structure of the protein, you said. I was wondering when you said MBL deficiency, because you also said that neutropenic patients have lower levels. What does this mean? Does it mean a less active MBL, or does it mean lower levels of protein?

In other words, if you want to study MBL deficiency, should we look at protein levels?

Turner: Good question. We believe that it is advantageous to both genotype and measure the protein levels. There is detectable protein in individuals with the mutations. But what there is not, is higher-order oligomers, which is absolutely critical for MBL function. If you cannot build it up to those higher-order structures, then you have a functional deficiency. But if you analyse what is circulating
by SDS page, for example, from someone who is homozygous for a mutation compared with my own MBL, which shows normal levels, you can see that there is a spike in the monomeric region in the person with the homozygous mutation and then a series of higher-order oligomers in my serum. So there is detectable protein there, but it is functionally lousy protein.

**Appelmelk**: The protein is evidently rather promiscuously binding to a variety of sugars. We as humans are full of high-mannose chains. So why are we not killed by MBL? When there is flexibility, you only need mannose. Why do we stay alive?

**Turner**: I think there are two possible answers to that. First of all, we tend to cap sugars with sialic acid on most cell surfaces. As a generalisation, I think you would agree that most oligosaccharide chains on human cell surfaces, protein oligosaccharides and so on, are terminating with sialic acid. Secondly, the sorts of characteristic repeating sugars that one sees on *Candida* for example, with mannan particularly, are much less commonly seen on mammalian cell surfaces. So the fact of the matter is, you have to have a repeating array of sugar groups. It is about this position and separation between them that the MBL is beautifully organised to respond to.

**Kullberg**: I am still intrigued by the *Leishmania* issue, because when there is a 40% incidence of polymorphism, one would think that there would be a strong selection pressure to keep these people in the population. Leishmaniasis obviously is not a disease that occurs everywhere, which would lead to this selection. So would not the *Leishmania* story act as a paradigm for other intracellular organisms? And the first one you would think of is *M. tuberculosis*, and maybe *Salmonella* may have a large impact. Are there any studies on that?

**Turner**: The reason why I have not discussed other organisms is because it is at this stage a rather confusing story. There are groups working on both *Mycobacterium tuberculosis* and leprosy, and initially the data seemed to be supporting the hypothesis, but I have recently examined a thesis from the University of Hong Kong. There was a large cohort of Chinese patients with tuberculosis, and instead of those individuals having the expected high frequency of wild-type MBL genotypes, in fact there was an increased frequency of mutations. It was against the hypothesis. I am again not going to put my neck on the block and say, I am totally wedded to the concept, because there are enough worrying stories coming through to make me a bit reserved on that front. Obviously, other diseases have also been considered: malaria was a candidate very early on because of its high incidence in Africa. The frequency obviously varies enormously around the world, as you saw, but what is very striking is that it is in the tropical regions of the world that we get the highest frequencies. I personally have not worked on this at all. I am just acting as a mouthpiece for some of the work of others. It is an extremely interesting question, because clearly the mutations have arisen independently of each other, the 57 and the 54 mutation, in different parts of the world and then both have risen to high frequencies in the population. It is quite a striking thing that that should have happened. It does not seem very logical that it is simply genetic drift, and that is really about as far as I can go at this stage. The malaria story is equally confused. There is one study by Bellamy in The Gambia which came to the conclusion that there was no strong association. Another study by a German group came to the contrary view. But that was in a much smaller cohort.

**Kullberg**: The other question is about the pathophysiology of this mechanism. Do we really know that the binding of a micro-organism like *Leishmania* and the subsequent invasion is the cause, or might it be that the macrophage activation is playing a role through differences in cytokine induction, which also would explain this fact?

**Turner**: I agree with you there.

**REFERENCE**

expression. IFN-β acts in an autocrine/paracrine manner to activate the transcription factor STAT1.10 TLR4-dependent STAT1 activation, in combination with NF-κB, results in the expression of several genes that mediate host responses against bacterial pathogens. These include iNOS, IL-12p40, IL-6, and several chemokines.10

Given the spread of drug-resistant Mtb strains, there is a pressing need to develop treatments that augment host innate immunity rather than to rely on new antibiotics. One novel approach would be to develop therapeutics that antagonise TLR proteins. This has been accomplished for one TLR4 agonist, Gram-negative bacterial lipopolysaccharide (LPS) and its pharmacophore lipid A. Three lipid A analogues, lipid IVA, Rhodobacter sphaeroides lipid A (RSLA) and E5531 have all been reported to function as LPS antagonists when tested both in vitro and in vivo.11-13 We subsequently demonstrated that RSLA could also block signalling by a TLR2 agonist, the mycobacterial glycolipid lipoarabinomannan.14 Together, these data suggest that certain lipid A structural antagonists are capable of blocking TLR-dependent activation by molecules that are chemically dissimilar to LPS. We later showed that the synthetic lipid

ABSTRACT

Mammalian toll-like receptor (TLR) proteins are pattern recognition receptors that mediate cellular activation by a wide variety of bacterial products. TLR activation leads to the expression of numerous mediators of innate immunity. We used the nonpathogenic mycobacterium M. bovis BCG (BCG) to define the roles of TLR proteins in the normal development of an immune response against the bacilli. We found that TLR2−/− mice were unable to effectively control the growth of BCG in vivo, compared with normal and TLR4−/− mice. Furthermore, splenic T cells isolated from infected TLR4−/− mice could proliferate in vitro following antigen challenge, but were unable to generate a strong Th1-type response. In contrast, splenic T cells isolated from infected TLR2−/− mice could neither proliferate in vitro following antigen challenge nor generate a strong Th1-type response. Together, these studies indicate that TLR proteins participate in the development of both innate and adaptive immune responses.

INTRODUCTION

Infection of macrophages with mycobacteria is accompanied by activation of the transcription factor NF-κB, secretion of inflammatory mediators (e.g. TNF-α, IL-1β), release of the reactive nitrogen intermediate nitric oxide (NO), and secretion of several chemokines.1 Until recently, the signalling pathways that elicit the production of these mediators have remained unknown. Members of the mammalian Toll-like receptor (TLR) family have been implicated in the activation of macrophages by a variety of chemically diverse bacterial products.2,3 We previously demonstrated that viable M. tuberculosis (Mt) bacilli contain distinct ligands that activate cells via TLR2 and TLR4, whereas heat-killed Mt failed to activate cells via TLR4.4 In contrast, M. avium appears to lack any TLR4 agonists.5 Several purified mycobacterial products have now been identified as TLR2 agonists, including arabinose-capped lipoarabinomannan,6 dimannosylated phosphatidylinositol,7 and the 19 kDa lipoprotein antigen.8 The identity of the Mt TLR4 agonist remains unknown. Interestingly, TLR2 agonists activate macrophages to express only some of target genes activated by TLR4 agonists.2,3 This difference is due, at least in part, to the capacity of TLR4 agonists, but not TLR2 agonists, to induce β-interferon (IFN-β) expression. IFN-β acts in an autocrine/paracrine manner to activate the transcription factor STAT1.10 TLR4-dependent STAT1 activation, in combination with NF-κB, results in the expression of several genes that mediate host responses against bacterial pathogens. These include iNOS, IL-12p40, IL-6, and several chemokines.10 Given the spread of drug-resistant Mt strains, there is a pressing need to develop treatments that augment host innate immunity rather than to rely on new antibiotics. One novel approach would be to develop therapeutics that antagonise TLR proteins. This has been accomplished for one TLR4 agonist, Gram-negative bacterial lipopolysaccharide (LPS) and its pharmacophore lipid A. Three lipid A analogues, lipid IVA, Rhodobacter sphaeroides lipid A (RSLA) and E5531 have all been reported to function as LPS antagonists when tested both in vitro and in vivo.11-13 We subsequently demonstrated that RSLA could also block signalling by a TLR2 agonist, the mycobacterial glycolipid lipoarabinomannan.14 Together, these data suggest that certain lipid A structural antagonists are capable of blocking TLR-dependent activation by molecules that are chemically dissimilar to LPS. We later showed that the synthetic lipid
A-like antagonist E5531 could block TLR4-dependent signalling induced by Mtb. E5531 could inhibit selected Mtb-induced macrophage responses, namely apoptosis and TNF-α secretion, but it did not block Mtb-induced NO production. Subsequent studies revealed that induction of NO production by Mtb was mediated by a TLR-independent mechanism and (unpublished observations). This underscores the concept that while purified bacterial TLR agonists can activate macrophages to express a variety of proinflammatory mediators in vitro, this is not predictive of TLR-dependent macrophage activation by intact bacteria. Here we have sought to determine the relative contributions of both TLR2 and TLR4 to innate and adaptive immune responses. In these studies we have used the nonpathogenic mycobacterium BCG to investigate the role of TLR proteins in host immune defence in vivo. We reasoned that the use of BCG would allow us to examine the contributions of TLR proteins to the normal development of host immunity in the absence of mycobacterial virulence factors that corrupt the normal development of these host responses.

**METHODS AND MATERIALS**

**Reagents**

*M. bovis* BCG (ATCC 35734) was purchased from the ATCC. Bacteria were grown in LPS-free Middlebrook 7H9 liquid medium, supplemented with AODC, Tween 80, and glycerol. Cultures were grown to a density of 0.5 to 0.6 (OD660). Numbers of BCG per ml of culture were determined by colony counting.

**Animals and cells**

TLR2<sup>−/−</sup> and TLR4<sup>−/−</sup> mice (female, 5 to 7 weeks old) were provided by Dr Shuzio Akira (Osaka University), and have been previously described. These mice had been previously backbred onto a C57Bl/6 background for four generations prior to their use in these studies. Inbred C57Bl/6 mice were used as control animals. Thioglycollate-elicited peritoneal exudate macrophages were isolated from uninfected mice, and cultured in vitro, as we have previously described. Each mouse was infected with 10<sup>6</sup> CFU of *M. bovis* BCG by intraperitoneal injection, and sacrificed 14 days later. Spleens were removed from the infected mice, and total splenocytes were prepared for culture in vitro, as previously described. Contaminating LPS levels in all media components were <10 pg/ml final concentration as measured by *Limulus* amebocyte lysate kit (BioWhittaker).

**Measurements of cytokine production by macrophages in vitro**

Peritoneal macrophages from TLR2<sup>−/−</sup>, TLR4<sup>−/−</sup> and normal mice were infected in vitro (5 BCG per macrophage) with live BCG for 18 hours. The culture supernatants were removed, filtered to remove any BCG, and then cytokine levels were measured using specific ELISA kits, as recommended by the manufacturer (R&D Systems and Pharmingen).

**Measurement of bacterial loads in the lung**

Lungs removed from infected mice were homogenised in a sterile blender, using a lysis buffer consisting of sterile water containing 0.025% SDS. Homogenates were diluted in the lysis buffer, and 1 ml aliquots were cultured on Middlebrook 7H11 agar plates supplemented with glycerol, L-arginine and cycloheximide (10 mg/ml). Colonies were counted 14 days later.

**Splenic T cell restimulation assay**

Spleens were recovered from uninfected and BCG-infected mice 14 days after inoculation. Total splenocytes were obtained by tissue disruption between sterile frosted glass slides, and erythrocytes were removed by lysis in Tris-buffered ammonium chloride (Sigma). Splenocytes were then cultured in 96 well plates (5 x 10<sup>5</sup> cells/well) in the presence or absence of heat-killed BCG (10<sup>3</sup> CFU/well). For proliferation measurements, splenocytes were cultured for two additional days and pulsed with [H] thymidine (1 mCi/well) eight hours prior to harvesting. Cells were harvested using an automated cell harvester (Skatron Instruments) and incorporation of radio labelled thymidine was measured by scintillation counting. For cytokine secretion, splenocytes were cultured for three additional days. Culture supernatants were then recovered and specific cytokine levels measured by ELISA.

**RESULTS AND DISCUSSION**

**TLR proteins are necessary for specific macrophage responses to BCG in vitro**

Peritoneal macrophages from TLR2<sup>−/−</sup>, TLR4<sup>−/−</sup> and normal mice were infected in vitro with live BCG for 18 hours. Cytokine levels in the culture supernatants were measured using ELISA and the Greiss assay respectively. As shown in figure 1, BCG-induced TNF-α and IL-6 secretion was substantially lower in the TLR2<sup>−/−</sup> macrophages compared with both TLR4<sup>−/−</sup> and normal macrophages. In contrast, secretion of IL-12p70 was similar in BCG-stimulated macrophages from all three mouse strains examined. This suggests that TLR2, but not TLR4, is necessary for BCG-induced TNF-α and IL-6 production, whereas IL-12 production does not depend on these TLR proteins. In these experiments, TNF-α production was strongly dependent on the presence of TLR2. Numerous investigators have shown that TNF-α expression in macrophages can be induced using purified TLR2 agonists. Intact bacteria,
different mycobacterial species are likely to dictate which TLR protein is most necessary for the induction of TNF-α expression. We had previously shown that Mtb possesses both TLR2 and TLR4 agonists, and that blocking TLR4 signalling with the lipid A-like LPS antagonist E5531 largely blocked TNF-α secretion induced by Mtb. In contrast, M. avium does not appear to be capable of activating cells via TLR4. It has been reported that BCG possess both TLR2 and TLR4 agonists, but the relative abundance of these agonists had not been determined. We hypothesise that BCG express lower levels (or fewer types) of TLR4 agonists than Mtb. Similarly, BCG may express higher levels (or more types) of TLR2 agonists, compared with Mtb. In either case, this could explain why TLR4 is not necessary for macrophage activation by BCG. In contrast to TNF-α and IL-6, IL-12 secretion by BCG-stimulated macrophages did not depend on the presence of TLR2 or TLR4. This finding was unexpected, but is reminiscent of Mtb-induced NO production, which is independent of TLR proteins. It remains to be formally determined whether BCG-induced IL-12 production, like NO production, is also mediated by a TLR-independent mechanism.

TLR2 is necessary for resistance to mycobacterial infection in vivo

TLR2−/−, TLR4−/− and normal mice were infected with live BCG for 14 days. The lungs were then removed and the number of bacteria in the tissues was counted. As shown in figure 2, the lungs from infected TLR2−/− mice contained more BCG bacilli than lungs from TLR4−/− and control mice.

Figure 1
Cytokine production by normal and TLR-deficient macrophages stimulated with BCG

Thioglycollate-elicited peritoneal macrophages (5 x 10⁵ cells/well) from wild-type, TLR2−/− and TLR4−/− mice were stimulated with live BCG (five bacilli/macrophage) for 24 hours, and supernatants assayed for TNF-α (A), IL-6 (B) and IL-12p70 (C) by quantitative ELISA. Data are presented as the mean values of triplicate wells ± SD. Results are representative of duplicate experiments.

Figure 2
Bacterial loads in the lungs of normal and TLR-deficient mice infected with BCG

Normal and TLR-deficient mice were infected intraperitoneally with 10⁶ CFU M. bovis BCG, and the lungs were harvested 14 days later. Lung homogenates were then prepared, diluted, and cultured on Middlebrook 7H11 agar plates for colony counting. Data are presented as mean of lung CFUs from three mice per genotype ± SEM. Results are representative of duplicate experiments.
Both normal and TLR4-deficient mice were fully capable of controlling the infection. Thus, the absence of TLR2 led to permissive growth of BCG in the lung. This finding is consistent with the inability of TLR2-/- macrophages to secrete substantial amounts of TNF-α following BCG challenge in vitro (figure 1). Studies performed using TNF-α/-/- mice have demonstrated the importance of TNF-α in controlling mycobacterial growth in vivo.21 It remains to be determined whether diminished production of TNF-α is responsible for the lack of mycobacterial growth control in the TLR2-/- mice. These data do indicate that TLR2 is necessary to generate an effective host response against mycobacterial infection. These findings do not completely exclude a role for TLR4 in the host response against mycobacterial infection. Our studies shown here used a background mouse strain that is genetically resistant to mycobacterial infection (i.e. C57Bl/6), as well as a relatively low inoculum of BCG. Preliminary studies performed using a mouse strain that is genetically sensitive to mycobacterial infection and lacks functional TLR4 (i.e. C57H/HeJ mice) have revealed that TLR4 does indeed contribute to the resistance to BCG infection in vivo (SN Vogel and MJF, unpublished observations). Furthermore, this protective role for TLR4 was only observed using a higher inoculum of BCG (>10⁷ CFU/mouse).

Splenic T cells from both TLR2-/- and TLR4-/- mice fail to generate a potent Th1-type response in vitro

In order to characterise TLR-dependent control of BCG growth in vivo, we sought to determine whether TLR-deficient mice failed to elicit an effective innate and/or adaptive immune response following BCG infection. To test these possibilities, we isolated total splenocytes from uninfected and BCG-infected normal and TLR-deficient mice. Splenic T cells were then stimulated in vitro with heat-killed BCG as a source of antigen. Activation of the T cells was assessed 48 hours later by measuring both cytokine production and T-cell proliferation (3H thymidine incorporation). As shown in figure 3, splenocytes isolated from uninfected mice did not respond to antigenic stimulus, as measured by either cytokone production or T-cell proliferation. In contrast, normal splenocytes from infected normal mice secreted IFN-γ following antigenic stimulation. This IFN-γ production was not observed using splenocytes from infected TLR2-/- or TLR4-/- mice. These findings suggest that TLR-deficient splenocytes fail to develop a potent Th1-type response in vitro. We do not believe that this failure to secrete IFN-γ represents a skewing of Th responses, as antigen-stimulated splenocytes from infected normal and TLR-deficient mice did not secrete measurable amounts of IL-4 or IL-5 in vitro (data not shown). In subsequent studies, we examined T-cell proliferation in vitro and observed that cells from normal and TLR4-/- mice proliferated in response to antigenic stimulation, whereas cells from TLR2-/- mice did not (figure 3B). Taken together, these data suggest that TLR2 and TLR4 contribute in a fundamentally distinct manner to the development of an effective Th1 response. Antigen-specific T cells are generated in BCG-infected TLR4-/- mice, as indicated by the proliferation of these cells in vitro following antigenic challenge. Nevertheless, these T cells fail to develop into effective Th1 responder cells, as indicated by the absence...
of IFN-γ secretion. This is not a consequence of skewing towards a Th2 phenotype, as there is no increase in IL-4 and IL-5 production by the antigen-stimulated TLR4−/− splenocytes. Thus, the immune defect in these cells appears to come from the inability of Th0 cells to commit to a Th1 phenotype. It should be noted that the absence of a strong Th1 response did not detract from the ability of TLR4−/− mice to control BCG infection in vivo (figure 2). This may be due, in part, to effective innate immunity (as evidenced by normal proinflammatory cytokine production, figure 1) additional to Th1-independent adaptive immunity. Furthermore, Th1 responses may not be absent in these mice, only diminished relative to control animals.

The finding that TLR2−/− splenocytes failed to both proliferate and secrete IFN-γ following antigenic challenge in vitro contrasts with the phenotype of the TLR4−/− cells. The BCG-infected TLR2−/− mice appear to possess a defect in the development of antigen-specific T cells. The inability of TLR2-deficient cells to secrete IFN-γ would then simply be a consequence of the lack of antigen-responsive T cells, rather than (or in addition to) a defect in Th1 commitment. This possibility is consistent with our finding that antigen-independent activation of TLR2−/− splenocytes, using cross-linked anti-TCR antibodies, induced both T-cell proliferation and IFN-γ secretion (data not shown). We do believe that TLR2−/− mice are capable of developing antigen-specific T cells, and published data report that these mice contain normal numbers and types of immune cells.16 Taken together, our data suggest that the absence of TLR2 renders the mice incapable of responding to the adjuvant activity manifested by the mycobacteria themselves. This adjuvant activity is critical for the development of T cells that recognise mycobacterial antigens, and for the host to mount an effective adaptive immune response. Because TLR2−/− macrophages fail to secrete critical proinflammatory cytokines in response to mycobacterial infection in vitro, it is likely that these cells also fail to express critical cytokines and co-stimulatory molecules in vivo during the course of infection. Dendritic cell maturation and function may also be defective in TLR2−/− mice due to the inability of these cells to respond to mycobacterial TLR2 agonists. Several laboratories have previously shown that TLR agonists induce dendritic cell maturation and activation.21,22 Furthermore, those dendritic cells that are incapable of responding to TLR agonists fail to mature and become functional in vitro.23 Studies are currently underway in the laboratory to characterise the immune defects observed in TLR2−/− and TLR4−/− mice.

REFERENCES

Van der Meer: I enjoyed that very much. Just to go back to the concept of the Toll-like receptor (TLR) as first line of response, can you tell us a bit more about the molecular interaction between bacterial components and TLR? Do they actually bind, and if so, how?

Fenton: Some of you may have noticed that I tried to stick to the word ‘agonist’ rather than to the word ‘ligand’. That is not a mere coincidence. With the exception of Gram-negative bacterial lipopolysaccharide (LPS) there has really been no clear biochemical demonstration of any of these molecules serving as classic ligands and we have little sense of what the affinity of ligands for these receptors is. In the matter of LPS, Richard Ulevitch’s lab and a few others have sought to demonstrate a physical interaction in using cross-linking approaches. They have been able to show a physical association between Gram-negative LPS and TLR4 in the presence of the coreceptors CD14 and MD2. If you transfected the cell with an expression plasmid encoding TLR4 in the absence of the coreceptors CD14 and MD2 you basically have to throw in milligram amounts of LPS to get an activation. So from the point of view of ligand-receptor interaction all these Toll-receptor agonists are very poor ligands by themselves. They probably operate in the context of a larger receptor complex that includes coreceptors such as CD14. I think it is reasonable to assume that there are a variety of coreceptors that may help TLR2 agonists or TLR9 agonists to also recognise the receptors and engage a signal. The other part of this paradigm relates to how strongly the receptor is engaged and what the kinetics of this interaction are. Several studies that have been published using FACS analysis to look at receptor complex interaction have shown that, if you use FITC-labelled LPS as your classic ligand, you can demonstrate a rapid and transient interaction between LPS, TLR4 and CD14. But interestingly, a few seconds or minutes after this initial interaction and activation the receptor components seem to move to different places on the cell and in some cases some of the components are internalised. Many of you here are familiar with Sam Wright’s work and the story of LPS internalisation. I think that if you take this together for LPS it suggests that there is a multireceptor component that is not assembled and only engaged on the cell surface for a very short period of time to allow a signal to be generated. The receptor components then disassemble and go elsewhere following the activation. There does not seem to be a strong high-affinity interaction between TLR proteins and any of their agonists in the absence of coreceptors.

Hermans: I have a question about the polymorphisms that are known to occur both in TLR4 and TLR2. In TLR4 there are amino acid substitutions known to lead to hyporesponsiveness. But as far as I am aware they do not show much of a link with the severity of or susceptibility to infectious diseases.

Fenton: As far as I am aware there is not a strong correlation in this case between TLR4 mutations and susceptibility to disease. In experimental models with normal human volunteers looking at the susceptibility to LPS by inhalation, David Schwartz has been able to show a correlation between certain polymorphisms in TLR4 and hyporesponsiveness of humans to LPS. But at least so far there does not seem to be an increased incidence of disease. The very few studies that have been published so far looked at the extracellular domains of the Toll-like receptor proteins. Most of the work today is focused on the intracellular domains looking at intracellular signalling. Some new studies in the Journal of Immunology have shown that the extracellular domain of TLR4 possesses a hypervariable domain and most of the polymorphisms seen in different human populations or amongst different species seem to cluster in this hypervariable region. It does seem to have an impact on the ability of TLR4 to recognise LPS or different forms of LPS as well. So we are beginning to get a sense of where within the molecule recognition really occurs, but so far the correlation with disease has been minimal.

Ottenhoff: I have a question about the IL-12. You said that TLR2 knock-out mice produce normal IL-12 upon BCG
stimulation. In vitro there is little interferon-α production. So my question actually is, what is the mechanism to explain that?

Fenton: That is a good point. Dr van der Meer said last night at dinner that we were supposed to expose all of our Achilles heels to the panel today. So it turns out to be a very complicated story. You really need to approach it from three different angles. One is to look at the question of how purified TLR agonists induce specific responses in macrophages in vitro. The next would be then to look at the whole bacterium as well, because those responses are going to be very different. A great example of this is if you look at nitric oxide (NO) production induced by mycobacteria. I am a bit slow maybe in getting to the answer to your question, but you can add purified LPS for example as a classic TLR4 agonist and show that you can activate nitric oxide production and that occurs through the TLR4 pathway. If you then use live mycobacteria to induce NO it turns out that in that setting it is a TLR-independent process that drives the NO production. We published those results a few years ago. So you have got to try to keep the two pathways apart. With the data I showed for IL-12, we have not yet determined whether the IL-12 production is dependent on TLRs or not in that setting. It may be in the setting of whole live mycobacteria that the macrophages do not need TLRs to make IL-12. Experiments are going on right now in the laboratory to determine that. Now in vivo you would have expected that the presence of IL-12 would have correlated with a fine ability to produce γ-interferon. So I think that is going to be the biggest Achilles heel of the data I showed you today, which are all unpublished and very preliminary, which is why do we see good IL-12 production and not good γ-interferon production? I think the reasons for that can differ for the two kinds of mice. In the case of the TLR2 knock-out mice, I think we are failing to get γ-interferon production because we failed to develop a large panel of antigen-specific T cells. The T cells are just not there. You can give them all the IL-12 you want and they will not do anything with it. The TLR4 knock-out animal is a bigger mystery because we – presumably – have antigen-specific T cells there but they are not making γ-interferon. I think part of that answer comes from the process of a Th0 cell maturing into a Th1 cell. So one possibility is that in the absence of TLR4 we are unable to fully activate the development of a commitment to the Th1 phenotype. I should point out that we do not have Th skewing here. We are not skewing the animals towards Th2. There is no production of IL-4 and IL-5 in these TLR4 knock-out animals. We therefore think that there is a defect in Th1 commitment and we are testing that possibility now. The other issue may be a threshold issue. We have not looked at IL-18 or at IL-23 as other components of these three cytokines leading to γ-interferon production. It may be that again we have plenty of IL-12 but not sufficient IL-18 and IL-23 to lead to a threshold of γ-interferon production. Lastly, in the C3H/HeJ model, where we now have a higher infective dose and we do see disseminated bacterial growth when you look at IL-12 levels in the serum of these mice, you do find in this case that the IL-12 levels in the animal are lower. I think that under those conditions we are seeing a correlation and γ-interferon levels are way down in these animals as well. So under the right conditions we can see it. All I can say to answer your question directly is that the splenocyte assay gives us an answer with regard to T-cell responses in the dish, but I do not think that it will really surprise anyone here that that does not necessarily correlate with what happens in vivo.

Netea: I have two questions. One is going back to the coreceptors for TLRs. When you mentioned all the TLRs and the agonists that are known, you did not include TLR6 and TLR1. They are described as possibly serving as coreceptors. Do you think that there are two classes of TLRs? TRLs which are really signalling and TLRs which are coreceptors? That is my first question, and a second one relates to the Toll reacting to Spätzle, an endogenous substance in Drosophila. In humans most of the data are done in the context of pathogens and we get more or less the same signals as in the context of IL-1 stimulation. My question is, why do you think that we also need an IL-1 system? We do have more or less the same intracellular signalling going through TLRs. Do you think that we in fact developed a kind of intention to amplify our TLR system by using IL-1?

Fenton: The TLR2 and coreceptor question is of course an important one. Those of you who are familiar enough with the data will probably agree that TLR2 probably does not work alone. TLR proteins probably function as dimers. In the case of TLR2 it probably functions only as a heterodimer in association with either TLR1 or TLR6. We do not have any data so far to answer the question whether TLR2-dependent responses also utilise TLR6 vs TLR1, so I cannot answer that question. In terms of whether they are coreceptors or actually contribute differently to the signalling in the intracellular responses, it is quite likely that they will. I think that if you look at responses mediated through TLR2.1 vs 2.6 you are likely to find some differences. Most people who have looked at TLR-dependent responses have focused on a similar set of cellular responses such as IL-6 or TNF production, IL-1 production. Those seem to be shared in common with all of the TLR receptors. It is only when you begin looking at different responses that you start to see differences: for example our findings that TLR4 engagement leads to type-1 interferon production, but engagement of TLR2
does not. I think you are likely to see differences between TLR2.6 and TLR2.1, but the data have not been published in that regard. It is also – just before I leave the topic of coreceptors – quite likely that non-TLR coreceptors are going to be involved as well. I think there is indirect evidence to support complement receptors as being Toll coreceptors, perhaps the macrophage mannose receptor or the scavenger receptor, maybe even certain Fc receptors as well.

To answer your second question, I think it ties in a bit to what I have just said, which is that there are certain common responses that seem to occur when you activate all of these receptors, not only all of the TLR receptors but also the IL-1 and IL-18 receptors. But clearly the functional responses of the cells are different. You can induce for example apoptosis in some cells triggered through TLR4, TLR2, but certainly not in cells stimulated through IL-1 or IL-18. So as usual the devil is in the details. There are certain responses that seem to be Toll dependent and certain responses that are specific for Tolls and not for IL-1 or IL-18 receptors. So what does that mean in the big picture of the biology? I think that like the IL-1 and IL-18 receptors, Toll receptors play an important role in the inflammatory response. The inflammatory response as a result of a pathogen invasion, but perhaps an inflammatory response mediated by endogenous factors as well. There certainly is an amplification loop going on here. IL-1 and IL-18 production is certainly going to be important in maintaining the inflammatory response and the duration of the response, and there is also the likely possibility that endogenous factors are being made that feed back into the Toll receptors themselves.

You pointed out the ligand for the Drosophila Toll, the Spätzle protein. Spätzle is produced and cleaved and feeds back into the Toll itself, but just as in the mammalian Toll agonist, no-one has actually demonstrated Spätzle binds as a ligand to Toll. It is all indirect evidence that supports that hypothesis. There are some studies suggesting that mammalian proteins can feed back into Toll receptors, heat-shock proteins being an important example. Cells that are damaged in the course of bacterial invasion may release these heat-shock proteins, they may be an endogenous danger signal as well. There is no evidence that these proteins can recognise IL-1 or IL-18 receptors. So I think we can draw a series of circles some of which will overlap. I think the IL-1 and IL-18 receptors and the Toll receptors play similar roles in the development and maintenance of inflammation. But I think they also play highly specific roles depending on the type of pathogen and the type of response and whether it is an organism possessing TLR4 antigens or not. I think it is almost as if we can say that the innate immune response is adaptive in that it can recognise a variety of different motives through this large variety of different TLR proteins that are available.
Human Fc receptor polymorphisms in relation to bacterial infection

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ABSTRACT

Human IgG receptors are very heterogeneous. Currently there are three Fc gamma receptor classes specifying at least 12 receptor isoforms to be distinguished. On top of this complexity, Fc gamma receptors (FcγRs) differ between different individuals. Polymorphisms have been identified for two FcγR classes, representing allelic variation of the FcγRIIa (CD16), FcγRIIIa and FcγRIIB (CD16). The FcγRIIa polymorphisms are now considered to be a heritable risk factor for infectious diseases and some manifestations of autoimmune disorders. A relevant role of the IIIb polymorphism in infectious disease has been suggested, though less convincingly. Detailed analysis of the exact contribution of each of these polymorphisms in relation to previously implicated risk factors for infectious or immunological disease should unravel the pathophysiological contribution of FcγR polymorphisms in the wide variety of factors now being investigated. The information obtained about the multiple genes that impact inflammatory responses of the host – and most likely in reaction to exogenous triggers and pathogens – is becoming overwhelming. The rapid development of molecular techniques makes it possible to determine the incidence of all these individual genetic polymorphisms. Although its relevance will be more difficult to ascertain, the information on all the different genes and their allelic variations involved in the host immune response will be very important for our understanding of infectious disease in modern times.

INTRODUCTION

Human genomics and the rapidly growing insight into the host inflammatory response explain the increasing interest in infectious disease genetics over the last five to ten years. Host genetic factors are major determinants of susceptibility to infectious diseases in humans. Candidate gene studies by association and human genome-wide analysis have been used to identify susceptibility and resistance genes in infectious diseases. However, a single gene defect has rarely been directly related to a devastating disease, such as interferon-gamma receptor (IFNγR) or interleukin-12 receptor (IL-12R) mutations leading to severe or fatal infections with mycobacterial strains. In clinical terms, gene polymorphisms of the host immune defence factors appear to have a much broader role and contribution to health and disease. These genetic variants, which modify the regulation or function of the mediators, have been associated with susceptibility to and/or outcome of severe sepsis and septic shock. All steps of the host response to bacteria may be affected by genetic factors. For example, Fcγ receptors (FcγRs), Toll-like receptors (TLRs), CD14 and mannose-binding lectin (MBL) mutations have all been shown to modify the host detection of pathogens leading to pneumococcal infections, Gram-negative bacteria septic shock, and meningococcal disease. Polymorphisms of cytokine genes (TNF-α, IL-1 receptor antagonist (IL-1RA), IL-10, etc.) have been reported to influence the level of secreted mediators and to unbalance the inflammatory cascade. Coagulation response to sepsis may also be affected by gene variants such as the plasminogen activator inhibitor 1 (PAI-1) common functional polymorphism that increases the risk of death from meningococcal infection. In this paper we will largely focus on the contribution of FcγRs in infectious disease.

PHAGOCYTES

The expression of FcγRs is limited to cells of the haematopoietic lineage (table 1). The consequence of IgG binding
to these receptors varies among the cells in relation to their primary function. In the case of infectious disease, it is clear that the phagocytes have the greatest impact on clearance and elimination of bacterial and fungal pathogens, both from tissues and the circulation. The professional phagocytes to be distinguished are mainly formed of neutrophilic granulocytes, monocytes and monocyte-derived tissue macrophages. Neutrophils constitute the major type of leucocytes in peripheral blood, with counts ranging from 40 to 70% under normal conditions. Neutrophils contain numerous proteases and other proteins in their granules and can produce – when activated – a large quantity of toxic oxygen metabolites through the NADPH oxidase activity to kill tissue-invading pathogens. Neutrophils protect our bodies against so-called extracellular bacterial and fungal micro-organisms, whereas the macrophages are particularly involved in and equipped for the killing of intracellular pathogens. Neutrophils have a high turnover rate. Once these cells have egressed from the bone marrow, their half-life in the peripheral circulation is about six to eight hours before they leave rather randomly into the extravascular tissue where the neutrophils roam for another 24 hours. In the case of inflammation, circulating neutrophils sense the site of infection, rapidly extravasate and crawl in large quantities towards the invading micro-organisms to ingest and kill them. During an infection monocytes follow only later to perform the role of scavenging cell, to engulf the remaining apoptotic neutrophils, and to prepare the local environment for recovery from the tissue damage inflicted during the first wave of neutrophil-mediated inflammation. Macrophages are tissue-dwelling cells derived from monocytes with an estimated half-life of three to four months. Macrophages can be found in any organ or tissue, though in different forms and endowed with different functions. These cells are well situated and actively involved in liver and spleen clearing the blood compartment from aged cells, oxidatively damaged material, as well as filtering out any bacterial pathogen that escaped the defence system of skin or mucosal lining, including the destructive power of tissue-infiltrated neutrophils. Thus, for proper functioning of this first line of defence by phagocytes, a number of prerequisites have to be fulfilled.

### PHAGOCYTOSIS AND MICROBICIDAL ACTIVITY

Phagocytes operate in concert with antibodies and complement factors, so-called opsonins. Micro-organisms covered with these opsonins are bound through specific receptors for these opsonins on the plasma membrane (table 1). Antibodies bind with their Fab regions to microbial antigens. In this way, the Fc regions of these antibodies are closely packed together. This spatial arrangement enhances complement activation, thus leading to binding of C3b and C3bi to the micro-organisms and subsequent binding of the microbes to the complement receptor type 1 (CR1)
and complement receptor type 3 (CR3) respectively. On the other hand, the proximity of the antibody Fc regions also promotes direct binding of the opsonised micro-organisms to the Fc receptors on the phagocytes.\(^5\)

Two types of Fcγ receptors are present on neutrophils: FcγRIIa and FcγRIIb. Only after long-term activation of neutrophils by interferons or growth factors is a third Fcγ receptor expressed, i.e. the FcγRI, which binds monomeric IgG with high affinity (table 2). In contrast, the constitutively expressed FcγRIa and FcγRIIIB bind monomeric IgG only with low avidity, but can efficiently bind immune complexes containing multiple IgG molecules. A polymorphism in FcγRIIa defines the intrinsic ability to recognise all four IgG subclasses or not. IgG2 antibodies, often formed as the most predominant IgG subclass of antibodies against the microbial carbohydrate structures, only react with the so-called L131 type of FcγRIIa (with a leucine at amino acid position 131). As will be discussed later, it is generally assumed that individuals with this isotype are better protected against infections with certain micro-organisms than individuals with the R131 type of FcγRIIa (arginine at position 131).

FcγRIII has two variants, a transmembrane form (FcγRIIIa) expressed on macrophages and natural killer cells, and a neutrophil-specific form (FcγRIIIb) linked to the plasma membrane by a lipid anchor, which allows very rapid redistribution and early localisation of opsonised material. Although there is a polymorphic site in the FcγRIIIB on neutrophils (NA1/NA2 depending on differences in glycosylation), its effect on clinical outcome is as yet not as clear as in the case of the FcγRIIa. In contrast to all other transmembrane FcγR members, the FcγRIIIB on neutrophils can be rapidly shed from the membrane during functional activation or during the process of programmed cell death (apoptosis) in the tissues. The presence of soluble FcγRIIIB plasma in combination with its relatively long half-life renders this molecule a prime candidate for the estimation of total neutrophil mass.\(^5\)

Monocytes express the FcγRI and FcγRIIa whereas macrophages show FcγRI, reduced FcγRIIa and a high level of FcγRIIIa. FcγRIIa has two polymorphic sites of which the FcγRIIa-158/V/F allotypes show some functional influence on the avidity of IgG subclass binding, of IgG4 in particular. The FcγRIIa-V/F158 allelic variation possibly influences autoimmune disease in its presentation, course and outcome. Even in one type of disease, the published data of groups of patients with various racial backgrounds are contradictory or at best inconclusive.\(^8,9\)

Studies on the inhibitory action of FcγRIIIB were largely limited to B-cell functions. With the current insight from experimental FcγRIIIB-knockout models,\(^10,11\) its expression on macrophages (and other phagocytes) and – as a consequence – its impact on the outcome in inflammatory responses as well as on the efficacy of intravenous immunoglobulin infusions in an experimental model for immune thrombocytopenia\(^12\) has been demonstrated. The precise working mechanism of the disease-mitigating role of FcγRIIIB should be elucidated in the near future, also in human disease.

**MICROBICIDAL ACTIVITY**

Binding of opsonised material to surface receptors leads to concentration of such receptors around the area of contact. Subsequently, the cell extends pseudopods that engulf the particle. By consecutive receptor binding, these pseudopods fit tightly around the particle and finally fuse with each other to form a closed membrane vesicle (phagosome) around the particle, within the phagocyte. Neutrophils may overeat themselves in infected areas and die of congestion. Macroscopically, this is manifested as pus formation. Apart from phagocytosis, receptor binding may also start two other processes, i.e. the generation of reactive oxygen compounds and the release of granule

---

Table 2  
*Function of Fcγ and complement receptors on phagocytes*

<table>
<thead>
<tr>
<th>NOMENCLATURE</th>
<th>EXPRESSION</th>
<th>LIGAND</th>
<th>PHAGOCYTOSIS</th>
<th>MEDIATOR RELEASE</th>
<th>CYTOTOXICITY</th>
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</thead>
<tbody>
<tr>
<td>FcγRI (CD64)</td>
<td>Constitutive/long-term activation</td>
<td>IgG</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>FcγRII (CD123)</td>
<td>Constitutive, stable expression</td>
<td>IgG</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>FcγRII (CD16)</td>
<td>Shed upon activation</td>
<td>IgG</td>
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<td>+</td>
<td>+</td>
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<tr>
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<td>IgA</td>
<td>+</td>
<td>?</td>
<td>?</td>
</tr>
<tr>
<td>CR1 (CD55)</td>
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<td>C4b/C3b</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>CR3 (CD11b/18)</td>
<td>Uregulated upon activation</td>
<td>C3bi</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>CR4 (CD11c/18)</td>
<td>Uregulated upon activation</td>
<td>C3bi/C3dg</td>
<td>+</td>
<td>+</td>
<td>?</td>
</tr>
</tbody>
</table>

* Constitutive expression on monocytes and macrophages, ** activation-dependent expression on neutrophils.
contents. Both reactions are localised events in that they are restricted to the release of microbicidal products into the phagosome. However, the secretion of these products begins before the phagosome is closed, and some of the oxygen compounds and granule enzymes may thus escape into the extracellular environment of the neutrophils. Moreover, neutrophils adhering to opsonised material that is too large to be ingested (e.g. immune complexes deposited along basement membranes) may secrete these products in large quantities into the extracellular space. Under such conditions, macrophages can fuse with each other forming large tissue multinuclear histiocytes as an important cell type, as is often present in granulomata.

Degranulation does not occur in resting neutrophils, monocytes, or macrophages. During phagocytosis or adherence of neutrophils to large substrates, intracellular signalling events induce the fusion of granules with the plasma membrane. Neutrophils contain at least two different types of granule; most likely the same holds true for monocytes. In macrophages, the granular content is less apparent. The azurophil granules resemble the lysosomes in other cell types in that they contain acid hydrolases, with a low pH optimum. Moreover, these granules also contain myeloperoxidase (MPO) and a number of serine proteinases (elastase, cathepsin G, proteinase 3). Further, the azurophil granules also contain large numbers of defensins, small peptides with a broad range of bactericidal activity, and bactericidal permeability-increasing protein (BPI), a very potent antibiotic against Gram-negative bacteria. Lysozyme, an enzyme that hydrolyses certain peptidoglycans of Gram-positive bacteria, is present in the azurophil as well as in the specific granules of the phagocytes. Proteins specifically found in the specific granules comprise lactoferrin, an iron-binding and therefore bacteriostatic protein, vitamin B₁₂-binding protein, and the metalloproteinases collagenase and gelatinase. Neutrophils possess far more granules than monocytes or macrophages. Finally, neutrophils also contain so-called secretory vesicles, which actively exchange their membrane-bound receptors and enzymes with the plasma membrane. In contrast, macrophages have a vesicular system of endosomal trafficking – although not as elaborate as the dendritic cell surface receptors is the active NADPH oxidase assembled to generate superoxide in phagocytes. Superoxide spontaneously dismutates into hydrogen peroxide that may then react with chloride ions to form hypochlorous acid (HOCI). This reaction is catalysed by MPO, when released into the phagosome or the extracellular space. HOCI is very toxic for a broad range of micro-organisms but is rather short-lived. However, it can react with primary and secondary amines, and thus give rise to N-chloramines, some of which are very stable microbicidal agents. Under normal phagocytosing conditions, neutrophils convert more than 75% of their superoxide into hypochlorous acid and N-chloramines, and thus create a highly toxic environment within the phagosomes and in the cell surroundings.

**Meaning of FcγR Polymorphisms in Inflection**

Since the FcγRIIa (CD32) is the sole IgG FcR capable of interacting with human IgG2, the main IgG subclass of bacterial capsular polysaccharides, most studies on infections with encapsulated bacteria have focused on the FcγR allotypes: i.e. FcγRIIa-R131 and IIa-H131. The retrospective study by Bredius et al. first showed in a small cohort of 25 children with prior fulminant meningococcal septic shock that almost half of the children were homozygous for FcγRIIa-R131, the poor IgG2-binding allotype. This allele frequency was significantly different from its frequency in a healthy white population (44% vs 23%, p=0.03). The relevance of this finding was further supported by the fact that neutrophils with the FcγRIIa-R131 allotype phagocytised *N. meningitidis* opsonised with polyclonal IgG2 antibodies less effectively than did IIa-H/H131 neutrophils. Another Dutch group had determined the FcγRIIa and FcγRIIb phenotypes of 48 children with recurrent bacterial respiratory tract infections. FcγRIIa-H/H131 was less than half that observed in 123 healthy adults (p=0.01). IgG2 responses were low in 25 out of 48 patients after immunisation with pneumococcal vaccine. The authors’ conclusion was that FcγRIIa polymorphisms contribute to increased susceptibility to infections with encapsulated bacteria in a childhood population with low IgG2 anti-carbohydrate antibodies. Similar variation in allele frequency was studied in small groups of patients with additional opsonisation defects in the complement system. The distribution of FcγRIIa and IIIb allotypes in 15 individuals with a deficiency in one of the late complement components (LCCD) and in 15 properdin-deficient patients with/without previous meningococcal disease was analysed. The combination of FcγRIIa-R/R131
with FcγRIIb-NA2/NA2 allotypes was associated with previous meningococcal disease (OR=13.9, p=0.036). No such relation was observed in the properdin-deficient patients. Another study in LCCD patients had previously shown that the distribution of FcγRIIa genotypes and disease demonstrated an apparently clear age effect. The R/R131, R/H131, and H/H131 genotype distribution was 0.14:0.29:0.57 for patients with their first disease episode <10 years of age, as compared with the distribution of 0.21:0.64:0.14 for those with their first episode >10 years (OR=8.0, p<0.05). Meningococcal disease had a more severe course in four out of 31 episodes in patients with the R/R131 or R/H131 allotypes, in contrast to one out of 18 in patients with H/H131 (OR=14.2, p<0.01). Thus, CD32-mediated phagocytosis may restrict the severity of meningococcal disease in LCCD patients with the H/H131 genotype. In a rather heterogeneous cohort of paediatric and adult HIV-positive individuals, skewing in FcγRIIa R/H131 allele frequency was not observed in relation to pneumococcal invasive disease. In 60 black children with sickle-cell anaemia (SCA) and well-documented bacterial infections, the R/H131 genotype distribution in the 51 individuals with a history of Streptococcus pneumoniae infection was also not statistically significantly different from that of the control population. In contrast, however, the H/H131 genotype was unexpectedly overrepresented in the 11 individuals with a well-documented history of Haemophilus influenzae type-b infection (64% H/H131, 27% H/R131, 9% R/R131, p=0.002) when compared with ethnically matched controls (14% H/H131, 60% H/R131, 26% R/R131). A case-control study on the risk and outcome of meningococcal disease in 150 patients with microbiologically proven meningococcal disease and 260 asymptomatic sex-matched controls indicated a lack of skewing in allele distributions of FcγRIIa allotypes. In comparison with meningococcal meningitis, however, both the fulminant meningococcal disease (OR=3.9, 95% CI 1.0 to 16, p=0.04) and sepsis without meningitis (OR=3.0, 95% CI 1.4 to 7.8, p=0.004) were associated more commonly with the FcγRIIa-R/R131 allotype than to those with meningococcal meningitis. Of the 42 patients with the R/R131 allotype, 31 (74%) had an adverse prognostic score, compared with 7% (4 of 59) of those with the R/H131 allotype and 3% (1 of 29) of those with the H/H131 allotype (p<0.0001).

Thus, the FcγRIIa-R/R131 allotype may not act as a strict susceptibility gene but – instead – a severity marker, associated with the more severe forms of meningococcal disease. This remains to be confirmed for other encapsulated pathogens.

**CONCLUDING REMARKS**

The meaning of polymorphic variations in the genes for the FcγRIIa, FcγRIIb and FcγRIIIb is far from clear at the moment. Most studies describe small and heterogeneous groups, and may at best tell us something about differences within a certain cohort. Then, the polymorphisms indeed show their most characteristic features, such as an age effect, a difference in outcome and symptomatology, and – presumably – a different treatment effect. The role of these polymorphisms seen as a separate issue in the host defence response indicates a subtle impact, more interesting from the perspective of pathophysiology than for the therapeutic options to date. This may change rapidly as soon as monoclonal antibodies enter the clinics for the reasons outlined above.

In the first phase of inflammatory responses or other forms of stress, chemokinas such as Cγa, lipid mediators, and so-called chemokines are produced. The secretion of chemokines can be firmly induced by the proinflammatory cytokines derived from tissue macrophage and T cells such as TNF-α, IL-1, and IFN-γ, or by bacterial products such as lipopolysaccharide (LPS) from Gram-negative bacteria, peptidoglycans from Gram-positive bacteria, or lipoarabinomannans from mycobacteria.

The process of recruitment is complex and still incompletely understood. Once recruited, the phagocytes – and neutrophils foremost – have a wide range of toxic mechanisms to fight any invading micro-organism, as described. These mechanisms are strongly regulated and delicately controlled because an over-excessive or premature induction of the toxic activities may result in the inactivation of protease inhibitors and activation of several cascades of activating substances (e.g. coagulation and fibrinolysis, the complement system). As a consequence, bacteraemia may progress to septic shock and disseminated intravascular coagulation, a community-acquired pneumonia may develop into acute or adult respiratory distress syndrome, and hypoxia/reperfusion injury can lead to fatal circulatory collapse.

In many of these early steps of inflammation, molecules are involved in which allelic variation has been characterised, often in the coding or promoter regions, as well as in the nontranscribed intronic sequences or 3'-regions. Their meaning in biological and – as a consequence – in clinical terms remains to be clarified. The FcγR allotypic variation is only a minute factor within the complex sequence of reactions in the host immune reaction to an invading pathogen.
REFERENCES


10. De Groot: I appreciate your remark about susceptibility and severity at the end of your presentation, which brings me to my question. It also relates to the first speaker, Dr Turner, who said, as I understand, that in the study on Mycoplasma pneumoniae infection there was a question of susceptibility. I fully agree with your statement that these molecules of innate immunity are more likely related to the severity of infectious diseases than to susceptibility. But if that is the case, could you comment on the type of studies that we have done so far, which are skewed, because most of them deal with retrospectively acquired material in highly selected populations from university settings and they are not prospectively done, i.e. they are not population-based. Can you give us your perspective on this? Maybe Dr Turner has a response to this question?

Kuijpers: First of all, we are now trying to do all these studies in a larger cohort of about 200 patients with recurrent respiratory tract infections more or less similar to the study already mentioned by Summerfield in which Dr Turner cooperated for his study of mannose-binding lectin (MBL). Once again, by checking all the known genotypic or allelic variation in these children, there is no clear-cut skewing in any of the polymorphisms presently known, not even for the MBL mutations. You can count the number of infections that these 200 children have, but indeed once again this is an anamnestic response by parents, and thus prone to recall bias. The only way to find out the truth is in a proper prospective study, preferably not in a tertiary centre, in order to have the broadest population possible. But what surprised us was that even the MBL mutations. You can count the number of infections that these 200 children have, but indeed once again this is an anamnestic response by parents, and thus prone to recall bias. The only way to find out the truth is in a proper prospective study, preferably not in a tertiary centre, in order to have the broadest population possible. But what surprised us was that even the MBL mutations were definitely not skewed to a particular mutation as compared to controls.

Turner: I would not disagree with that. I think most of the studies on MBL today should have been done in centres where there have been tertiary referral hospitals collecting the samples. That is one of the reasons why we are doing a large study in the West of England – it is called ALS-PAC, the Avon Longitudinal Study of Pregnancy And...
Childhood – which Professor Jean Golding set up in the early 1990s to follow 14,000 pregnancies, and we are just completing a study of 8000 children to see what correlates we can find for disease associations in those children. That is a true prospective study. These sorts of studies are desperately needed for these innate immune markers.

Van der Meer: Just to get back to the point of the *Mycoplasma* infection as a complication in hypogammaglobulinaemic patients, the question there as well is whether it is a severity or a susceptibility marker.

*Turner*: You are right, it was mainly infection due to *M. hominis*, and the patient cohort was a mixture of common variable immunodeficiency and also some X-linked agammaglobulinaemia patients who had started off as a study of common variable immunodeficiency – the *Mycoplasma* association was discovered as an incidental part of that. So we then enlarged the cohort for *Mycoplasma*.

*Kuijpers*: I want to point out the study already mentioned by Peter Garred in cystic fibrosis. Considering a drop of eight years in lifespan, it is crucial when you are also MBL-deficient. Then you may think about prospective treatment options being available nowadays for those CF patients who are MBL-deficient. But that can only be done in a proper setting with a multicentre study. Without such collaboration we probably remain stuck with the question, is it susceptibility or severity? A severity marker is already important, but only in certain cohorts.

*Appelmelk*: Dr Kuijpers, first can you explain to me, when you have an allele in a low-affinity receptor causing inactivity, why doesn't the high-affinity receptor take over? It sounds as though there is some redundancy in the system. So how does that work?

*Kuijpers*: I think you are completely right in mentioning this. Of course, all comes down to the initial thought and idea that these polymorphic sites in case of IgG2 opsonising mechanisms were of importance because there was a strict difference in whether you had the one or the other genotype, FcγRIIIα. Of course, the other studies were a kind of follow-up to that, first of all trying to confirm their ideas, and then suddenly these genotypes for the IIIα were showing different expression patterns and especially so in the autoimmune diseases. If a macrophage expresses so many Fcγ-receptors, having the opportunity to bind IgG-laden material, it is indeed questionable why it would not be taken over by other Fcγ receptors. I think a lot of the work in autoimmune diseases in fact confirms the genotype skewing. There are more molecules involved in immune reactivity as such. Think about the IL-6 or proteins related to apoptosis. Nobody knows in fact. This might simply be a way to look at something different in that particular genetic locus, not meaning that it is that particular receptor as such.

*McAdam*: Are these same receptors expressed on a placenta to facilitate the passage of immunoglobulin across the placenta? Would it be useful to look at babies with neonatal infections?

*Kuijpers*: The only receptor believed to be important in the transport of IgG from the mother to the child is thought to be the FcRN, so the neonatal receptor, which shows homology to the HLA class-I molecules. This is not even related to the FcγRI, II or III. So it is a very different mechanism. There is, as far as I know, no information about allelic variation in that receptor. Of course, I just mentioned the polymorphic sites in the FcγRIIb: they might be another thing to study, and especially that it is not in the extracellular part, where it may have an effect on the function of the other receptors. That is of course something that may or may not affect the outcome of an inflammatory reaction. But once again, I wonder whether that would tell us very much about susceptibility as such.

*Van Agtmael*: I would like to ask you a question from a clinical point of view. In March 2001 there was a study in Cochrane Review on the use of intravenous immunoglobulins (IVIG) for sepsis and septic shock and it showed a moderate effect. It would be interesting to look at this group of patients to find factors in those patients who would benefit from the intravenous immunoglobulins. Do you think that it would be useful to look at the Fc polymorphisms in this broad group of patients with sepsis and to identify those who might benefit from the IVIG?

*Kuijpers*: Well, it would not be the first molecule I would look at, although potentially IVIG may be beneficial. I think it will be very hard to see in which patients they are effective. Of course, I am talking very much as a paediatrician seeing a lot of meningococcal infections – that is a very homogeneous population. But when you are practising internal medicine, there is a huge variation. There are so many parameters that you have to exclude or include to come up with a firm idea about which group is definitely helped by IVIG. The follow-up of those patients studied is difficult. Did they show a normal humoral response etc? All that crucial information is completely lacking in these cohorts. So I don't know.

*De Groot*: A small remark on the question concerning the neonatal infection, which brought me back to the presentation by Dr Turner in the beginning, where he said that surfactants may play a role as part of innate immunity. There is data to show that mutations in the genes for...
surfactants A and D are associated with an increased risk of chronic recurrent lower respiratory tract infection. It is all very preliminary, and that actually brings me to my question. I will turn the gun onto myself immediately after I have said this because so far all these studies – if you have read Kimman’s nice book – have been done on associations between single-gene polymorphisms and diseases. You have already said so, but knowing the literature for instance on leucocytes or chronic granulomatous disease (CGD), even in a clear-cut serious mutation disease as CGD there is a tremendous variability in the expression of the disease. This varies from patients who do not become ill at all to those who are very seriously ill with many in between. The way we study these diseases as clinicians is at this point in time very simplistic. We try to take one gene mutation and apply it to a population and look for an association, whereas it might very well be possible that there are a hundred genes involved and that the effects of twenty genes are upregulating severity and there are thirty down-regulating it.

Verbrugh: I have to intervene as Chairman, because we have a time problem here. Could you answer that briefly, because we would like to have two more comments from speakers before we go on to the next topic?

Kuijpers: This is one of the main points set out by the Dutch Society for Science, that you have to enter this field by doing gene arrays and snip arrays, and that may not even bring a clear answer to your question, because if you have twenty different genes or snips being characterised in a certain cohort of patients you come up with the same question. You have then characterised only a limited number of these snips. You may be more susceptible, but then also of course it is a matter of meeting the agent that can potentially affect you.

Kimman: Are Fcγ-receptors involved in the response to vaccinations, and has anybody looked for associations between response to vaccination and Fcγ-receptor polymorphisms?

Kuijpers: I would say yes, most likely, but whether somebody has studied that, I am not aware of that.

Van Furth: Just in emulation of the discussion with Van Agtmael and you, Dr Kuijpers, is there a difference between persons regarding the turnover of IgG, given intravenously or just autologous? Have these studies been done?

Kuijpers: I don’t think anybody has done that in a detailed fashion, and the only thing I could say is that of course the turnover of IgG very much relates to the FcRN effect. So I think that a different receptor is involved in rescuing IgG from being cleared and broken down.

REFERENCE

Genetic susceptibility to *Neisseria meningitidis* infections

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**ABSTRACT**

The clinical presentation of infections by *Neisseria meningitidis* is highly diverse. Some patients with invasive meningococcal infections develop meningitis, while others present with sepsis or even septic shock. Three major host defence systems are activated after transepithelial passage and invasion of the bacteria into the bloodstream. These include the complement pathway, the inflammatory response by cytokines and chemokines, and the coagulation and fibrinolysis pathway. These three systems are mutually dependent. Genetic polymorphisms among components of these pathways (co)regulate the susceptibility, severity and outcome of meningococcal disease. In this paper the current knowledge of polymorphisms which are known to be associated with susceptibility to and severity of meningococcal infection is reviewed.

**INTRODUCTION**

Despite ongoing improvements in the treatment of infections by *Neisseria meningitidis* the mortality rates in patients with invasive disease are still very high, ranging from 4 to 40%. This is a reflection of the different clinical presentations of infection. The disease spectrum varies from meningitis to sepsis and septic shock. The first entity has a mortality rate of 4 to 6%, while in septic shock mortality rates up to 40% have been reported. The observation that septic shock can develop within several hours of onset of meningococcal invasive disease implies a major role for the innate immunity in host defence. Meningococcal lipopolysaccharide (LPS) is one of the major factors to induce the host response during bacterial invasion. This response is complex and involves the activation of three major host response systems (figure 1). The first is the complement pathway that apart from contribution to phagocytosis of the bacteria also functions as an inducer for the inflammatory reaction through C3a and C5a. The second system is the inflammatory reaction mediated by different chemokines and cytokines among which TNF-α and IL-1β play a central role. The third cascade is activation of the coagulation and fibrinolysis, which result in a prothrombotic stage. Activation of the host response in patients with sepsis results in a sudden onset of fever and a petechial or purpuric rash followed by hypotension. In patients with septic shock, disseminated coagulation and multiple organ failure develop. For an extensive review of the pathophysiology we refer to previous reports.1,2

The broad range of clinical presentations of *N. meningitidis* infections raises the question why some patients show hardly any clinical symptoms while others die within several hours of onset of symptoms. Variations in host genetic factors are known to contribute to these differences. Genetic polymorphisms are relatively stable in the human population. Single-nucleotide polymorphisms (SNPs) are distributed throughout the human genome at an estimated overall frequency of one in every 2 kb.3 It has been shown that these polymorphisms may affect susceptibility to and severity of meningococcal disease. This review focuses on the current knowledge of genetic variability in the susceptibility to and severity of meningococcal infections (table 1).

**INNATE IMMUNITY**

**TLR**

The innate immunity plays an important role in the initial recognition of invading pathogens. This recognition was, until recently, believed to be nonspecific. However, elucidation of the function of Toll-like receptors (TLR) has shown...
otherwise. TLRs sense different microbial molecules, covering a range of pathogens that cause infections in the host. TLR4, for example, recognises bacterial LPS. C3H/HeJ mice, having a point mutation in *tlr4* that abolishes LPS responses, are hyporesponsive to Gram-negative infections. The common Asp299Gly polymorphism in TLR4 alters the extracellular domain of the receptor. Airway epithelial cells of patients carrying this polymorphism are hyporesponsive to LPS. However, no association has been found between the Asp299Gly polymorphism and the susceptibility to or severity of meningococcal infection. Smirnova et al. have found an excess of rare amino acid polymorphisms in TLR4 of which the clinical relevance has not yet been studied. TLR2 recognises other bacterial components, such as lipopeptides and peptidoglycan. Until now the relation between polymorphisms in TLR2 and meningococcal infections has not been studied. TLRs recognise ligands in the presence of CD14 and MD-2 (TLR4) and activation of the diverse TLRs results in the activation of different signalling pathways, leading to NF-κB activation. Polymorphisms in the factors which are involved in these signalling pathways may also result in different phenotypes.

**LBP and BPI**

In blood LPS binds to lipopolysaccharide-binding protein (LBP) to form a complex that binds TLR4. In a recent study the Cys98Gly and Pro436Leu polymorphisms of LBP were not correlated with the susceptibility to or severity of meningococcal infection.
of bacterial sepsis in all patients but a relationship was found with the outcome of bacterial sepsis in males. It has been proposed that these polymorphisms may partially explain the worse outcome of bacterial infections observed in males. In the same study the clinical effects of polymorphisms in bactericidal/permeability-increasing (BPI) protein were also evaluated. BPI is another protein binding to LPS which inhibits LPS-induced host cell responses. Neither the A645G, the G545C silent polymorphism, nor the PstI in intron 5 were associated with outcome and severity of bacterial sepsis. However, in this study the limited number of patients prevented a separate analysis of patients with Gram-negative versus Gram-positive infections, thus introducing a bias with respect to LPS-related susceptibility. This may have limited the sensitivity in detecting an association.8

**COMPLEMENT**

**MBL**

Activation of the complement system forms a significant part of the innate immunity. Besides beneficial, also deleterious effects are associated with complement activation. The severity of hypotension is in part regulated by complement activation. At present, three activation pathways are considered (figure 2).9 Firstly, the classical pathway which is activated by antibody-antigen interactions, and secondly, the two pathways of the innate immunity, which do not require antibody.

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**Table 1**

Genetic polymorphisms possibly associated with meningococcal infection (for details see text)

<table>
<thead>
<tr>
<th>PATHWAY</th>
<th>GENE</th>
<th>POLYMORPHISM</th>
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<td></td>
<td>IL1RN</td>
<td>86 bp repeat in intron 2</td>
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<td></td>
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<td>T2018C</td>
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<td></td>
<td>IL1B</td>
<td>C-511T</td>
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<td></td>
<td>IL-6</td>
<td>G-174C</td>
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**Figure 2**

The three pathways of complement activation, connecting into a common late pathway generating the membrane attack complex (MAC) and inflammatory mediators C3a and C5a

Adapted from Hibberd et al.9
The alternative pathway of innate immunity is activated through interaction of C3 with factor b, factor d and properdin to generate C3b. The additional innate activation pathway is activated through mannose-binding lectin (MBL). All three pathways converge in a common final pathway. MBL first forms trimers, which in turn further assemble to form multimers. The MBL multimers bind to sugars and LPS on the bacterial surface. This complex then activates the mannose-associated serine proteases MASP1 and MASP2. MASP3 activate C4 of the classical pathway. Three allelic variants of MBL have been described in codons 52, 54 and 57 of exon 1. A mutation in codons 54 and 57 causes the disruption of the axial glycine repeats (Gly-Xaa-Yaa) resulting in aberrant trimers. These trimers cannot form correct multimers and are unstable. Through an unknown mechanism, the codon 52 mutation also results in unstable trimers. Heterozygotes for the variant alleles show a decrease in MBL serum levels to 10% of normal, while in people homozygous for any of the three mutations levels drop to 1% of normal.9,10 In children the variant alleles were associated with an increased susceptibility to meningococcal infections. Patients homozygous for the variant alleles showed a trend towards slightly less severe disease than heterozygous and wild-type individuals. This observation, however, did not reach significance.11

LCCD and factor D
Patients with late complement component deficiency (C5-C9) (LCCD) are known to suffer from recurrent Gram-negative bacterial infections. Failure to form a membrane attack complex (MAC) might underlie this increased susceptibility. Interestingly, these infections result in milder disease severity than observed for the total patient population, suggesting that there are also adverse effects of complement activation during meningococcal infections. Complement D deficiency was found in members of a family suffering from severe N. meningitidis infections. The alternative pathway for complement activation was impaired. This pathway, in contrast to the classical pathway, appears to be prominent in meningococcal infection.12

ACQUIRED IMMUNITY

Fcγ receptors
Fcγ receptors (FcγRs) belong to a heterogeneous family of receptors and are grouped in three classes (FcγRI, II and III). Three subtypes of receptors responsible for IgG-mediated signalling, FcγRIa, FcγRIla and FcγRIIb, are thought to be important in host defence against meningococci. FcγRIa is located on leucocytes and mononuclear macrophages and is sensitive to IgG2 and IgG3. Two alleles are known to differ at amino acid position 131 because of single-nucleotide polymorphism (SNP) in exon 4. The 131Arg allele confers lower interaction efficiency on IgG2 and IgG3 than the 131His haplotype. Two allotypes known for FcγRIIa, 158Phe and 158Val show different binding of IgG1, IgG3 and IgG4, as interaction with FcγRIIa-158Val is stronger. FcγRIIb is expressed on neutrophils and has the neutrophil antigen (NA) polymorphism representing four amino acid substitutions in the membrane-distal loop of the receptor. FcγRIIb-NA2 binds IgG1 and IgG3 less efficiently than FcγRIIb-NA.14 One can imagine that differences in efficiency in binding IgGs result in different host response effectiveness and thereby variable susceptibility to and/or severity of disease.

A study in survivors of meningococcal disease and first-degree relatives of survivors and nonsurvivors revealed no differences in FcγR distribution. The FcγRIla-131Arg allele was more often found in meningitis patients compared with sepsis patients. The FcγRIIa-158Val allelic frequency was markedly increased in relatives of meningitis patients compared with relatives of patients presenting with haemodynamic instability. The Arg/Arg-Phe/Phe-NA2 frequency that represents the least efficient FcγR combination, and is responsible for diminished phagocytosis, was tripled in first-degree relatives compared with healthy nonrelated controls. These data suggest an association between FcγR haplotype and susceptibility to and severity of meningococcal disease.14

COAGULATION

Activation of coagulation and fibrinolysis is the result of the acute inflammatory response in patients with invasive meningococcal disease. The prothrombotic endothelium surface results from activation by cytokines. Subsequently, tissue factor production results in activation of the extrinsic pathway of coagulation and the production of platelet-activating factors. The fibrinolytic system is initially activated but is subsequently inhibited. This results in a marked imbalance in coagulation and fibrinolysis resulting in a net procoagulant state and ultimately disseminated intravascular coagulation (DIC). This leads to deposition of fibrin, the formation of microthrombi and bleeding. Multiorgan failure and death are the most severe clinical findings regarding this imbalance.

t-PA
Tissue-type plasminogen activator (t-PA) is a serine protease that converts plasminogen into its active form, plasmin, which in turn leads to fibrinolysis. Impaired t-PA function leads to insufficient lysis of thrombi. Differences in t-PA production or impaired function can therefore affect the severity of meningococcal disease. An insertion/deletion polymorphism of an Alu element in t-PA considered to affect the basal levels of t-PA has been investigated in
relation to meningococcal disease. No association could be observed between the different alleles and the severity or outcome of meningococcal disease. The authors have regarded the use of an intensive care unit (ICU) as a criterion for severe meningococcal disease. In our opinion this only holds partially true, since not all patients admitted to the ICU for observation because they are at risk of septic shock actually develop septic shock. This might have prevented them from finding significant differences between the study populations. Further research regarding polymorphisms in t-PA with respect to meningococcal disease is therefore indicated.

**PAI-1**

Plasminogen activator inhibitor type 1 (PAI-1) is responsible for the inhibition of fibrinolysis both directly and indirectly through inhibition of t-PA (figure 3). In turn PAI-1 is inhibited by activated protein C. In septic shock, laboratory findings show decreased levels of all coagulation factors including protein C. The gene encoding PAI-1 has several polymorphic loci, including a 3′-HindIII site, a CA(n) repeat in intron 3 and a 4G/5G insertion/deletion polymorphism at -675 in the promoter. PAI-1 activity has been shown to be significantly higher in control subjects homozygous for the 4G allele than in subjects homozygous for the 5G allele. The production of PAI-1 mRNA after IL-1 stimulation appeared to be higher in HepG2 cells bearing the 4G allele. In patients with meningococcal sepsis the levels of PAI-1 are positively related to severity of disease, outcome, cytokine levels, acute-phase proteins and coagulation parameters. In nonsurvivors the PAI-1 levels were shown to be 1.9 times higher for the same TNF-α levels than in survivors. In children suffering from meningococcal disease a relationship has been observed between genotype, PAI-1 levels and outcome of disease. The subjects with the 4G homozygous genotype had higher PAI-1 levels and had an increased risk of death. No association was observed with severity of disease.

A similar study performed by Westendorp et al. showed a higher incidence of the 5G/5G genotype among relatives of patients with meningitis. Patients whose relatives were carriers of the 4G/4G genotype had a sixfold higher risk of developing septic shock than meningitis.

**FV<sup>+</sup>**

Factor V Leiden (FV<sup>+</sup>) is associated with thrombotic events, and is therefore an interesting candidate for involvement in the development of meningococcal purpura fulminans. A study comparing children with meningococcal disease, healthy controls and parents of children with meningococcal disease did not reveal an association between the FV<sup>+</sup> mutation and susceptibility. Patients heterozygous for the mutation showed increased complications, as assessed by requirement for skin grafting, referral to plastic surgeon and/or amputation. A significant effect on mortality was not observed.

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**Figure 3**

*Involvement of PAI-1 and t-PA in coagulation and fibrinolysis*
**CYTOKINES**

**TNF-α**

Tumour necrosis factor α (TNF-α) plays a central role in the activation of the inflammatory response, and serum levels are raised in all patients with meningococcal disease. TNF-α activates adhesion-promoting receptors and ligands enabling leucocytes to cross the endothelium and reach the site of inflammation. Other inflammatory mediators such as IFN-γ, IL-6 and IL-8 are activated by TNF-α. A procoagulant state is promoted by the induction of tissue factor release. TNF-α blood levels are positively associated with disease severity, coagulopathies and outcome. Westendorp et al. found a higher TNF-α response in ex vivo blood samples after stimulation with endotoxin in patients who had experienced a moderately severe disease course compared with patients with a mild course. The TNF-α response was low again in survivors of fulminant disease. On admission for meningococcal disease, patients who did not survive had initial TNF-α levels three times higher than those in survivors with a clinical disease presentation of similar severity.

The G-308A polymorphism in the TNF-α promoter region has been shown to be associated with outcome of meningococcal disease. The TNF-α allele (G308A) is associated with an increased risk of death. Controversial opinions exist about the role of this polymorphism and the severity of disease. The diverse results of the various studies may reflect the differences in patient and control populations. Some researchers study meningococcal sepsis only, while others look into the relevance of the G-308A polymorphism in the A2 allele of IL1RN at +2018 was significantly associated with survival. In this study no association between the TNF-308 genotype and fatal outcome was demonstrated. These data suggest that IL-1 genotype influences the outcome of meningococcal disease.

**IL-6**

Interleukin 6 (IL-6) is a major pyrogen and is responsible for the induction of hepatic acute-phase proteins and antibody production by B cells. IL-6 blood levels are increased in meningococcal infection. The G-174C polymorphism in the promoter region of IL-6 is associated with outcome in meningococcal infection, since the -174G/G genotype is associated with an increased mortality risk. However, this polymorphism is part of a complex haplotype associated with differences in IL-6 production. The -579C, -572G, -373A/T11, -174G haplotype shows higher transcription of IL-6 in an ECV304 cell line after IL-1 induction than the other polymorphism combinations. This study clearly shows that different polymorphisms can have an influence on transcription, but they are not functioning independently. When assessing the contribution of the G-174C polymorphism in meningococcal disease, the complete haplotype should be considered.

**DISCUSSION**

Meningococcal disease comprises a complex pathophysiology resulting in a spectrum of disease presentation in affected individuals. Assessing the contribution of host factors in infection therefore requires a strict definition of the patient population. Patients suffering from meningococcal meningitis might have different ‘susceptibility genotypes’ to septic shock patients, as different pathophysiological pathways are activated. Combining these study populations is therefore not advisable. The same problems occur when comparing patients with sepsis of unknown microbiological origin. Host response to Gram-positive microbes might differ from the response towards Gram-negative bacteria. It must be noted, however, that in approximately 10% meningococcal infection cannot be proven with microbiological techniques, while the clinical presentation is typical. In addition, it might be difficult to obtain patient groups of sufficient numbers to show an association between disease
susceptibility, severity and outcome when investigating genotypes with extremely low allele frequencies. Ethnic differences in the study population might also interfere with the supposed associations. Studies including relatives of patients as controls might overcome this problem. These studies compare the observed and expected inheritance of the different alleles. One must, however, consider the possibility that disease is not linked to the studied gene, but to another gene in linkage with the first.

Another interesting focus of genetic investigations is the interaction of the polymorphisms and the cumulative effect on the course of meningococcal disease. These interactions might be either synergistic or counteracting. In the IL-1 family such interactions have been found for IL-1B(-511) and IL1RN (2018). The development of high-throughput molecular genetic techniques is of great importance in our efforts to unravel the immense complexity of genetic interactions.

REFERENCES

Discussion following lecture by P.W.M. Hermans

Netea: I would like to ask you two questions; one is regarding the tumour necrosis factor (TNF) levels in meningococcal sepsis. You told us that they are high and that this increases the severity and the risk of death. Is this really an increased production capacity leading to death and leading to increased circulating levels, or is there actually a reduced production capacity leading to multiplication of bacteria, which leads to a lot of stimulus, which then leads to high amounts of cytokines? I am thinking of first-degree relatives of patients with meningococcal sepsis. If I remember rightly, they have a reduced production capacity of TNF. My second question is a more conceptual one, which is more or less for everybody. As we are now looking at Toll-like receptor (TLR) polymorphisms in various diseases, what are our chances of finding something important with a genetic approach? Because at the moment we find a very significant polymorphism or a very significant mutated gene, the host is already dead. So the closer we are to the truth in looking for a determinant gene, the smaller the chance we will ever find it. Only less significant polymorphisms are found which are compatible with survival, whereas the really significant ones are not detected since the hosts are already dead. I am thinking of TLRs, because if it is really a polymorphism which leads to a TLR-2 defect, I do not think this is compatible with survival. It may be the same with some important polymorphisms for TNF. For example, I do not know anyone who is really deficient in TNF.

Hermans: Quite complex comments, but starting with the last part, I think it is absolutely true that quite a few interesting polymorphisms have been studied now, and as soon as new polymorphisms pop up, I immediately get the feeling. OK, we have to increase the number of patients again to see any relevance in interaction. You are in fact driving towards a complete human-specific genetic passport for that particular human being. If I have got your point right, I think that these extremely complex and difficult studies might not give us the appropriate answers we were hoping for. Coming back to TNF, TNF-α expression actually, for many cytokines, when patients come in, as far as I understand from the clinicians, the cytokine responses and the cytokine levels are extremely high. Immediately after admission they tend to decrease, do you agree, Dr van Deuren?

Van Deuren: Yes.

Hermans: The turnover is extremely high, which means that the half-life is quite short.

Netea: I am just thinking that the circulating levels that you are measuring are in fact a result of the interaction between our capacity to make it and how many bugs are multiplying in our system. It is very difficult to discern and to say, a sick person has a lot of TNF, so that is a bad thing. It might very well be possible he was unable to make enough in the beginning to suppress the multiplication of the bacteria.

Hermans: I agree with that.

Van Deuren: I would like to ask a few questions and make a few remarks on meningococcal disease. Of course, it is a blood-borne infection with an impressive clinical picture and blood is the most easily obtained tissue. So a lot of measurements have been done in blood. But it is really the question whether that is the most important site of the body to look at. The gate for the meningococcal bacterium is the oronasal mucosa. At that site there are several interactions between the bacterium and our immune system: the meningococcal pilius is attached to CD46 for instance, the meningococcal pore A outer membrane protein is attached to the carcinoembryogenic antigen CEA, CD66a, b and c. And there are a lot of polymorphisms in these types of receptors or ligands too, for instance relating to the intramucosal survival of the meningococcus, because it is able to survive passing through the cells. There are
some studies showing that they are influencing bactericidal proteins, enabling them to survive and to pass through the bloodstream. Are you aware of any studies looking at the polymorphisms in this site of the body? Because that will really determine our susceptibility, because all the rest in the blood really is a matter of severity.

Hermans: As far as I know, such studies have not been undertaken, but the initial point you made that has not been studied either, in detail at least, is the genetic differences among these bugs, and it is definitely not only man C versus man B, but there are many more molecules showing a huge variety within this particular species.

Van Deuren: That is the second important property of the bug, of course, its switching off and switching on molecules so rapidly enabling it to enter the bloodstream. A second remark about the levels of TNF: the higher the concentration of endotoxin in your blood, the more TNF you produce. And really the best predictor of mortality is not the TNF level but the endotoxin level, as already mentioned by Brandtzaeg in his series of 150 patients. There is a good correlation between the level of TNF and endotoxin. So for me it is not the genetic trait or the capacity of the person to produce TNF, but it is the amount of endotoxin that he tolerates, and that will determine the amount of TNF produced and, thus, the amount of procoagulant and anticoagulant activities.

Appelmelk: You showed that you get an impressive increase in relative risk when you add the various polymorphisms. Where will this end? From a scientific point of view you can go on, but do we need to know all this? Which knowledge regarding polymorphisms will lead to clinical actions? You read in the papers about DNA passports and you see companies eager for dollars, but how important is it for the actual patient management?

Hermans: Your question actually was the main reason for me to show this study on tissue-type plasminogen activator (t-PA) therapy, which is in part guided by the existing polymorphisms and genetic variability. Indeed, when you have these details, there is a possibility of performing patient-specific therapy in the long run. At the moment that is not feasible. But I think such data are of definite value for the patient. It is not so that you are just born with a ‘genetic passport’ and that nobody can change anything about that. I think when you have these data in advance and you know where to interact, you can intervene in these processes.

Appelmelk: Do you think that it is realistic when we have a patient and are at the bedside to take his blood, for us to put it on a chip and then decide what to do?

Hermans: By that time it is too late!

Kusters: Can I give one brief comment or ask a question? You are now looking at only one type of disease and one type of bug trying to find the ideal ‘genetic passport’, but obviously evolution has gone a long way and the so-called wrong passport may in fact be an ideal passport for survival. Maybe an increased risk of a certain type of disease is the flip side of a better survival of other types of disease.

Hermans: When a patient comes in with a meningococcal sepsis, having an excellent overall survival passport, still at that time his survival clock has started ticking towards zero. When you know the disadvantages of that particular passport, if you can alter it, that would be a major advantage. Of course, such an intervention might be disadvantageous with another infection.

Kuipers: Whether lipopolysaccharide (LPS) and the levels of TNF strictly correlate, depends on which test system you use, which ELISA, or especially which firm you have addressed to purchase this ELISA system from. Just comparing TNF ELISA test systems as such would already give you two or three papers probably. It is very difficult. With genes you cannot lie – that is an advantage, but on the other hand it is of course a disadvantage that if you then start to shift from genes to concepts, as for instance TNF-induced responses, and one observes the staggering lack of effect of blocking TNF for instance in meningococcal disease or sepsis, I very much doubt whether this approach will have any impact in the short run on how to treat patients.

Kimman: It is nice to comment on this issue of course, whether we should do this work in order to improve the treatment of individual patients. I do not see a future in which patients will be treated only after their genotype has been assessed, but on the other hand, you nicely showed that this kind of work can lead the way to pathways which can be influenced whatever the genotype of the patient is. For instance, you identify a PAI/t-PA pathway and then you have a lead for treatment irrespective of the genotype of the patient. Unfortunately it did not work, but you identified something which you can tackle.

De Groot: I would like to support Dr Hermans in relation to the question from Dr Appelmelk and the point that is raised here. I will give you a practical example why I think this genetic approach will have additional value and how it could already have in the current situation. Let’s consider a polytrauma patient and suppose you knew the genetic profile in advance when he came in, thus being able to predict whether he was in a high-risk group or in a low-risk one. That would be helpful in the choice of therapy. Now Dr Hermans mentioned one therapy, t-PA, but another one
is known to all clinicians from a publication in the New England Journal of Medicine last year, namely activated protein C. Both therapies have serious potential side effects in terms of cerebral haemorrhage. The selection of patients who would benefit from these very invasive therapies would therefore be balanced depending on their risk. So this is the way of thinking I believe we should pursue as clinicians in terms of making a choice actually for these drugs where we know that in these desperately ill patients there certainly will be a very narrow kind of safety margin.

Van Deuren: Just to address a limitation of this approach. In meningococcal disease I have looked at the moment – I call it the kinetics of dying – the patient dies from that disease. From literature and from my own experience I have collected approximately 300 deaths, not cases, but deaths, and from that it can be seen that one-third of the patients who will die have already died within six hours of admission, half have died within 12 hours, 66% within 24 hours and 80% within 48 hours. So already one-third of your patients have been lost within six hours. I do not know how long it takes to run a chip array.

Verbrugh: It is quite interesting that we are here discussing the value of our core business as a science, the creation of new knowledge. We would rather like to pose the question beforehand or we would like to know which knowledge we can use and what knowledge we cannot. This is a poor question to ask. Sometimes we do have to ask, because there are financial constraints, but primarily the business is to get new insights and new knowledge.

REFERENCE

Genetics of type-1 cytokines in human intracellular infectious diseases: a spectrum of novel genetic deficiencies demonstrates the essential role of type-1 cytokines in immunity against nontuberculous mycobacteria, *M. bovis* BCG and salmonellae

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**Abstract**

Human genetic factors play an important role in determining the outcome of infections caused by intracellular pathogens, including mycobacteria and salmonellae. The genetic elements involved and the mechanisms by which these control disease susceptibility vs resistance, however, remain incompletely characterised. Recent studies on patients with idiopathic severe infections due to otherwise poorly pathogenic mycobacteria (nontuberculous mycobacteria or *Mycobacterium bovis* BCG) or *Salmonella* species have revealed that many of these patients are unable to produce or respond to IFN-γ. This inability results from causative, deleterious genetic mutations in any one of five different genes in the type-1 cytokine cascade, encoding IL-12p40, IL-12Rβ1, IFN-γR1, IFN-γR2 or STAT1. The mutational events can lead to complete or partial deficiency, and are mostly autosomal recessive but can be dominant negative as well. The immunological, clinical and histopathological phenotypes resulting from the 11 groups of genetic type-1 cytokine (receptor) deficiencies that have been identified thus far differ significantly. These findings are summarised, discussed and placed in a broader context in relation to genetic disease predisposition and molecular and cellular mechanisms of protective immunity to these intracellular pathogens.

**Outline**

Protective immunity to intracellular pathogens such as mycobacteria and salmonellae depends on effective cell-mediated immunity (CMI) in which T-cell-macrophage interactions play a crucial role. A major effector mechanism of CMI is the activation of infected macrophages by type-1 cytokines, particularly interferon-gamma (IFN-γ). IFN-γ is produced by antigen-specific T-helper 1 (Th1) cells and natural killer (NK) cells, and binds to IFN-γR1/R2 receptor complexes at the cell surface of macrophages.

The production of IFN-γ by T cells and NK cells itself is tightly regulated by another cytokine, interleukin-12 (IL-12). IL-12 is a heterodimer, composed of a p40 and a p35 subunit, and is produced by antigen-presenting cells such as macrophages, monocytes and dendritic cells following the activation of Toll-like receptors by bacterial ligands. Thus, IL-12 plays a major role in promoting and linking both innate and adaptive immunity. IL-12 binds to IL-12 receptor β1/β2 complexes at the surface of Th1 and NK cells. Whereas IL-12p40 predominantly interacts with the IL-12Rβ1 chain, IL-12p35 primarily binds to IL-12Rβ2. Two additional cytokines with IL-12-like activities have recently been identified, namely IL-18 and IL-23, both of which are produced by antigen-presenting cells. IL-18 acts mainly in synergy with IL-12 and plays an accessory role in promoting optimal IFN-γ production. Interestingly, IL-23 shares one subunit
with IL-12, notably p40, which is coupled to a unique second chain, p19. Similarly, the receptor for IL-23 consists of an IL-12Rβ1 subunit which is complexed to an as yet unidentified p19R chain. As expected, IL-12 and IL-23 display similar functions, including the stimulation of IFN-γ production, although their functional profiles are not completely identical. Other cytokines can act as additional factors in promoting Th1 development and IFN-γ production, such as the recently identified TCCR ligand, interferon-α and chemokines.

IFN-γ, in synergy with TNF-α, is able to activate microbicidal mechanisms with antimonococcal activity in murine macrophages. Although IFN-γ is clearly able to affect the growth of M. bovis BCG as well as human macrophages, reports on a similar role for IFN-γ in M. tuberculosis-infected human macrophages have been conflicting. Recent evidence now suggests that IFN-γ may require the presence of other factors, such as 2,3-dihydroxy-vitamin D3 and TNF-α, or human lymphocytes, in order to exhibit anti-M. tuberculosis activity in human macrophages, but this issue clearly needs further study. Furthermore, IFN-γ is well known to enhance MHC class I and II expression and to modulate the expression of other molecules involved in antigen presentation, such as proteasomes and transporter-associated-antigen-processing (TAP), thus promoting antigen presentation, such as proteasomes and transporters-to modulate the expression of other molecules involved in

Recently, several patients have been reported with unusually severe and sometimes fatal infections due to usually poorly pathogenic mycobacteria, in the absence of any recognised primary or secondary immunodeficiencies. These patients mostly suffered from infections due to M. avium, other nontuberculous mycobacterial species or M. bovis BCG, but also other pathogens have been reported including salmonellae and M. tuberculosis. The patients described thus far often fail to form well-organised granulomata at the sites of their lesions. A common feature of these individuals was their inability to produce or respond to IFN-γ in vitro. This appeared to be due to deleterious mutations in any one of five different genes in the type-1 cytokine cascade, notably IL12B (encoding IL-12 p40), IL23R (encoding IL-23R), IFNGR1, IFNGR2 (encoding IFN-γR1 and IFN-γR2 chains, respectively) or STAT1 (encoding IFN-γR-associated STAT1). The mutational events resulted in either (i) recessive, nonfunctional null alleles, (ii) recessive, partially functional alleles, or (iii) dominant-negative alleles, causing partial functionality. Upon further analysis, these deleterious mutations appear to comprise a spectrum of genetically controlled deficiencies in which the extent of the defect correlates with the severity of the clinical, immunological, and histopathological phenotypes observed. Recent developments and findings regarding defects in the IL-12/IL-12R and IFN-γ/IFN-γR/STAT1 systems respectively will be discussed. These novel defects reveal essential molecular and cellular mechanisms of protective cell-mediated immunity against intracellular pathogens. The intriguing observation that these patients appear to be selectively susceptible to otherwise poorly pathogenic mycobacteria and Salmonella species will be discussed as well.

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Discussion following lecture by T.H.M. Ottenhoff

Van der Meer: Regarding the interaction between the T lymphocyte and the macrophage, you did not point to defects of IL-18. The question is, of course, is IL-18 an irrelevant molecule, didn’t we look carefully enough, or could it be that the IL-23/IL-12 combination takes out enough of the redundancy to cause trouble.

Ottenhoff: We have not been able to find any defects in IL-18 production and IL-18 receptor expression in those patients we have analysed. Other laboratories did not find any mutations or defects in that system either. In my view IL-18 is mainly an amplifier of IL-12 and perhaps also IL-23. Maybe IL-18 deficiency is not sufficient to cause a dramatically enhanced disease susceptibility to mycobacteria.

Netea: You have also investigated the patients with receptor defects for IL-12 and interferon-γ and found no difference in IL-18 receptor expression?

Ottenhoff: Correct.

Netea: One of the mechanisms for the synergism between IL-12 and IL-18 could be that IL-12 actually induces expression of IL-18, and IL-18 would do a lot of the work.

Ottenhoff: If you activate the cells with phytohaemagglutinin (PHA), you see normal expression of the IL-18 receptor α component. So that certainly is not IL-12-dependent in that system, or at least not IL-12-receptor-β1-dependent.

Netea: But I don’t know whether PHA is a relevant stimulus. Could it be going to the T cell directly without the need of a macrophage?

Ottenhoff: PHA is a good system to screen for major defects, but physiologically IL-18 actually could contribute.

Netea: Have you looked at the IL-18 receptor in these patients with IL-12 receptor defects?

Ottenhoff: Yes, we looked at it, but in these patients there is no defect in IL-18 receptor α expression.

Netea: That would imply that those who are saying that IL-12 is working through induction of IL-18 receptor are probably wrong?

Ottenhoff: That is true. We have published this.1 If you activate T cells in patients with IL12R-β1 defects, there is a small residual IL-12 response. This is of course β1 STAT4-independent, and most likely works through MAP kinase. Perhaps that pathway would be sufficient to induce IL-18 receptor expression in these patients.

Van Furth: Do you have an explanation for the occurrence of tuberculosis, which only arose in three patients, and the other mycobacterial infections, while activation of macrophages is only mildly affected? In contrast, AIDS patients develop tuberculosis early on, and when the CD4 count is really low infections with other mycobacteria develop.

Ottenhoff: One explanation for this paradox is that there is no exposure of these patients, who are mainly from Western countries, to M. tuberculosis. Another explanation is that in endemic areas these patients die prematurely and a genetic diagnosis is never made. A third option is that once a patient presents with TB, a genetic defect is not considered. In the three TB cases that have been reported so far this was more or less discovered by coincidence. These defects may be more common in tuberculosis. A fourth, less likely and more academic option is that M. tuberculosis inhibits, at least in part, signalling through the interferon-γ receptor STAT1 pathway in macrophages. Because M. tuberculosis does this, the macrophage may be less sensitive to interferon-γ, and therefore in TB such defects would have less impact than for instance in BCG or M. avium.

De Jongh: Sarcoidosis has many similarities with tuberculosis. Are there defects in patients with sarcoidosis?

Ottenhoff: We have tested about ten sarcoidosis patients, but it is too early to say.

Kuijpers: Interferon-γ receptor-deficient patients may have an increased susceptibility to viral diseases.2 It is a very weak association, but isn’t it the biggest surprise that it is so monogenic?

Ottenhoff: I agree. That is why I concluded that quantitative ligation of the interferon-γ receptor is important. It indicates how important full-blown activation through the interferon-γ receptor pathway is for protection. I think in the case of viral infections or toxoplasmosis, there may be sufficient backup pathways to compensate for these defects, but in the case of mycobacterial and salmonella infection these are not sufficient.

McAdam: What about the ages of the patients with the defects? You suggested the poor life expectancy in the tropics. Certainly we have screened for type-1 pathway defects in
our adult TB patients and have not found any, but that probably means that the others died of viral infections or something else much younger.

Ottenhoff: Patients with complete interferon-α receptor 1 and 2 defects usually present during early life and quite often die before the age of ten. So that is really a severe, often fatal syndrome. IL-12 receptor deficiencies are a little less severe. Those patients can present at an early age but even at 30 years and older. They often survive quite long.

De Groot: Do you have data on the genetics of parents, grandparents and other family members, and have you gone back some generations to see if there were comparable diseases?

Ottenhoff: Yes, all the families we have analysed from Turkey are consanguineous. They can be traced back to one precedent generation. The parents are always heterozygous for the mutations. We performed extensive family analyses and showed that these really segregated recessive traits, as you would expect. At the moment we are investigating whether there are founder effects in Turkey, if certain alleles are more common in the population than other alleles, and if these alleles are maintained in the population and sometimes cause major disease in these families.

De Groot: How would this fit in with the theories on HLA and genetic susceptibility at population level? By changing the HLA make-up over generations apparently disease becomes modified? How does this relate to these cellular defects?

Ottenhoff: That is a difficult question. The defects I described work at the level of innate immunity as well as of the adaptive immunity: first there will be a major deficiency in innate immunity, and this will later on also lead to a major defect in acquired immunity. At that stage there is interaction with HLA leading to enhancement or a decreased susceptibility. These genes I have discussed have a major impact, especially on the early, innate phase, at that stage of course apart from HLA.

De Vries: Also, such a rare mutant, which results in a rather severe phenotype, works out in a recessive way. The genetic situation is completely different when you are talking about HLA alleles which are polymorphic at relatively high frequencies, and which are working in a dominant or co-dominant way. This situation is open to selection.

Netea: Regarding IL-12 p40, could it be, for example, that there are TB patients who produce too much p40 and in that way would be blocking the normal p40/p35 heterodimer action?

Ottenhoff: There is great variation in p40 production between different individuals, that I know, but I am not aware that this is related to tuberculosis.

Appelmelk: I am curious, how are you planning to go on?

Ottenhoff: It is difficult to decide. Should we opt for a candidate gene approach? That is something we are doing. One of these is the interleukin-10 gene. If you want a totally unbiased approach you should go for a genome scan and do linkage analysis and then try to positionally clone the genes involved. That is not easy. It would be a good idea to start using micro-arrays and compare genetic expression profiles of tuberculosis patients with exposed but protected individuals, and try to find which pathways light up in susceptible vs protected individuals and to define the different cascades.

Van Agtmael: Has this pathway been evaluated in the patients with Legionella, for instance during the recent outbreak in Bovenkarspel in the Netherlands?

Speelman: I can answer that: with Professor van Dissel we are investigating this. So far the results have not been very exciting.

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NRAMP1 (SLC11A1) and vitamin D receptor genes: disease associations

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Abstract

Resistance to infectious diseases is complex, being regulated by multiple genes, and so far no one locus has been shown to dominate the susceptibility in outbred human populations. Multi-case families have contributed greatly to defining important host immune response pathways using a candidate gene approach. It is likely that genome scans will identify novel genes for resistance to disease that could help define new approaches to drug and vaccine development.

Introduction

Susceptibility to infectious diseases is under polygenic control, as exemplified by genetic susceptibility to malaria. Severe Plasmodium falciparum malaria exerts enormous selective pressure on populations living in malaria-endemic areas. In the era before the advent of antimalarial medicines, those who could not survive malaria and develop effective immunity were wiped out at a young age and only those who survived were able to pass on their genes to the next generation. The sickle-cell haemoglobin mutation (S) confers protection against malaria in its single-dose heterozygote form (AS) and provides a selective advantage, despite the disadvantage conferred by the two-dose (SS) form in homozygotes.1 Many genes have now been described as providing resistance against malaria, including various haemoglobin variant genes giving rise to thalassaemia2 and glucose-6-dehydrogenase deficiency, as well as class I and II HLA molecules. HLA B53 is found in 30% of the Gambian population whereas it is uncommon in Europe. The nine-amino-acid peptide that fits best in the groove of HLA-B*53 codes for a portion of the malarial liver-specific antigen LSA-1, presumably demonstrating that the selective advantage of B*53 identifies a vulnerable target in the parasite life cycle. Following on from this work in The Gambia, new malaria vaccine constructs have been designed to include this and other liver-stage antigens not previously considered as vaccine candidates. The promise that identification of susceptibility/resistance alleles can lead to the development of new approaches to vaccines or therapeutic agents has encouraged us in The Gambia to pursue studies of the genetics of disease susceptibility. We have focused on important endemic infectious diseases in Africa including malaria, tuberculosis, hepatitis B, chlamydia and HIV. This paper briefly summarises our efforts on two candidate genes, NRAMP 1 and vitamin D receptor, to define susceptibility to tuberculosis.

Genetic Susceptibility to Tuberculosis

Heritability of tuberculosis has been suggested by various studies in twins,3 by racial differences in resistance to TB4,5 and by animal studies in rabbits and inbred strains of mice.6,7 Families expressing a high rate of mycobacterial disease have been important in defining various Mendelian susceptibilities in the interferon-γ and IL-12 pathways.8,9,10 Most people who breathe in aerosol droplets containing M. tuberculosis become infected. However, only 5 to 10% of close contacts of a case of open pulmonary TB go on to develop tuberculosis, and it has been assumed that this susceptibility is related to the effectiveness of the immune system. Many factors including genetic background influence the innate and acquired arms of the immune response. Poor nutrition, alcoholism and immunosuppression due to drugs or other infections, including HIV and measles, have been implicated in an increased susceptibility to TB.
An increasing number of genes have been implicated in susceptibility to tuberculosis. HLA is perhaps the best documented, with conflicting positive and negative associations reported. An increased frequency of HLA-DR2 is the most consistent association but has not been found in all populations examined, nor was there clear linkage to the MHC in a genome-wide screen carried out on patients from The Gambia and South Africa. When the Scottish missionary Dr David Livingstone travelled through Central Africa in the mid 19th century he did not see a lot of TB, though he would have observed plenty in Britain. Senegalese troops who fought in the 1914-18 war contracted TB at a higher rate than European soldiers, suggesting that they were nonimmune and had not been exposed to M. tuberculosis previously, or perhaps were more susceptible genetically. Stead reported that black Americans in Arkansas nursing homes had twice the risk of acquiring M. tuberculosis infection compared with white subjects. Crowle confirmed a similar trend in vitro, showing that macrophages from blacks were more easily infected and less activated by vitamin D.

**VITAMIN D RECEPTOR AND TUBERCULOSIS**

Historically, there has been circumstantial evidence for an association between vitamin D and tuberculosis. Prior to effective chemotherapy, patients were sent off to sanatoria where they were exposed to fresh air and sunlight, which was thought to provide the best environment for recovery. Patients with skin TB or lupus vulgaris responded well to vitamin D therapy but some patients with pulmonary tuberculosis fared badly. Rook showed that macrophages stimulated with vitamin D were activated, providing a rationale for these anecdotal clinical observations. The active form of vitamin D, 1,25 dihydrocholecalciferol \( (1,25 \text{D}_3) \), binds the vitamin D receptor (VDR) in the cytoplasm of macrophages and activated lymphocytes. VDR is a zinc-finger DNA-binding transcription factor which migrates to the nucleus, resulting in the expression of a number of hormone-sensitive genes.

VDR maps to chromosome 12q13-14, and belongs to the steroid/thyroid hormone receptor family with 11 exons. Polymorphisms within the VDR gene include a Taq I site at codon 352, an Apa I site and a Bsm I site in intron 8 and a Fok I site in exon 2 which leads to an alternative transcription site. Although the association between VDR polymorphisms and bone mineral density has been hotly debated, the homozygous ‘Taq I genotype ‘TT’ has been associated with decreased bone mineral density (osteoarthritis). Bellamy et al. found this genotype less commonly in 400 TB cases in The Gambia than in the 400 ethnically matched controls (odds ratio 0.53, 95% confidence limits 0.31-0.88, \( p=0.01 \)). Wilkinson et al. undertook a case-control study of Gujarati Indians in West London, demonstrating an association between TB and a combination of VDR genotype and serum 1,25\( \text{D}_3 \) concentration. Another study in India did not confirm an association with VDR, though the TT genotype was overrepresented in female cases compared with controls. Vitamin D receptor polymorphism has been shown to be relevant to susceptibility to leprosy in Calcutta, where ‘T’ was overrepresented in tuberculoid cases and ‘TT’ was associated with lepromatous disease. Interestingly, ‘T’ has also been associated with enhanced clearance of Hepatitis B virus, suggesting that 1,25\( \text{D}_3 \) and VDR may play a more central role in regulating immune responses against infections.

**NATURAL RESISTANCE ASSOCIATED MACROPHAGE PROTEIN 1**

Natural resistance associated macrophage protein 1 (NRAMP1) has recently been renamed SLC11A1 (Solute Carrier family11 member1). Originally described in inbred mouse strains, this locus was confirmed to be a single gene on chromosome 1 when a knockout mouse proved NRAMP1 was responsible for resistance to several intracellular infections. A single amino acid change on the 4th transmembrane domain of the protein resulted in an absence of the protein in susceptible mice. This naturally occurring mutation led to a Gly-Asp substitution at amino acid 169, which enhanced susceptibility in mice to intracellular infections with leishmania, salmonella, toxoplasma, candida and mycobacteria.

In humans the NRAMP1 gene is located on chromosome 2q35 and has been associated/linkd to various infectious diseases (tuberculosis, leprosy, meningococcal meningitis), leishmaniasis and HIV and autoimmune diseases (rheumatoid arthritis, diabetes, sarcoidosis, and Crohn’s disease). In 400 cases and controls in The Gambia, Bellamy and colleagues have shown that four variants of the NRAMP1 gene are significantly associated with an increased risk of developing cavitary pulmonary tuberculosis. In the patient group there was an increased risk (odds ratio 4.08, 95% confidence interval 1.86-9.12, \( p<0.001 \)) of TB in individuals heterozygous for both a single nucleotide polymorphism (SNP) in intron 4 and a ‘TGTG’ deletion in the 3’untranslated region (3’UTR). A family-based study from Guinea-Conakry confirmed the association with the intron 4 polymorphism and a case-control study has confirmed the association with the 3’UTR deletion in Koreans. Gao et al. have found associations with a 5’ promoter region polymorphism in
Japanese patients. Linkage to a chromosome 2 region, which includes the NRAMP1 gene, has been documented in a Canadian aboriginal family. However, the results from a linkage study in a Brazilian population showed no evidence of NRAMP1 involvement in susceptibility to TB. Moreover, a genome-wide screen demonstrates that NRAMP1 is not a major susceptibility gene in Gambians, in whom only a weakly positive linkage was shown to q23.5.

Slc11a1 is found in late endosomes and lysosomes but not in early endosomal membranes. It is unclear how Slc11a1 functions in the maturation of the phagosome nor in the reduced acidification found in mycobacterium-containing lysosomes. Slc11a1 is a proton/divalent cation transporter (Fe, Zn, Mn) which can move divalent cations in either direction against a proton gradient. Thus cations can be delivered from the cytosol to the acidic compartment of late endosomes/lysosomes, where they catalyse the production of reactive oxygen intermediates (ROI) including hydroxyl radicals. Killing of mycobacteria probably involves both ROIs as well as reactive nitrogen intermediates (RNI) generated by nitric oxide synthetase NOS2, and by apoptosis of macrophages induced by ATP through the P2X7 receptor.

Blackwell has defined four alleles containing different numbers of DNA repeats at positions (i)203, (ii)201, (iii)199 and (iv)189, with allele frequencies of (ii) and (iii) being 0.25 and 0.75 respectively. Using a reporter gene system, LPS drives five to eightfold higher gene expression by allele (iii) and significant reduction in expression by allele (ii). They proposed that the higher expressing allele (iii) with (GT)n polymorphism would be associated with autoimmune disease and the low-expressing allele (ii) with infection. Allele frequencies for SLC11A1 allele(ii) are in the range 0.14 to 0.20 in West and Southern Africa, compared with 0.25 to 0.29 in Northern Europe and 0.36 in Brazil. Individuals homozygous for iii/iii produced higher concentrations of TNF and were at significantly higher risk of severe clinical meningococcal disease (Hibbard, Levin & Blackwell).

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Discussion following lecture by K.P.W.J. McAdam

Fenton: Are there any data suggesting that similar susceptibility loci are involved in other populations and racial groups?

McAdam: Quite a large number of different places have been looked at, for instance for HLA. The NRAMP work has been done in South America, the USA and in Canadian aboriginals.

De Vries: For the known four associations – HLA, the vitamin D receptor, the NRAMP1 and interleukin-1 – there are several ways to get an idea to what extent they explain the genetic variability. Has that been studied?

McAdam: My understanding is that the heritability has been derived from the twin studies. In terms of the individual genes, not one of those comes up on the whole genome scan as a susceptibility area for linkage. So I suspect the contribution is quite small.

Ottenhoff: There was a recent paper by Adrian Hill’s group showing that there is a major locus at chromosome 10 estimated to contribute up to about 40% of the total genetic component in leprosy.¹ So that is actually quite a large contribution for a single locus.

De Groot: The paper by Wilkinson et al. on West Gujarati Indians clearly showed the gene-environment interaction in an infectious disease.² Do you know what happened in the follow-up of this population? Are they prescribing vitamin D for these people, and does it have an effect on the susceptibility to tuberculosis?

McAdam: I am told that the authors are not using vitamin D therapy or suggesting any intervention. I would actually like to know whether anyone else is considering vitamin D therapy and how this would be tested. Vitamin D has been used historically and in the book by Dubos & Dubos it is recorded that quite a lot of people did worse with vitamin D therapy.³ They seemed to lyse their lungs. So I’m not sure about this intervention, except for skin tuberculosis – there vitamin D is very effective.

Van der Meer: We would rather use vitamin A and zinc supplementation in view of a placebo-controlled study in Indonesia in which we were involved.⁴ After two months the supplement had a distinct effect on both wellbeing and the X-ray signs of the tuberculosis. This effect was lost after six months, probably because there was no resistant tuberculosis among the patients, and all of them responded well to the antituberculous drugs which were given concomitantly.

McAdam: And the people on isoniazide, did they do as well as the people on isoniazide plus zinc and vitamin A?

Van der Meer: The latter group did better. All this has still to be confirmed in a larger independent study.

McAdam: How are we, as a clinical investigating community, going to respond to genes that are going to be accumulative in terms of their effect? If you select patients with a particular vitamin D receptor genotype, you do not actually know – unless you type their genes – what other susceptibility loci they have. Ottenhoff’s suggestion of using the array technology to develop a haplotype might have to be followed before one can actually look at functional genomics.

El-Omar: Quite a number of populations that are predisposed to tuberculosis also have a high incidence of starvation, malnutrition, malabsorption enteropathies and so forth.
To what extent do you think these environmental factors are modifying the genetic constitution in terms of expression of the disease, either towards susceptibility or towards responding to the infectious agent?

McAdam: That is a very pertinent question, to which I do not know the answer. Common sense says it must make a huge difference, and if you look at animal studies, it does make a dramatic difference. When you look at guinea pigs that are fed a protein-deficient diet and then are challenged with aerosol tuberculosis they die very rapidly, whereas protein-sufficient animals do not. Of course, many of these patients, by the time you see them, have a nutritional problem. With tuberculosis they have lost weight, they have had fever, they have got lots of inflammatory cytokines on board. We are doing a prospective case-contact study at the moment trying to analyse that, but it is not easy to investigate.

Appelmelk: I am confused about how vitamin D works, if it works. You stated that it causes macrophage activation and then bacteria are killed, but at the same time, as you said, it causes a shift from Th1 to Th2, meaning the opposite.

McAdam: It originates from studies done by Graham Rook and the supposition is that vitamin D modulates the cytokine profile, leading to proinflammatory cytokine production.1

Netea: I wonder whether we are on the right track if we are not taking into account that susceptibility to mycobacteria may vary depending on the strain. This would hold for M. tuberculosis versus atypical mycobacteria but perhaps also within M. tuberculosis isolates. I am thinking for instance of the Beijing strains.

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The role of interleukin-1 beta in \textit{Helicobacter pylori}-associated disease

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\textbf{A B S T R A C T}

\textit{Helicobacter pylori} infects half the world’s population and is associated with serious human diseases including peptic ulcer disease and gastric neoplasia. The clinical outcome is largely dependent on the severity and distribution of the \( H. \text{pylori} \)-induced gastritis. The reasons for such variable clinical outcomes remain poorly understood. Bacterial virulence factors contribute to the pathogenicity but do not explain the divergent outcomes. There is emerging evidence that host genetic factors play a key role in determining the clinical outcome to \( H. \text{pylori} \) infection. In particular, proinflammatory genotypes of the interleukin-1 beta (IL-1\( \beta \)) gene are associated with increased risk of gastric cancer and its precursors. The effects are most likely mediated through induction of hypochlorhydria and severe corpus gastritis with subsequent development of gastric atrophy. In this article we discuss the role of IL-1\( \beta \) and other host genetic factors in the pathogenesis of \( H. \text{pylori} \)-related disease.

\textbf{IN T R O D U C T I O N}

It has long been established that human susceptibility to infectious agents is at least partly under genetic control. Several observations from twin, adoptee, pedigree, and candidate gene studies point to host genetic factors as key determinants of this susceptibility.\(^1\) The recent explosion in genetic knowledge, accelerated by the human genome project, is helping to unravel the molecular pathways that mediate genetic susceptibility to human diseases, including infections and cancer.\(^1\) While genetic susceptibility may apply to the risk of acquisition of an infectious agent, it is becoming increasingly recognised that host genes also influence the pathophysiological response to infections, which ultimately determines the clinical outcome.

The role of infectious agents in carcinogenesis has commanded significant scientific interest culminating in five Nobel prizes in the 20\(^{th} \) century.\(^5\) Infections can cause cancer by a variety of mechanisms including direct transformation of cells, induction of immunosuppression with consequent reduced cancer immunosurveillance, or by causing chronic inflammation. The last-mentioned is becoming increasingly recognised as an essential component of many epithelial cancers by virtue of its combined effects of generating genotoxic by-products and increased cellular proliferation, thus maximising the potential for DNA damage.

In this article, I hope to demonstrate how interactions between an infectious agent, host genetic makeup, and environmental factors could influence the pathogenesis of a cancer. The infectious agent in question is \textit{Helicobacter pylori}, the world’s commonest chronic bacterial infection, and the malignancy is gastric cancer, second only to lung cancer in its global incidence and impact. We demonstrate how this gastric infection could be utilised as a paradigm for gene-environment interactions in human disease, one that could help unravel a multitude of other microbially induced malignancies.

\textbf{HE LICOBACTER PYLORI INFECTION}

The \textit{Helicobacter} genus consists of at least 24 species found in the GI tracts of animals and humans.\(^6\) One of these species is \textit{Helicobacter pylori} (\( H. \text{pylori} \)), a Gram-negative, spiral-shaped, micro-aerophilic, urease-positive bacillus, which is known to chronically infect the stomachs of over half the world’s population. The infection is acquired during childhood, most probably via the faecal/oral or gastric/oral routes, and if not treated with antibiotics, will persist throughout life.\(^7\) The organism is 2.5 to 5 micrometers long...
with four to six unipolar flagellae. These flagellae are thought to allow it to move through the mucus layer within the stomach and come to reside between this layer and the gastric epithelium. Eighty percent of the bacilli are free; however the remainder are attached to epithelial cells. Once attached, the organism induces ultra-structural changes in the gastric epithelial cells. Although the bacteria mainly reside on the surface mucus gel layer with little invasion of the gastric glands, the host responds with an impressive humoral and cell-mediated immune response. This immune response is largely ineffective, however, as most infections become chronically established with little evidence that spontaneous clearance occurs.

*H. pylori* can only proliferate on gastric epithelial cell surfaces and in the overlying mucus layer. Thus *H. pylori* has to survive in one of the harshest and least hospitable niches in the human body. Gastric acidity acts as a formidable first line of defence against food-borne pathogens, and the constant outpouring of gastric secretions, coupled with regular peristalsis, ensure that gastric contents, including microbial agents, are constantly flushed away. Despite this, *H. pylori* seems well equipped and adapted for habitation within this harsh environment. Recent studies show that *H. pylori* maintains its periplasmic pH within viable limits through possession of an acid-induced urea channel that regulates intra-bacterial urease activity. Essential nourishment for *H. pylori* is drawn from host gastric tissue through the inflammatory exudate it induces.

Since its original description and culture by Marshall and Warren in 1982, *H. pylori* has been causally implicated in a variety of gastric diseases including simple gastritis, gastric and duodenal ulcer disease, and gastric cancer. While the link between *H. pylori* and peptic ulcer disease was established soon after successful culture of the bacterium, the association with gastric cancer lagged almost a decade before credible evidence was presented. The major reason for this delay was inability to demonstrate the presence of active infection in gastric tissue of cancer patients. In order to understand how this bacterium can predispose to such variable clinical outcomes, it is necessary to understand the basic pathophysiological consequences of its presence within the human stomach.

**H. pylori and Chronic Gastric Inflammation**

The key pathophysiological event in *H. pylori* infection is the initiation of an inflammatory response. This response is mostly probably triggered by the bacterium’s lipopolysaccharide, urease, and/or cytotoxins and is mediated by cytokines. Cytokines, including the interleukins, are soluble peptide molecules that mediate the interaction between immunocompetent and haematopoietic cells and between the immune and neuroendocrine systems.

In addition to their pro- or anti-inflammatory properties, some *H. pylori*-induced cytokines have direct effects on gastric epithelial cells that have a profound effect on gastric physiology. For example, the proinflammatory cytokine interleukin-1 beta (IL-1β) is the most potent of known agents that are gastric cytoprotective, antiulcer, antisecretory, and inhibitory of gastric emptying. Wolfe and Nompleggi estimated that on a molar basis, IL-1β is 100 times more potent than both prostaglandins and the proton pump inhibitor omeprazole and 6000 times more potent than cimetidine in inhibiting acid secretion. Another important proinflammatory cytokine that is upregulated by *H. pylori* infection is tumour necrosis factor alpha (TNF-α), which also inhibits gastric acid secretion, but to a lesser extent than IL-1β.

In physiological terms, the stomach could be divided into two main compartments: an acidic proximal corpus that contains the acid-producing parietal cells, and a less acidic distal antrum that does not have parietal cells but contains the endocrine cells that control acid secretion. *H. pylori* infection is first established in parts of the stomach that have a higher pH such as the antrum. This is most likely due to the bacterium’s attempt at energy preservation, for although *H. pylori* is well equipped for survival at low pH, this is achieved at a high cost of energy expenditure. Thus, high acid production by the parietal cells probably protects the corpus mucosa from initial colonisation. Both animal and human ingestion studies suggest that successful colonisation of the gastric mucosa is best achieved with the aid of acid suppression. Furthermore, pharmacological inhibition of acid secretion in infected subjects leads to redistribution of the infection and its associated gastritis from an antral to a corpus-predominant pattern. Thus lack of gastric acid extends the area of colonisation and also maximises the tissue damage resultant from this colonisation.

**H. pylori Infection and the Divergent Clinical Outcomes**

*H. pylori* infection is associated with divergent clinical outcomes that range from simple asymptomatic gastritis
to more serious conditions such as peptic ulcer disease and gastric neoplasia. The extent of this remarkable divergence is made more striking by the observation that certain outcomes of the infection, such as duodenal ulcer disease, are actually protective against others, such as gastric cancer. The key determinants of these outcomes are the severity and distribution of the *Helicobacter pylori*-induced gastritis. There are three main gastric phenotypes that result from chronic *H. pylori* infection: (1) the commonest by far is a mild pangastitis that does not affect gastric physiology and is not associated with significant human disease, (2) a corpus-predominant gastritis associated with gastric atrophy, hypochlorhydria and increased risk of gastric cancer, and (3) an antral-predominant gastritis associated with high gastric acid secretion and increased risk of duodenal ulcer disease. The association of *H. pylori* with such variable outcomes poses a most fascinating scientific challenge, the unravelling of which will not only explain how ulcers and gastric cancer develop, but will also act as a paradigm for gene-environment interactions in most human diseases.

**H. pylori Induces Variable Gastric Phenotypes: The Gastric Cancer Versus Duodenal Ulcer Phenotypes**

There is accumulating evidence that acid secretory capacity is crucial in determining the distribution and natural history of *H. pylori* infection. In hosts with low secretory capacity (genetically determined or secondary to pharmacological inhibition) the organism is capable of colonising a wider niche than would be possible in the presence of high volumes of acid. Colonisation of a wider niche, including the corpus mucosa, leads to corpus gastritis with resultant functional inhibition of acid secretion. This inhibition is mediated by *H. pylori*-induced inflammatory cytokines (such as IL-1β and TNF-α) and the net effect is the establishment of a more aggressive gastritis that accelerates the development of gastric atrophy. Once atrophy develops, acid secretion is not only attenuated by the functional inhibition caused by inflammatory mediators but by a more permanent morphological change that is harder to reverse. This situation is very relevant to the subgroup of humans who develop the gastric cancer phenotype in the presence of chronic *H. pylori* infection.

In contrast to subjects who have an increased risk of gastric cancer, subjects who develop duodenal ulcer disease are known to have a large parietal cell mass that is relatively free of *H. pylori*-induced inflammatory activity. This pattern of antral-predominant gastritis with high acid output characterises the duodenal ulcer diathesis. The high acid output is associated with the development of duodenal gastric metaplasia (DGM), a protective mechanism against the persistent delivery of an increased acid load to the duodenum. The presence of gastric epithelium (DGM) in the duodenum is an invitation for antral *H. pylori* infection to colonise this new niche. The ensuing gastritis with the production of proinflammatory cytokines such as IL-1β and TNF-α greatly weakens the resistance of this mucosa, and in the presence of large volumes of acid, and a reduction in duodenal mucosal bicarbonate production, ulcers develop.

As mentioned above, the effect of acid secretion on changing the distribution of *H. pylori* colonisation and gastritis is most markedly exposed in subjects in whom acid secretion is manipulated by pharmacological means. Thus *H. pylori*-infected subjects on long-term proton pump inhibitors undergo a shift in the pattern of gastritis from antral- to corpus-predominant, and they have a higher risk of developing gastric atrophy, a precursor lesion for gastric neoplasia. This observation provided a clue as to the role of potential endogenous substances that could also inhibit acid secretion, such as IL-1β and TNF-α. As will be discussed later, these two cytokines were prime candidates as host genetic factors that may increase risk of gastric cancer. IL-1β is the archetypical pleiotropic cytokine being produced by many cells and exerting its biological effects on almost all cell types. IL-1β is a very potent proinflammatory cytokine and is involved in the host’s response to many antigenic challenges.

**Genetic Polymorphisms in the IL-1 Gene Cluster Increase the Risk of Gastric Cancer and Its Precursors**

The key question in *H. pylori* research is how this infection could be associated with such divergent clinical outcomes as gastric cancer and duodenal ulcer disease. A large volume of research has focused on the role of bacterial virulence factors in the pathogenesis of these diseases, and although these factors undoubtedly contribute to the degree of tissue damage, they do not distinguish between the two key outcomes. This prompted us to concentrate on the host genetic factors that may be relevant to this process. The search for the appropriate candidate genes had to stem from a profound understanding of gastric physiology and how it is disrupted by *H. pylori* infection. Since *H. pylori* achieves most of its damage through induction of chronic inflammation, it was reasonable to consider genes that control this process as appropriate candidates.

The IL-1 gene cluster on chromosome 2q contains three related genes within a 430 kb region, IL-1A, IL-1B and IL-1RN, which encode for the proinflammatory cytokines...
IL-1α and IL-1β as well as their endogenous receptor antagonist IL-1ra, respectively. IL-1β is upregulated in the presence of H. pylori and plays a central role in initiating and amplifying the inflammatory response to this infection. IL-1β is also an extremely potent inhibitor of gastric acid secretion; on a molar basis it is estimated to be 100-fold more potent than proton pump inhibitors and 6000-fold more potent than H2-antagonists. Three di allelic polymorphisms in IL-1β have been reported, all representing C-T transitions, at positions -511, -31, and +3954 bp from the transcriptional start site. There are conflicting data regarding the functional effects of these polymorphisms on IL-1β production. The IL-1RN gene has a penta-allelic 86 bp tandem repeat (VNTR) in intron 2, of which the less common allele 2 (IL-1RN*2) is associated with a wide range of chronic inflammatory and autoimmune conditions. IL-1RN*2 is associated with enhanced IL-1β production in vitro, but data regarding its effects on IL-1ra production are contradictory. The gene also has a number of functionally relevant polymorphisms that could be correlated with high or low IL-1β production. This provided an ideal opportunity to design the appropriate hypothesis-driven epidemiological studies.

We first studied the correlation of these high IL-1β genotypes (two polymorphisms in the IL-1B and IL-1RN genes) with hypochlorhydria and gastric atrophy in a Caucasian population of gastric cancer relatives. These relatives are known to be at increased risk of developing the same cancer and have a higher prevalence of the precancerous abnormalities, but only in the presence of H. pylori infection. We found that the high IL-1β genetic markers significantly increase the risk of these precancerous conditions. In a logistic regression model including both genotypes, the estimated age-adjusted odds ratios for IL-1B-511/311*2 and IL-1RN*2/*2 were 7.5 (95% CI: 1.8-31) and 2.1% (95% CI: 0.7-6.3) respectively. We proceeded to examine the association between the same IL-1β genetic polymorphisms and gastric cancer itself utilising another Caucasian case-control study comprising 366 gastric cancer patients and 429 population controls. We confirmed the same positive association between these genotypes and gastric cancer. In a logistic regression model including both genotypes, the estimated odds ratios for IL-1B-511/311T* and IL-1RN*2/*2 were 1.5 (95% CI: 1.2-2.2) and 2.9 (95% CI: 1.9-4.4) respectively.

Although IL-1β was the perfect candidate gene, other genes involved in the H. pylori-induced gastritis cascade are also legitimate targets. Our most recent search has confirmed a positive but weaker role for polymorphisms in the TNF-A gene that correlate with high TNF-α levels (El-Omar et al., unpublished data). The TNF-α polymorphism increases the risk of gastric cancer and its precursors in a similar fashion to the IL-1β polymorphisms. This proinflammatory cytokine is also upregulated in H. pylori infection and has acid-inhibitory properties, albeit weaker than IL-β. So it is clear that the targeted and hypothesis-driven search for these host genetic factors will aid in unravelling the pathogenesis of H. pylori-related diseases.

But how do these IL-1β/TNF-α polymorphisms explain the divergent outcome to H. pylori infection? We speculate that the effect of these polymorphisms operates early in the disease process and requires the presence of H. pylori infection. When H. pylori infection challenges the gastric mucosa, a vigorous inflammatory response with a high IL-1β/TNF-α component may appear to be beneficial, but it has the unfortunate side effect of switching acid secretion off, thus allowing the infection to extend its colonisation and damaging inflammation to the corpus mucosa, an area that is usually well protected by secretion of acid. A decreased flow of acid will also undermine attempts to flush out these toxic substances, causing further damage to the mucosa. More inflammation in the corpus leads to more inhibition of acid secretion and a continuing cycle that accelerates glandular loss and onset of gastric atrophy. It is apparent that this vicious cycle ultimately succeeds in driving the infection out, but at a very high price for the host. This is amply demonstrated by the finding that H. pylori density becomes progressively lower with the progression from mild gastritis through severe gastritis, atrophy and intestinal metaplasia. Indeed, by the time gastric cancer develops, it is extremely hard to demonstrate any evidence of the infection.

**ROLE OF ENVIRONMENTAL FACTORS IN GASTRIC CARCINOGENESIS**

A very obvious question at this juncture is why only a few H. pylori-infected subjects with these polymorphisms develop gastric cancer. Why isn’t everyone with such a genetic makeup at risk of this outcome? The answer lies in the polygenic and multifactorial nature of most complex human diseases. These genetic factors operate only in the presence of an infectious agent and lead to the development of an atrophic phenotype. Progression of atrophy towards cancer depends on other components of the host genetic constitution acting epistatically, as well as dietary and other factors in the environment. While H. pylori infection and host genetics interact to initiate a hypochlorhydric and atrophic phenotype, environmental co-factors may mediate subsequent neoplastic transformation, even after disappearance of the infection. Diet may be particularly relevant, with greater consumption of fresh fruits and vegetables shown to protect against the risk of gastric as well as several other cancers. Dietary vitamin C reduces the formation of...
N-nitroso-compounds and scavenges mutagenic reactive oxygen metabolites generated by gastric inflammation, and supplemental vitamin C is associated with significantly lower risk of noncardia gastric cancer. Furthermore, vitamin C concentrations and bioavailability are reduced in the presence of *H. pylori* infection. Another important co-factor is cigarette smoking, which was found to nearly double the risk of transition from atrophic gastritis to dysplasia in a high-risk population. Thus, cytokine gene polymorphisms represent only one component of a complex interplay among host, pathogen, and environmental factors involved in gastric carcinogenesis.

These proinflammatory polymorphisms, therefore, can distinguish between subjects who will develop the hypochlorhydric atrophic phenotype in response to *H. pylori* infection and those who will manage to limit the infection to a smaller area and offer relatively better protection of their corpus function. Another valid question is whether these proinflammatory polymorphisms actually offer protection against the other extreme clinical outcome, namely, duodenal ulcers. Could it be that a low IL-1β/TNF-α response to *H. pylori* infection, and a consequently lower inhibition of acid secretion, is the determinant of the antral-predominant, corpus-sparing gastritis pattern seen in duodenal ulcer patients? To date, no reports have been published addressing this specific question. It would be tempting to speculate that this would be the case, but my gut feeling is that the large parietal cell mass frequently seen in duodenal ulcer patients is determined by other genetic factors, hitherto undescribed, that relate to parietal cell development and the endocrine receptors they express. This genetically determined capacity to secrete large volumes of gastric acid will probably neutralise any subtle contribution of a genetic polymorphism in a cytokine gene.

**CONCLUSIONS AND A LOOK TO THE FUTURE**

IL-1β is a very important proinflammatory cytokine with profound effects on gastric physiology. Its acid-inhibitory properties uniquely qualify it as a major player in the host’s response to *H. pylori* infection and the diseases associated with it. Polymorphisms in the gene for IL-1β that correlate with higher levels of this cytokine have been found to increase the risks of hypochlorhydria and gastric atrophy in response to *H. pylori* infection and to increase the risk of gastric cancer itself. These host genetic factors that affect IL-1β may determine why some individuals infected with *H. pylori* develop gastric cancer while others do not. Future research should focus on identifying the molecular pathways that mediate this increased risk. The search for other host genetic factors that contribute to the pathogenesis of the disease should continue, particularly in view of the wonderful new opportunities made possible by the human genome project. A special effort should be directed at understanding these host genetic factors in non-Caucasian populations, and in populations with high and low incidences of gastric cancer. We should also target other upper GI diseases that may be linked indirectly to these genetic polymorphisms that alter gastric physiology. Prime amongst these are oesophageal cancers and gastro-oesophageal reflux disease.

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Van der Meer: Being a person who performs research with interleukin-1, I would be interested to hear why you left interleukin-1α out. Conceptually, IL-1α would also be an interesting candidate. I wonder if you did consider that and if you have data on it?

El-Omar: It is a very good point. We did not ignore interleukin-1α. IL-1α does not have any effect whatsoever on this particular model.

Kimman: Your genetic data appear very convincing, but are they supported by physiological data? Do people with a proinflammatory genotype really have higher IL-1β levels in their gastric lesions than people with a less inflammatory genotype?

El-Omar: Polymorphism has to be functional. There are some data showing these proinflammatory genotypes to be associated with higher IL-1β levels, but it is pretty weak. The IL-1 receptor antagonist is probably the strongest. Allele 2 of that VNTR polymorphism is probably the strongest that we have. It is actually very difficult to measure the cytokine content and correlate that with genetic polymorphisms. In the presence of the infection, depending on the severity, it may be quite difficult to correct for the degree of inflammation in that particular locus. We lack tools to address this question appropriately and we are lagging behind in terms of explaining the physiological effects of these polymorphisms, but the epidemiological data are pretty powerful.

Netea: IL-1 receptor antagonist is approved for treatment of rheumatoid arthritis and anti-TNF treatments have already been in use for a couple of years. Is there anything known about whether this pattern of gastric pathology is changing in some of the patients who also have *Helicobacter* infections?

El-Omar: A very interesting question. We have not been studying this. Rheumatologists are probably not going to look for changes in the stomach. It is a very worthy experiment to perform, perhaps in an animal model.

Netea: Would patients with a duodenal ulcer, who receive anti-TNF for rheumatoid arthritis, get worse as a result of the treatment?

El-Omar: Nothing is known about that, but people with rheumatoid arthritis who get ulcers usually get them because of nonsteroidal anti-inflammatory drugs. So you are dealing with two different issues, which makes it difficult.

Van der Meer: The nonsteroidal anti-inflammatory drugs should inhibit prostaglandins and thereby upregulate cytokine production. So you get into complicated counterregulatory mechanisms.

El-Omar: And the link between the effect of NSAIDs and *H. pylori* is very controversial.

Van Deuren: It is even more complicated, because IL-1 upregulates cortisol. High IL-1 producers may have higher cortisol levels and therefore a higher acid secretion. On the other hand IL-1 would decrease acid secretion. Physiological tests would be decisive, I think.

El-Omar: I do not think experiments have been conducted that address these questions.

Van Deuren: We are often considering whether we should perform a repetitive gastroscopy in patients with atrophic gastritis and if so, how many times – once every three years, once or twice a year? Do you envisage that in the future, genetic make-up will be decisive in the scheme for endoscopic control?

El-Omar: It is of course much simpler to test for HP infection and if you find it, get rid of it. The genetic make-up becomes unimportant. The value of these genetic studies and genetic markers, from my point of view, is in understanding the pathogenesis.

Kusters: Clearly there are markers for severity and for susceptibility. Could it be that your population is biased regarding the susceptibility to infection with *H. pylori* and how would that affect your data?

El-Omar: What I have shown is that these markers influence the severity and the outcome of the infection, not necessarily the susceptibility. We looked at susceptibility originally and found that high IL-10 genotypes will increase the risk of contracting a chronic *H. pylori* infection. This suggests that an anti-inflammatory Th2-driven response allows this infection to persist. We found this in two populations in two studies, but in a third, much larger study I could not reproduce the same data, and that made me reluctant to claim that high IL-10 genotypes increase the risk of acquiring the infection. However, mice that consecutively produce more IL-10 have persistent *Helicobacter* infection, while mice with a vigorous Th1-driven cytokine response clear the infection.
Appelmelk: I can understand how inflammation shuts down acid production, but I am puzzled how a shutdown of acid would act the other way around. In your view, the cause is the shift of the bacteria from antrum to corpus, but what is the evidence? In the mouse colonisation is exclusively localised in the antrum. Yet there is strong atrophy in the corpus. Could you envisage a model where the bacteria are not needed and still an acid-induced increased inflammation occurs in the corpus?

El-Omar: There are only two experiments where people have either ingested or acquired acute H. pylori infection. When Marshall and Morris just took a preparation and swallowed it, there was colonisation only when they took acid inhibitors. So it looks as though you have to switch off the acid secretion to allow the bacteria to take hold in the stomach. The other fact is that when H. pylori is first acquired, it tends to settle in the less acidic parts of the stomach. That is why you get maximal colonisation in the antrum. Although Helicobacter is unique in surviving in an acidic environment, it is at the cost of high energy expenditure. It has to use a lot of its machinery to try and protect itself from the acid exposure. Acid secretion seems to determine how extensive the colonisation in the stomach will be. Now, if interleukin-1β is poured out to fight this infection and at the same time acid secretion is switched off, the infection does extend from the antrum to the corpus leading to a more severe corpus gastritis. But the counts are probably even slightly reduced in both areas. What is happening here is a pouring out of acid from the glands trying to flush out all the toxins and all the mediators. If the acid secretion is switched off, you have basically got a dry part of the stomach where maximal concentrations of these damaging genotoxic substances can exert their effect.

McAdam: In West Africa the babies seem to be getting infected at weaning or before. By the age of one, using noninvasive tests, we have a Helicobacter infection rate of approximately 80%. This has been ascribed to all sorts of things, but certainly to malnutrition. Around the age of approximately 80%. This has been ascribed to all sorts of infected at weaning or before. By the age of one, using H. pylori infection. Does it look as though you have to switch off the acid secretion to allow the bacteria to take hold in the stomach? The other fact is that when H. pylori is first acquired, it tends to settle in the less acidic parts of the stomach. That is why you get maximal colonisation in the antrum. Although Helicobacter is unique in surviving in an acidic environment, it is at the cost of high energy expenditure. It has to use a lot of its machinery to try and protect itself from the acid exposure. Acid secretion seems to determine how extensive the colonisation in the stomach will be. Now, if interleukin-1β is poured out to fight this infection and at the same time acid secretion is switched off, the infection does extend from the antrum to the corpus leading to a more severe corpus gastritis. But the counts are probably even slightly reduced in both areas. What is happening here is a pouring out of acid from the glands trying to flush out all the toxins and all the mediators. If the acid secretion is switched off, you have basically got a dry part of the stomach where maximal concentrations of these damaging genotoxic substances can exert their effect.

El-Omar: Theoretically, if the infection is acquired at a much earlier age, at the time when the stomach is not fully developed in terms of its acid secretion, the phenotype should be more in keeping with the gastric atrophy and low acid secretion and that should increase the risk of developing gastric cancer. In addition, the Africans tend to have a so-called proinflammatory genetic make-up. Yet we do not see such a dramatic increase in gastric cancer. Whether they do not live long enough to develop it, or whether there are other conditions that are modifying the inflammatory response, has not been addressed. One very interesting experiment came from Fox et al. They looked at the role of co-infection with helminths. It showed that in an animal model, if you co-infect with a helminth the system tries to switch the immune response from a Th1 to a Th2, which attenuates your inflammatory response and prevents gastric atrophy. It may be that in these populations, where you have such a high prevalence of H. pylori, yet you have very little clinical disease, there are other factors, other bacteria that may be modulating this inflammatory response.

Peña: There is a great difference between duodenal ulcer and gastric ulcer. There are families that either develop gastric ulcers or duodenal ulcers. Did you study this kind of polymorphism?

El-Omar: It is fascinating that in the West duodenal ulcer and gastric cancer so seldom both strike in one patient. Classically, the people who develop gastric cancer are the ones in whom there has been manipulation of acid secretion: they either have had a vagotomy or surgery that basically attenuates their acid production. Some people would argue that inhibition of gastric acid over many years could be the reason why these people basically switch from being protected towards being at risk. Some fascinating data from Japan recently showed that regarding the proinflammatory genotype, this genetic constitution in people who have DU disease at the beginning, at an early age, when they are in their teens or in their early twenties, if you follow them long enough, you will see very few people with this proinflammatory genotype actually having duodenal ulcer disease or a relapse of duodenal ulcer disease. So it may increase the risk at an early age, but it burns out, and the reason it burns out is presumably because of the effects on the corpus mucosa, discontinued inflammation, the onset of atrophy, and eventually they basically become less protected against gastric cancer and more likely to show the hypochlorhydria atrophic phenotype. The question of looking at gastric ulcers vs duodenal ulcers has not been addressed properly and there is one study looking at the effect of these polymorphisms on peptic ulcer disease.3

References
The role of polymorphisms in chemokines and chemokine receptors in the clinical course of HIV-1 infection

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Abstract

The outcome of HIV-1 infection is highly variable: not all individuals exposed to HIV-1 will become infected, and among individuals who do become infected the time from infection to clinical AIDS is highly variable. This variability is thought to reflect the complex interactions between virus and host. An important role for host genetic factors in the pathogenesis of HIV-1 infection is increasingly being appreciated. Many novel genetic polymorphisms have been identified and analysed for their role in HIV-1 transmission and disease progression. Here an overview is provided of polymorphisms in chemokines and chemokine receptors that influence HIV-1 disease.

Introduction

The clinical course of HIV infection

HIV-1 infection is characterised by a gradual and progressive loss of CD4+ T cells, ultimately leading to the acquired immunodeficiency syndrome (AIDS), which is characterised by opportunistic infections, neurological symptoms and malignancies. Among patients, the clinical course of HIV-1 infection is highly variable. Before antiretroviral therapy became available, the asymptomatic phase of infection could take only months (rapid progressors) or last for more than 15 years (long-term asymptomatics, LTA). Between these extremes, the median time from infection to AIDS diagnosis is eight to ten years.1

The course of HIV infection may be influenced by both viral and host factors. The host fights infection by generating HIV-specific cytotoxic T cells and antibodies. The error-prone nature of HIV-1 reverse transcriptase results in the generation of a spectrum of HIV-1 mutants in each replication cycle (viral quasi-species). The growth advantage of mutants with altered antigenic structures (escape mutants) allows the virus to escape from the suppressive action of the immune system. The variable nature of HIV-1 also results in the evolution of other biological characteristics, such as replicative capacity, cytopathicity and cellular tropism.

Though the significance of the humoral immune system to protect against AIDS remains controversial, cytotoxic CD8+ T cells have been shown to significantly influence HIV-1 disease progression. Depletion of CD8+ T cells in simian immunodeficiency virus (SIV)-infected macaques leads to a rapid increase in viral replication.2 In humans, the presence of CTL has been associated with reduced viral load and a more benign disease course.3-5 The importance of the viral phenotype for HIV-1 pathogenesis is supported by multiple studies: experimental infection of macaques with late-stage SIV variants resulted in a more rapid disease progression than infection with early isolates;6 extremely slow progression of disease was observed in haemophiliacs who were infected with an attenuated virus that lacked the regulatory viral gene nef;7 and long-term nonprogressors more often harbour virus variants with slow in vitro replication kinetics.8

Another aspect of the HIV-1 phenotype is the so-called syncytium-inducing (SI) capacity. SI HIV-1 variants first got their name as they are able to infect and induce fusion of cells into multinucleate cells (syncytia) in T-cell lines, due to their ability to use chemokine receptor CXCR4 as a viral coreceptor (therefore SI HIV variants are also referred to as X4 HIV-1 variants).9 Nonsyncytium-inducing (NSI)
HIV-1 variants are in general restricted to CCR5 usage (R5 HIV-1 variants). Whereas HIV-1 infection is in general established by a homogenous population of macrophage tropic NSI / R5 HIV-1 variants. SI / X4 HIV-1 variants may evolve from these R5 variants in approximately half of the HIV-1 infected patients. The emergence of these X4 variants in patients is associated with a more rapid loss of CD4+ T cell numbers and a more rapid progression to AIDS.\textsuperscript{10,11}

Chemokines, chemokine receptors and HIV-1

Chemokines are small, structurally-related molecules involved in chemotaxis of a large variety of cell types via interaction with G protein coupled 7-transmembrane spanning receptors. Chemokines play a role in a variety of biological processes, such as lymphocyte migration to sites of inflammation, migration through various lymphoid organs during lymphocyte development and in angiogenesis.\textsuperscript{12-14} In 1996, chemokine receptors were identified as coreceptors for entry of HIV-1 (for references see table 1). Viral entry is a multistep mechanism, in which the envelope protein gp120 in succession binds to the CD4 molecule and a chemokine receptor. This results in a series of conformational changes, which eventually leads to fusion of the viral and cellular membrane. Several members of the chemokine receptor gene family have been identified as HIV-1 coreceptors (table 1). Of these, CCR5 and CXCR4 are thought to be the most relevant \textit{in vivo}, whereas the \textit{in vivo} role of the additional chemokine receptors remains to be established. Cellular tropism of HIV-1 variants is primarily determined by coreceptor expression on the cell surface and coreceptor preference of the virus. Thus, CCR5 expressing cells, such as macrophages and memory CD4+ T cells, can be infected by R5 variants, whereas CXCR4 expressing cells, such as memory and naive CD4+ T cells, can be infected by X4 variants.\textsuperscript{15,16} Since naive cells are crucial in the process of T-cell renewal, the capacity of X4 HIV-1 variants to infect and eventually kill these cells may explain the more rapid CD4+ T-cell decline associated with the presence of X4 HIV-1 variants. It should be noted that post-entry restrictions on HIV-1 replication may also influence tropism, as shown for macrophages and resting T cells, that may not efficiently support HIV-1 replication despite expression of the appropriate coreceptors.\textsuperscript{7,18}

The natural ligands of the HIV-1 coreceptors, MIP1\textalpha, MIP1\textbeta, RANTES (ligands of CCR5) and SDF-1 (ligand of CXCR4), have been shown to inhibit virus replication \textit{in vitro}\textsuperscript{19-23} and enhanced \textit{in vitro} chemokine production by patient peripheral blood mononuclear cells (PBMC) has been associated with slow disease progression.\textsuperscript{24,25} Furthermore, expression levels of CCR5 have been shown to influence infectibility \textit{in vitro}.\textsuperscript{26,27} Therefore, it can be expected that genetic differences that influence the pattern and level of expression of chemokines and chemokine receptors may have a major impact on the course of HIV-1 disease.

<table>
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<tr>
<th>CHEMOKINE RECEPTOR FAMILY\textsuperscript{a}</th>
<th>RECEPTOR</th>
<th>LIGAND</th>
<th>NEW NOMENCLATURE FOR LIGAND\textsuperscript{b}</th>
<th>REFERENCE\textsuperscript{c}</th>
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<tr>
<td>CC</td>
<td>CCR2</td>
<td>MCP1-4</td>
<td>CCL2, CCL8, CCL7, CCL13</td>
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<td>CCR3</td>
<td>Eotaxin, Eotaxin-2, RANTES, MIP1\textalpha</td>
<td>CCL11, CCL24, CCL15, CCL13</td>
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<td>CCR5</td>
<td>MIP 1a, MIP 1b RANTES</td>
<td>CCL13, CCL4, CCL5</td>
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<td></td>
<td>CCR8</td>
<td>I-309</td>
<td>CCL1</td>
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<td></td>
<td>CCR9</td>
<td>TECK</td>
<td>CCL25</td>
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<tr>
<td>CXC</td>
<td>CXCR4</td>
<td>SDF-1</td>
<td>CXCL12</td>
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<tr>
<td></td>
<td>CXCR6/BONZO/STRL13\textsuperscript{d}</td>
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<td>CXCL16</td>
<td>113,114</td>
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<td>CX3C</td>
<td>CX3CR1</td>
<td>Fractalkine</td>
<td>CX3CL1</td>
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<tr>
<td>Orphan</td>
<td>BOB/GPR15</td>
<td>Unknown</td>
<td>CX3CL1</td>
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<td></td>
<td>GPR1</td>
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<td>AP1</td>
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<td>ChemR23</td>
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<td>Chemoattractant receptor</td>
<td>BLTR</td>
<td>LTB4</td>
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<td></td>
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<td>Virally encoded\textsuperscript{e}</td>
<td>US28</td>
<td>Broad spectrum of CC Chemokines, fractalkine</td>
<td>109,120</td>
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</tr>
</tbody>
</table>

\textsuperscript{a}Chemokines can be divided into four families on the basis of the spacing between two N-terminal cysteines. Chemokine receptors are named according to the family of chemokines they bind.\textsuperscript{b}A new nomenclature for chemokines based on chemokine family names, which consists of family name (C, CC, CXC, CX3C), 1. (for ligand) and the numbering of the respective gene, has recently been proposed.\textsuperscript{13,121} \textsuperscript{c}References for the papers first to describe the molecule as an HIV-1 coreceptor are cited.\textsuperscript{d}Given the recent identification of a ligand and assignment of a systematic name for this molecule, alternative naming is also given.\textsuperscript{e}This chemokine receptor is encoded by human cytomegalovirus.
POLYMORPHISMS IN CHEMOKINE RECEPTORS AND HIV-1 DISEASE PROGRESSION

CCR5 D32
Soon after the identification of chemokine receptors as the coreceptors for entry of HIV-1 into human CD4⁺ T cells, individuals were identified who had frequently been exposed to HIV-1, and yet remained uninfected due to a homozygous genotype for an inactivating deletion of 32 base-pairs in the CCR5 gene.⁴⁻⁶ This polymorphism in the CCR5 gene (CCR5 D32) leads to a premature frameshift and a nonfunctional protein that is not expressed on the cell surface. As with other polymorphisms, a large racial variation in the prevalence of the CCR5 D32 allele is observed. It is common among Caucasians, whereas it is virtually absent in African-Americans and Africans (table 2). The effects of CCR5 D32 on the course of HIV-1 disease have been widely studied, though primarily in cohorts of subtype B-infected homosexual men.⁷⁻¹⁰ In these studies, heterozygosity for CCR5 D32 has been associated with a delayed progression to AIDS. In an international meta-analysis of individual patient data from ten well-characterised cohorts of seroconverters, a relative hazard of 0.74 for progression to AIDS was obtained for CCR5 D32 heterozygosity.⁴⁵ The mechanism of protection most likely involves a reduction of the number of CCR5 positive cells and hence the number of potential target cells for HIV-1, which may result in reduced virus replication already during primary infection and subsequently a lower viral set-point.⁵⁰,⁵¹

In HIV-1-infected intravenous drug users, haemophiliacs and recipients of contaminated blood,⁴⁸⁻⁵⁰ no effect of CCR5 D32 on disease progression was observed, whereas a protective effect was observed among HIV-1-infected children.⁴⁴⁻⁴⁶ It remains to be established whether this is due to study design or whether the effect of CCR5 D32 is indeed dependent on risk group and route of transmission.

CCR5 promoter
The CCR5 5’ untranslated region (UTR) consists of three exons and two introns. In this region, 12 single nucleotide polymorphisms (SNPs) have been described,⁴⁴⁻⁴⁵ which may, in part, explain differences in basal expression levels of CCR5 among individuals homozygous for the wild-type non-deleted CCR5 gene. To standardise the different numbering systems for the CCR5 promoter in literature, a numbering system was recently proposed in which the first nucleotide of the translation start site is designated as position 1, the nucleotide immediately upstream of this position as position -1, and so on.⁴⁶ In the paragraph below, we will use this numbering system and show the alternative nomenclature between brackets.

Among SNPs in the promoter region of CCR5, a high degree of linkage disequilibrium exists, allowing the identification of four common haplotypes (P1 to P4) and six rare haplotypes (P5 to P10), consisting of different combinations of 10 SNPs.⁴⁵ The P1 haplotype, including T-2135C (alternative nomenclature G59029A or G303A) was independently described to be associated with a more rapid course of disease. SNP G-2459A (alternative nomenclature C927T or G59653T) is now considered to be part of the P1 haplotype. The association of these SNPs with enhanced disease progression was observed in different risk groups, such as homosexuals, haemophiliacs and perinatally-infected children.⁴⁴⁻⁴⁵ It is likely that these SNPs or linked mutations are involved in the regulation of transcription of CCR5, but results from reporter assays have been inconsistent thus far.⁴⁴⁻⁴⁵

CCR2 64I
A valine-to-isoleucine transition in the second transmembrane region of CCR2 (CCR2 64I) has been associated with a delayed progression to AIDS.⁴⁶ The protective effect of CCR2 64I is similar to the effect of CCR5 D32 (RH of 0.76 in meta-analysis of combined cohorts,⁴⁵ results from individual cohorts).⁴⁵⁻⁴⁷⁻⁴⁹ Though the effect of CCR2 64I on disease progression is obvious, the mechanism is still not understood. CCR2 is rarely used as a coreceptor and the mutated CCR2 molecule does not alter in vitro infectibility of cells,⁵¹⁻⁵² therefore it is unlikely that the polymorphism directly influences infection. The mutation in CCR2 is in strong linkage disequilibrium with a single-nucleotide polymorphism in the promoter of the CCR5 gene, C-1835T (alternative nomenclature C927T or G59653T)⁴⁴⁻⁴⁵ and may thus indirectly be involved in the regulation of expression of CCR5. However, neither basal expression levels of CCR5 nor transcription levels in primary lymphocytes were reduced in CCR2 64I heterozygotes.⁵¹⁻⁵² An effect on CCR5 expression has been suggested by the finding that re-expression of CCR5 after internalisation by N-terminal modified RANTES was less rapid in two out of three CCR2 64I heterozygotes.⁵¹ An alternative explanation for the effect of CCR2 64I was provided by Mellado et al., who showed that CCR2 64I protein was able to form dimers with CXCR4 after sensitisation with the cognate chemokines, whereas the normal CCR2 protein was unable to do so.⁴⁶ This capacity may thus reduce the amount of CXCR4 available on the cell surface among CCR2 64I carriers. This, however, does not explain the finding that CCR2 64I already affects the viral load early in infection, when in general only NSI / R5 variants are present.⁵²

CX3CR1 249I 280M
Although CX3CR1 is only used by a minority of HIV-1 variants as a coreceptor, an enhanced progression to AIDS was observed among patients homozygous for CX3CR1 variant V249I T280M. These two amino acid substitutions result in a reduced capacity to bind the cognate ligand.
Table 2
Common polymorphisms described in chemokines and chemokine receptor genes, reported to significantly influence HIV-1 disease progression in prospective cohort studies, for details see text

<table>
<thead>
<tr>
<th>GENE POLYMORPHISM (NAME)</th>
<th>REFERENCES</th>
<th>POLYMORPHISM FREQUENCY</th>
<th>ALLELIC EFFECT ON GENE PRODUCT</th>
<th>EFFECT ON HIV-1 DISEASE PROGRESSION</th>
<th>DISEASE MODIFYING GENOTYPE VS REFERENCE GROUP</th>
<th>REFERENCES</th>
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<tbody>
<tr>
<td>Deletion of 32 basepair (D32)</td>
<td>28-30</td>
<td>C: 0.08 A: 0.07</td>
<td>Defective protein, no expression on cell surface</td>
<td>Delayed, RH 0.76</td>
<td>D32/+ vs +/+</td>
<td>31-34</td>
</tr>
<tr>
<td>Val to Ile in first transmembrane region (64I)</td>
<td>50</td>
<td>C: 0.098 A: 0.151 H: 0.172</td>
<td>Amino acid substitution</td>
<td>Delayed, RH 0.76</td>
<td>64I/+ and 64I/64I vs +/+</td>
<td>31.3-34</td>
</tr>
<tr>
<td>SNP in promoter region G-2459A</td>
<td>44</td>
<td>C: 0.57 A: 0.43 H: 0.28</td>
<td>Enhanced promoter function</td>
<td>More rapid, RH 1.74</td>
<td>A/A vs G/G</td>
<td>47-49</td>
</tr>
<tr>
<td>SNP in promoter region G-2459A</td>
<td>45</td>
<td>C: 0.560 A: 0.4316 H: 0.009</td>
<td>Unknown</td>
<td>More rapid, RH 1.53</td>
<td>P1/P1 vs all other genotypes</td>
<td>47-49</td>
</tr>
<tr>
<td>Two amino acid substitutions (V249I T280M)</td>
<td>55</td>
<td>C: 0.135</td>
<td>Reduced ligand binding</td>
<td>Conflicting results</td>
<td>280 M/M vs T/T</td>
<td>56-57</td>
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<td>SNP in 3’ untranslated region (3’A)</td>
<td>62</td>
<td>C: 0.52 T: 0.48</td>
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<td>Conflicting results, RH 0.99</td>
<td>A/A or T/T</td>
<td>42-62-64</td>
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<tr>
<td>Two SNP in promoter region (G-28G, G-403A)</td>
<td>58</td>
<td>C: 0.148 T: 0.85 H: 0.160</td>
<td>Increased promoter activity</td>
<td>Delayed, RH 0.65</td>
<td>II/I vs II/I</td>
<td>n.a.</td>
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<tr>
<td>Intron variant (In1.1C)</td>
<td>61</td>
<td>n.a.</td>
<td>Reduced promoter activity</td>
<td>More rapid</td>
<td>n.a.</td>
<td>n.a.</td>
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*aReference for the study in which the polymorphism was originally described. **Allelic frequencies of the polymorphisms may vary between different races. Here, allelic frequency of Caucasians (C), Hispanics (H) and African Americans (A) are shown, if available. ***22 additional mutations leading to an amino acid substitution have been described in the coding region of CCR5. Of these, only one allele was associated with reduced entry of HIV-1, and three with a limited ability to bind MIP1α. Due to the low prevalence of the mutations, effects on disease progression cannot be established in a cohort study. **Relative hazard as obtained in meta-analysis of individual cohorts. **According to recently proposed nomenclature. **G-2459 is now considered a part of the P1 haplotype. As the study population in both studies is partially overlapping, the results obtained should not be considered confirmatory. **Allelic frequency of the disease modifying haplotype (P1) is shown. **Due to the linkage disequilibrium between these SNPs, three haplotypes were identified (haplotype I: -403G -28C, II: -403A -28C and III: -403A -28G). Prolonged survival was observed among individuals carrying haplotype I and II as compared with homozygotes for haplotype I. **Allelic frequency for haplotype I is given. **A strong linkage disequilibrium between intron variant In1.1C and SNPs at position -28, -403 of the RANTES promoter is observed. In1.1C almost always occurs in conjunction with -403A. Therefore, results from these survival studies should be considered as conflicting. **This study is not available in print yet, therefore, further details are missing.
The effect on the course of HIV-1 infection could, however, not be confirmed in three US-based cohort studies.37

POLYMORPHISMS IN CHEMOKINES AND HIV-1 INFECTION

RANTES promoter
Beta-chemokines can block HIV-1 infection via CCR5 in vitro39-41 and high production levels of these chemokines have been associated with less rapid disease course.44-45 In vitro RANTES production levels can vary widely among PBMC from different individuals, which in part may be due to differences in the genetic make-up of the RANTES gene. Two SNPs were identified within the RANTES promoter region (C-28G and G-403A)58-60 and recently a variant in intron 1 (In1.1C) was identified.61 These variants are in strong linkage disequilibrium: almost all subjects who carry In1.1C also carry -403A, whereas -28G always occurs in combination with -403A / In1.1C. Both promoter SNPs display increased promoter activity.58,59 whereas In1.1C is associated with a strong downregulation of promoter activity.61 In a cohort of Caucasian homosexuals the -403A -28C haplotype was associated with a reduced progression of disease,59 which could not be confirmed in an analysis of five US-based cohorts.61 In the latter study, In1.1C was associated with more rapid disease progression in both Caucasians and African Americans.

SDF-1 3’A
Initially, a very strong protective effect was reported for homozygosity for a G-to-A mutation in the 3’ untranslated region of the SDF-1 gene (SDF-1 3’A),62 encoding the ligand for CXCR4. This effect could not be confirmed in other studies,42,63-67 including an international meta-analysis of individual cohorts (RH=0.99).35

CHEMOKINE RECEPTOR POLYMORPHISMS AND THE ACQUISITION OF SI/X4 HIV-1 VARIANTS

The development of X4 / SI HIV-1 variants is a hallmark of disease progression, and their appearance has invariably been associated with a more rapid progression to AIDS.56,60,65,66 It is still not understood why X4 variants develop in some patients and not in others. Several factors have been suggested to influence the development of X4 variants, including structural restrictions35 and loss of fitness during the adaptive process of gp120,71 levels of proteins that bind to CXCR4, such as SDF-1,40 and HIV-1 tat protein28, and immune control.70 Recently it was shown that host genetic factors may play a role in the appearance of X4 HIV-1 variants.

As compared with the CCR5 WT genotypic group, the acquisition of SI variants was delayed in the group of CCR5 D32 heterozygotes. An unexpected finding was the association of the CCR2 64I allele with an increased conversion rate toward X4 variants.35,47,49 As this mutation is linked to the promoter mutation in CCR5, enhanced X4 conversion may be due to altered levels or patterns of CCR5 expression.

CHEMOKINE RECEPTOR POLYMORPHISMS AND HIV-1 TRANSMISSION

HIV-1 may be transmitted from mother to child, via sexual contact, needle sharing, or exposure to contaminated blood products. Exposure to HIV-1 does not invariably lead to persistent infection. A multitude of factors influence transmission rates, such as frequency and magnitude of exposure, inoculum size, disease stage, CD4+ T cell numbers and immune response of the patient.26-29 Early in infection, a homogenous population of mainly macrophage tropic, NSI / R5 virus variants can be found, suggesting a strong selection pressure with regard to virus phenotype in acute infection. Indeed, susceptibility of cells from the exposed individual to R5 HIV-1 variants has been correlated with transmission.50,51 One of the most prominent determinants for transmission is the viral load in the donor, irrespective of whether it involves homosexual, heterosexual, parenteral or perinatal transmission.45,49,50 The role of host genetic factors in viral transmission is typically studied in a case-control setting, in which the prevalence of a genetic marker in a population of HIV-1-infected patients is compared with the prevalence of this marker in an HIV-1-negative control group or, more extremely, with a group of individuals who are known to have been exposed to HIV-1, yet remain uninfected (exposed uninfected). There has been considerable debate about the role of host genetic factors in protection against transmission of HIV-1. Part of these conflicting results may be due to differences in the composition of the study population and selection of the HIV-1-negative control group. Diverging results have indeed been reported upon selection of highly exposed uninfected individuals or nonexposed HIV-1-negative individuals as a control group.52,56 Furthermore, confounding factors, such as viral load in donor, should preferentially be taken into account in transmission studies. Considerable efforts have been undertaken to study the role of CCR5 D32 in transmission of HIV-1. Homozygosity for CCR5 D32 has been associated with protection from transmission in all risk groups studied.36,39-40 This indicates an absolute requirement for CCR5 in the establishment of infection, irrespective of the route of entry. Despite the near complete resistance, the few case reports of infected CCR5 D32 homozygotes52-53 and the identification of laboratory workers accidentally infected.
with T cell line adapted, X4 restricted virus variants,\textsuperscript{9,6} indicate that transmission via X4 variants can occur in selected cases. The role of CCR5 D32 heterozygosity in protection from transmission has been more controversial. Though protective effects of CCR5 D32 heterozygosity have been reported,\textsuperscript{39,37,40,87,88,90,98-100} the majority of studies fail to show a protective effect of CCR5 D32 heterozygosity on transmission.\textsuperscript{88,95,98,100}

Polymorphisms in RANTES (-G403A, -C28G, In1.1C), the ligand for CCR5, were shown to be associated with increased risk of homosexual transmission.\textsuperscript{59,61} This fits the finding that CD4\textsuperscript{+} T cells from exposed uninfected individuals express higher levels of MIP1a, MIP1b and RANTES upon in vitro stimulation.\textsuperscript{20,101,102}

Kostrikis et al. reported a significant increase of HIV-1 transmission to African-American infants homozygous for a promoter allele CCR5 C-2132T (or CCR5 C59356T, C630T).\textsuperscript{99} This mutation was rare in Caucasians and Hispanics, and a potential role for this allele could not be assessed in these children. John et al. showed that maternal SDF 3'A heterozygosity was associated with an increased risk in transmission, which was more pronounced when transmission occurred via breastfeeding.\textsuperscript{102}

**CONCLUDING REMARKS**

Our insights into the role of host genetic factors in the course of HIV-1 infection are growing. However, it is important to note that the majority of genetic factors described so far only have a relatively mild influence on the course of disease and can only partly explain differences in disease course among patients. Of note, only a minority of long-term nonprogressing HIV-1-infected individuals carry known protective alleles and, conversely, the presence of a protective allele does not warrant a benign disease course. Furthermore, the majority of frequently exposed but uninfected individuals do not contain CCR5 D32 homozygous or other protective genotypes, and therefore other mechanisms, such as a potent CTL response or reduced infectibility of CD4\textsuperscript{+} T-lymphocytes, may contribute to the resistance to infection in these individuals.\textsuperscript{79,103,104} 

Without doubt, the identification of novel HIV-1 disease-modifying genetic factors will be ongoing in the coming years, yielding further insights into the complex interplay between virus and host and the relative role of host genetic factors therein. Besides expanding our understanding of the pathogenesis of HIV-1 infection, this will hopefully lead to the identification of critical targets for therapeutic interventions.

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Discussion following lecture by H. Schuitemaker

Hoepelman: The first studies with anti-CCR5 antibodies were performed in heavily pretreated AIDS patients. Surprisingly, a rapid decline in the viral load is seen in these patients. That decline persists at least 16 weeks. I would have expected there would have been a rapid shift of the virus, because many patients probably harbour R4 virus. Do you think this is due to short follow-up or is there another explanation?

Schuitemaker: When CCR5 is not properly functioning in the CCR5 D32 heterozygotes, we see a protective effect, even in individuals who have X4 viruses, so I guess you achieve benefits by blocking only the R5-using population. In really late-stage patients with very low CD4 counts, we sometimes see a natural infection which the X4 viruses do not survive, because at that time, X4 viruses mainly use naïve T cells as their targets, whereas R5 viruses use memory cells and this leads to a depletion of naive T cells. So it might be by this shift in the predator-prey relation that at that time there are no longer any T cells that could serve as target cells.

Hoepelman: My second question concerns the prostitutes in Kenya who do not get infected. I thought this was due to homozygosity for the deletion, but you stated you do not see that in Africa. So what is the explanation?

Schuitemaker: These women are highly protected by cytotoxic T lymphocytes and it is assumed that when these women keep working, they are protected. There is continuous antigenic stimulation of their immune system. However, when they take a holiday, there is an increase in infection. It is completely opposite to what was expected.

De Marie: Persistent viraemia with a GB virus type C has been recently recognised as a protective factor, even in HIV patients treated with antiretroviral therapy. Did you study the presence of these viruses in relation to the CR5 gene?

Schuitemaker: We are going to do that. It is very difficult to set up a proper study, because the GBVC viraemia is normally transient, and only viraemia is associated with a protective effect.
De Groot: The disease course in perinatal infection is much more rapid with incubation time of about a year. Is there information on the expression of CCR5 on neonatal T cells?

Schuitemaker: I am not aware of those data. HIV infection being a viral disease, the loss of cells was thought to be a result of virus-mediated killing. The more recent idea is that it is chronic immune stimulation that consumes the T cells, rather than virus-mediated killing. All cells go through the process of becoming infected and dying a natural death from apoptosis. And since neonates respond more strongly to all kinds of infection, you can imagine that HIV infection may have a more dramatic course.

Verbrugh: Since AIDS is a relatively new disease, the R5 polymorphism was presumably there before the virus hit mankind and also the difference across the globe probably was there as far as the dissolution of this polymorphism is concerned. What would the role of this receptor have been in other types of disease?

Schuitemaker: When people ask me this question, I always say that CCR5 protects you from the negative effects of eating polar bears. I say this because in the northern regions like Scandinavia there is up to 40% of that genotype. SCCR5 is an activation marker and allows T cells to respond to inflammation and lead to immunopathology. For some infections it is not good to overreact. It is pure speculation, but having this polymorphism could be advantageous. It is of interest that individuals that are CCR5 D32 homozygous have no record of immune deficiency.

Kimman: Is CCR5 used as a receptor by other pathogens? I am thinking of endogenous retroviruses. Our genome harbours many retroviruses. Have they used CCR5?

Schuitemaker: Not that I am aware of.

Van Strijp: The finding of a coreceptor may turn the main receptor also into a coreceptor. Are there experiments with overexpressing one of these receptors, CD4 or CCR5, to see whether one of the receptors can do it on its own? Which is the most important one?

Schuitemaker: It is possible to change the chemokine receptor, but you need CD4 in addition. Therefore, CD4 is still assumed to be the main receptor. So in artificial systems you can use CCR5, but also CCR2 and CCR4 next to CD4, and it works. However, HIV-2 virus can become CD4-independent after passage, and also SIV, the related virus in macaques, is very frequently CD4-independent. It could very well be that the HIV was first using only chemokine receptors and, after introduction into humans, the virus adapted to using CD4 because of the proximity of CCR5 and CD4. High expression of the coreceptor does not change the susceptibility of the cell and that CD4 is always the limiting factor. That is also why macrophages are not susceptible to SI / X4 viruses, despite the presence of CXCR4 and CD4 on macrophages. When you upregulate CD4, these cells become susceptible to X4 viruses. So it seems that CD4 is the main receptor.

Kuijper: To give it a different perspective, the CCR5 D32 deletion seems also to be a susceptibility marker of asthma. I also have a question: Is there a difference in proliferative potential between NSI and SI viruses? How easily do they disseminate?

Schuitemaker: Among individuals dissemination of NSI viruses is more efficient than of SI viruses. The viral load however is not very different between NSI and SI carriers, being slightly higher in SI individuals. The burst size of the viruses, however, is different and SI viruses may be able to kill cells earlier, thereby not allowing as much reproduction as NSI viruses do. This more or less compensates for the fact that SI viruses have more target cells, due to the availability of more CXCR4 CD4 positive cells than CD4 CCR5 positive cells.

Kuijper: So you take away the disseminating potential of the NSI part? And this could perhaps explain the anti-CCR5 monoclonal effect?

Appelmelk: Where is the DC sign in your scheme with the coreceptors?

Schuitemaker: DC sign is only expressed on dendritic cells. It is still a matter of debate however whether DCs themselves really become infected via DC sign or whether this molecule only facilitates the infection of T lymphocytes. I know that people have found polymorphisms in DC sign, but considering the fact that I heard about this two years ago and that nothing has been published on a correlation between these polymorphisms and the clinical course, I assume that there are no correlations.

Appelmelk: What happens to the virus when it makes these new variants at a molecular level? Does it change its outside, maybe in the sugar chains? Because, as you know, GP120 uses a ligand to attach to the DC sign.

Schuitemaker: Looking at the envelope, the variable domain 3 (the loop that sticks out and is important for the interaction with the coreceptor) becomes more positively charged in SI viruses. There are two specific amino acid residues in the SI viruses at position 11 and 28. One or both are positively charged in SI viruses.
McAdam: You mentioned the differing use of receptors for HIV-2. Could that account for the slowness of its natural history and the low viral load?

Schuitemaker: HIV-2 is a very different story. Even when you provide an optimal situation, the virus still hardly grows, in contrast to HIV-1. I think something in the genome attenuates the virus and therefore it takes so long before the HIV-2 leads to disease. I think that it is not just due to coreceptor use.

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