Monocytes Heterozygous for the Asp299Gly and Thr399Ile Mutations in the Toll-like Receptor 4 Gene Show No Deficit in Lipopolysaccharide Signalling

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Abstract

Toll-like receptor 4 (TLR4)-mediated recognition of lipopolysaccharide (LPS) is required for efficient recognition of Gram-negative bacterial infections. Two commonly occurring mutations in the human TLR4 gene (Asp299Gly and Thr399Ile) have recently been shown to be associated with blunted physiological responses to inhaled LPS, and with increased risk of Gram-negative bacteraemia in sepsis patients and reduced risk of atherosclerosis in an Italian population. Here we show that monocytes from individuals heterozygous for both mutations in the TLR4 gene exhibit no deficit in recognition of LPS of E. coli, Neisseria meningitidis, Bacteroides fragilis, Yersinia pestis, Chlamydia trachomatis, Porphyromonas gingivalis, or Pseudomonas aeruginosa. We propose that the relatively high frequency of these mutations in the Caucasian population may reflect modified responses of carriers to alternative TLR4 agonists.

Key words: lipopolysaccharides • Toll-like receptor 4 • single nucleotide polymorphism • monocytes • innate immunity

Introduction

The innate immune responses of mammalian species have evolved to provide the host with a rapid detection of and reaction toward microbial products. Such responses are essential to allow efficient combatting of infection. A family of pattern recognition proteins termed the Toll-like receptors (TLRs) has recently been discovered and shown to be capable of recognizing a wide range of conserved pathogen-associated molecules. The human genome contains genes coding for at least ten TLRs (1), most of which have been shown to be capable of recognizing microbial products. The majority of bacterial lipopolysaccharides, for example, are recognized by TLR4, though there have been reports that the LPS of Porphyromonas gingivalis and Leptospira interrogans may be recognized by TLR2 (2, 3).

Two common mutations in the human TLR4 gene, Asp299Gly and Thr399Ile, have been observed to occur at a frequency of between 6 and 10% in Caucasian populations (4). Individuals heterozygous for these, typically co-segregating, mutations have been shown to have reduced airway responsiveness to inhaled Escherichia coli LPS (5). Furthermore, primary airway epithelial cells of individuals heterozygous for these mutations were shown to be incapable of producing IL-1α in response to LPS challenge, whereas this response was intact in cells extracted from wild-type individuals (5).

As these mutations have been shown to exist at a relatively high frequency in the Caucasian population (4), we set out to determine whether expression of the mutant allele conferred on carriers any advantage in terms of their ability to respond to the LPS of organisms other than E. coli. The component of LPS recognized by TLR4 has been determined to be the lipid A moiety (6). For this reason, we assembled a panel of seven different LPS types representing diverse lipid A structures (for a review, see reference 7) to determine if presence of the mutation altered responses to the LPS of other bacterial species.

Materials and Methods

Detection of TLR4 Polymorphisms. 80 Scottish residents were screened for the presence of the Asp299Gly and Thr399Ile alleles according to the method of Lorenz et al. (4). Briefly, DNA was prepared from whole blood using the ReadyAmp genomic DNA purification system (Promega) according to manufacturer’s instructions. Genomic DNA (5 μl) was added to 25 μl of ReadyTag PCR mix (Sigma-Aldrich) supplemented with 0.2 μl (20 pmol) of each primer and 19.6 μl of nuclease free water. Primers for the Asp299Gly allele were (forward: 5'-GATTTAGCATCTTAGACTACTACCTCCATG-3', reverse: 5'-GAT-
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Results and Discussion

A screen of 80 Scottish residents revealed 8 individuals heterozygous for the Asp299Gly and Thr399Ile polymorphisms in the TLR4 gene. Each individual carried both mutations, confirming the earlier observation that these mutations are rarely seen to segregate individually (10). Fig. 1 shows the results of genotyping of three individuals heterozygous for the TLR4 mutations and three individuals expressing wild-type TLR4. Monocytes from these six, roughly sex and age matched, volunteers were challenged with LPS of E. coli, N. meningitidis, B. fragilis, Y. pestis, C. trachomatis, P. gingivalis, and lipoteichoic acid of S. aureus. Fig. 2 shows that no appreciable difference exists in the responses of wild-types and heterozygotes to any of the LPS tested. Statistical analysis reveals that no significant difference exists in the response of wild type or heterozygote monocytes to any of the panel of LPS investigated at any of the concentrations tested (Table I). It is also clear when viewing the data in this way that the capacity of the different LPSs to stimulate cells varies substantially. For example, responses to the LPSs of E. coli and N. meningitidis are strongest, while responses to B. fragilis, P. gingivalis, and Y. pestis LPS are somewhat reduced and LPS of C. trachomatis and P. aegyptiaca show the lowest activity.

It was expected that the responses of wild-type and heterozygote monocytes to S. aureus LTA should be broadly similar as the signaling of this molecule is thought to be TLR4 independent (11). This differential signaling could also explain the identical responses made toward P. gingivalis LPS as this molecule has been shown to be capable of signaling via TLR2 (2), though it should be pointed out that the LPS of at least one strain of P. gingivalis has been shown to signal via TLR4 (12). However, the responses of heterozygotes to every other LPS tested are at odds with recent reports of the reduced functional capacity of cells isolated from such donors. Arbour and coworkers have reported that individuals heterozygous for these mutations have blunted physiological responses to inhaled endotoxin and while airway epithelia from wild-type individuals are capable of secreting IL-1α in response to LPS in vitro, cells from heterozygotes were shown to be incapable of this response (5).

There are several possible explanations for the discrepancy between the findings of these workers and the current study. First, airway responses to LPS are known to be highly variable between healthy donors (13). Arbour and colleagues categorized study subjects challenged with inhaled endotoxin as ‘LPS responsive’ if their forced expiratory volume in one second (FEV1) was reduced by 20% or more from baseline, and ‘LPS nonresponsive’ if the FEV1 was reduced by less than 20%.

Figure 1. Detection of wild-type, Asp299Gly, and Thr399Ile alleles in the human TLR4 gene. Genomic DNA of individuals recruited into the current study was amplified according to the method of Lorenz et al. (reference 4). PCR products of S. aureus were digested with the enzymes NcoI (299 allele) or HinfI (399 allele). Lanes 1 and 14, 100 bp base pair marker. Lanes 2–7, RFLP of the 299 section of TLR4 gene from three wild-type donors and three heterozygotes. Lanes 8–13, RFLP of the 399 section of TLR4 gene from three wild-type donors and three heterozygotes. Top band represents presence of wild-type allele, bottom band indicates presence of mutant allele. Genotypes were confirmed by sequencing.
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Tory volume in one second (FEV$_1$) was reduced by at least 20% at any stage following endotoxin challenge. Using this cut off, they state that the mutation was present in 3 of 52 normal responders and 7 of 24 hyporesponders. Using Fisher’s one-tailed exact test of these ratios, the group cite a P value of 0.029, though the more appropriate chi-squared analysis of these ratios would have indicated no significant difference in allele frequency between these two groups (P = 0.0539). Most significantly, however, the authors point out that not everyone in their study with the TLR4 mutation was hyporesponsive to LPS and that some of the individuals hyporesponsive to inhaled LPS in their study expressed wild-type TLR4. With this in mind, we feel it is more likely that the differences in airway responsiveness to LPS observed by Arbour and colleagues are determined not by the presence of these mutations, but instead by such factors as the circulating levels of LBP and soluble CD14, the number of LPS responsive cells present in the airway at time of testing and the current expression level of TLR4 – itself understood to rise and fall in response to various stimuli.

To remove bias from modulating factors such as these, we investigated the LPS responsiveness of monocytes derived from different donors in vitro. Using this approach allowed much of the interindividual variability to be removed, as factors such as cell number and differences in serum constituents could be controlled for. Arbour and colleagues investigated the in vitro responses of airway epi-

Figure 2. IL-1β secretion of wild type and Asp299Gly/Thr399Ile heterozygote TLR4 monocytes in response to LPS and LTA challenge. Human monocytes were challenged with ten-fold serial dilutions of E. coli, N. meningitidis, Y. pestis, C. trachomatis, B. fragilis, P. aeruginosa, P. gingivalis LPS or S. aureus LTA, or medium alone (C). Supernatants were assayed for IL-1β content after 4 h incubation. Open circles represent mean IL-1β secretion ± SEM from three wild-type donors. Filled squares represent mean IL-1β secretion ± SEM from three donors heterozygous for both TLR4 mutations.
used in their study (100 ng/ml) was their preparations. Certainly, the concentration of LPS heat shock protein or another TLR4 agonist present in et al. occurred as a result of impaired recognition of either able to facilitate efficient purification). Thus, it remains possible that expression of variant TLR4 is capable of altering the host response to TLR4 ligands other than LPS. Indeed, several other microbial and host-derived products have also been shown to signal via this molecule. For example, F-protein of respiratory syncytial virus (19), extra domain A of fibronectin (20), and both human (21) and bacterial heat shock protein (22) have all been shown capable of activating cells via TLR4. Therefore, while the responses to LPS may be identical between wild-types and heterozygotes, this does not preclude the possibility that these mutations may alter the ability of individuals to detect other microbial products. Larger association studies may yet therefore discover a correlation between presence of the mutation and disease progression. It is possible, for example, that efficient recognition of Gram-negative heat shock proteins may be significant in combat-

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<th>Minimum concentration activating TLR4+/− monocytes (ng/ml)</th>
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<tr>
<td><em>E. coli</em> LPS</td>
<td>0.01</td>
<td>0.01</td>
</tr>
<tr>
<td><em>N. meningitidis</em> LPS</td>
<td>0.1</td>
<td>0.1</td>
</tr>
<tr>
<td><em>B. fragilis</em> LPS</td>
<td>1</td>
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<tr>
<td><em>P. gingivalis</em> LPS</td>
<td>10</td>
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<td><em>Y. pestis</em> LPS</td>
<td>10</td>
<td>10</td>
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<tr>
<td><em>C. trachomatis</em> LPS</td>
<td>100</td>
<td>100</td>
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<tr>
<td><em>P. aeruginosa</em> LPS</td>
<td>100</td>
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<tr>
<td><em>S. aureus</em> LTA</td>
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Homozygous wild-type or Asp299Gly/Thr399Ile heterozygous (TLR4+/−) human monocytes were challenged with 10-fold serial dilutions of *E. coli, N. meningitidis, Y. pestis, C. trachomatis, B. fragilis, P. aeruginosa, P. gingivalis LPS,* or *S. aureus LTA* or medium alone.

Minimum concentration represents the lowest concentration at which individual stimuli induce production of significantly more IL-1β (P < 0.05) than cells incubated with medium alone.

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Table I. Comparison of Homozygous Wild-Type and Wild-Type/Asp299Gly, Thr399Ile Heterozygote TLR4-bearing Monocyte Recognition of Various LPS

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ting infection and it has already been shown that recognition of human heat shock proteins has a role to play in atherogenesis (23).

In summary, our initial hypothesis that the described mutations in the TLR4 gene may alter host responses to the LPS of bacteria other than E. coli has proven to be unfounded. Instead, we have shown that presence of these mutations (at least in heterozygote carriers) has no effect on the capacity of human monocytes to detect LPS of seven different strains of Gram-negative bacteria. The marked differences in in vivo LPS responsiveness between individuals is therefore determined far more significantly by other genetic and acquired traits of individuals, than by the presence of the Asp299Gly and Thr399Ile TLR4 mutations. Further experiments will be required to determine whether expression of these variant receptors results in modified capacity to respond to alternative TLR4 agonists.

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