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**Schwartz et al.**

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(54) **VARIANT TLR4 NUCLEIC ACID AND USES THEREOF**

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(51) **Int. Cl.**<sup>7</sup> ..... **C12Q 1/68**; C12P 19/34; C07H 21/04

(52) **U.S. Cl.** ..... **435/6**; 435/91.2; 536/23.5; 536/24.31; 536/24.33; 424/9.1

(58) **Field of Search** ..... 435/6, 91.2; 536/23.5, 536/24.31, 24.33; 424/9.1

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(57) **ABSTRACT**

The invention provides methods to identify polymorphisms at the human TLR4 locus, as well as methods to identify individuals at risk of indications that increase their morbidity and mortality.

**18 Claims, 15 Drawing Sheets**

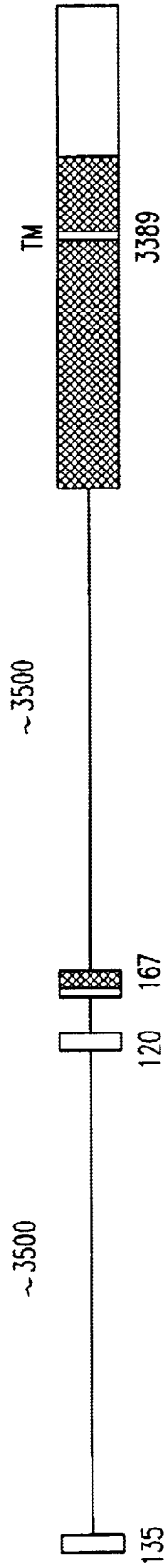


FIG. 1A

Intron	Position	5' to 3' sequence at EXON/intron boundary
1	135 - 136	GCGTGGAGgtatgtggctggagtcagct ---- atttgttttgtttttaaagACTTGGCC
2	255 - 256	TCACGGAGgttagaatgctgagcacgta ---- gtcattgtgtaatcat tgcagGTGTTCC
3	422 - 423	TTATCCAGgtaatgaatccacttttaca ---- atgtctttttattcctgtagGTGTGAAA

FIG. 1B

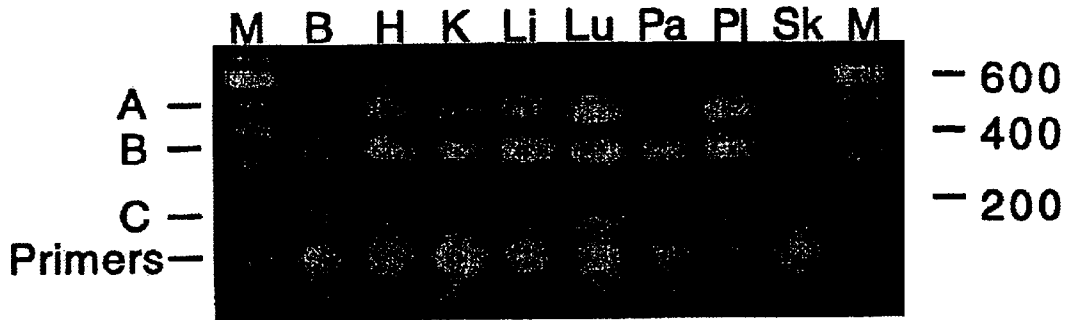


FIG. 2A

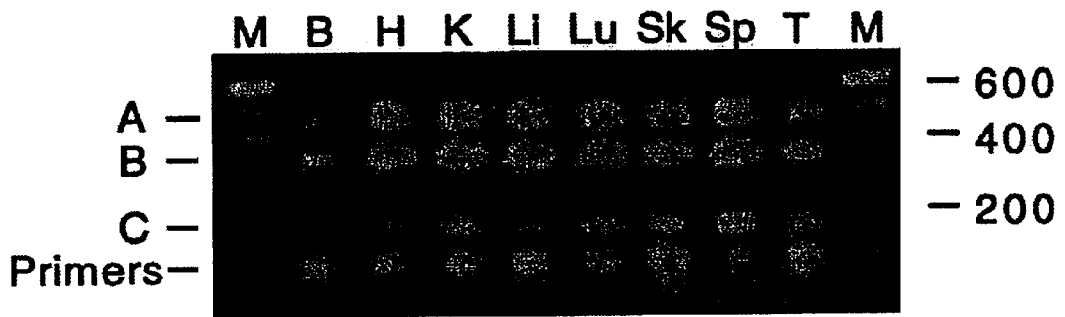


FIG. 2B

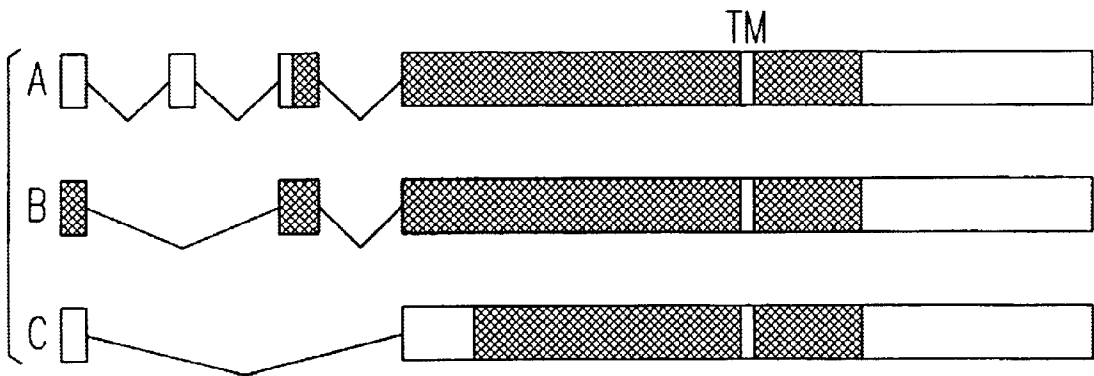


FIG. 2C

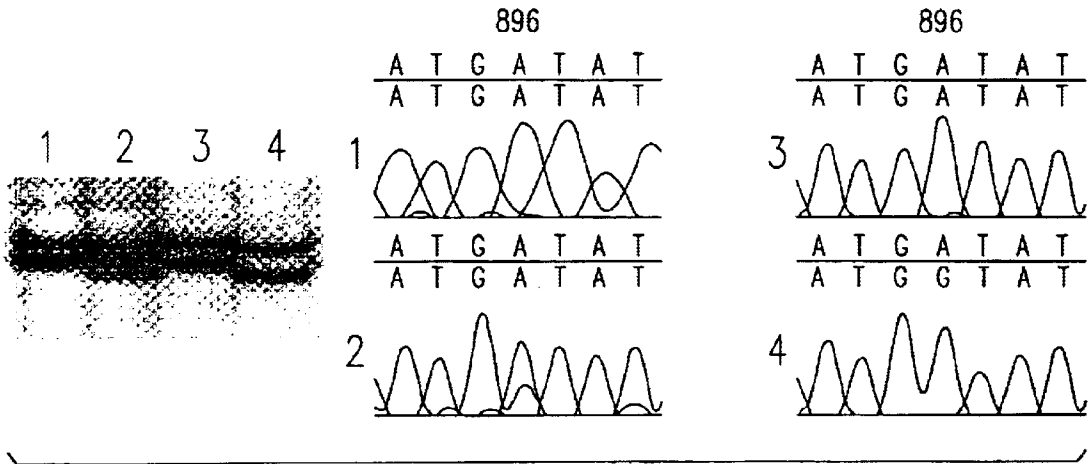


FIG. 3A

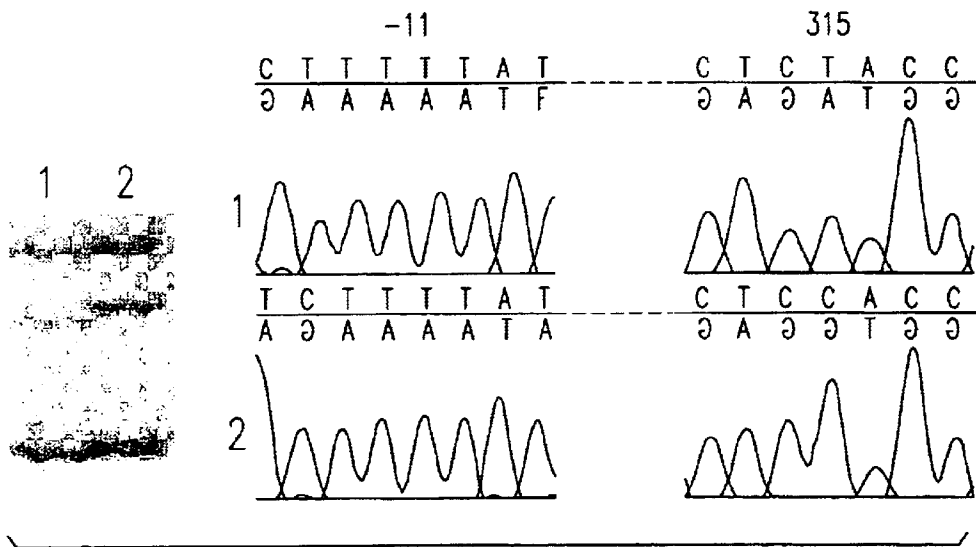


FIG. 3B



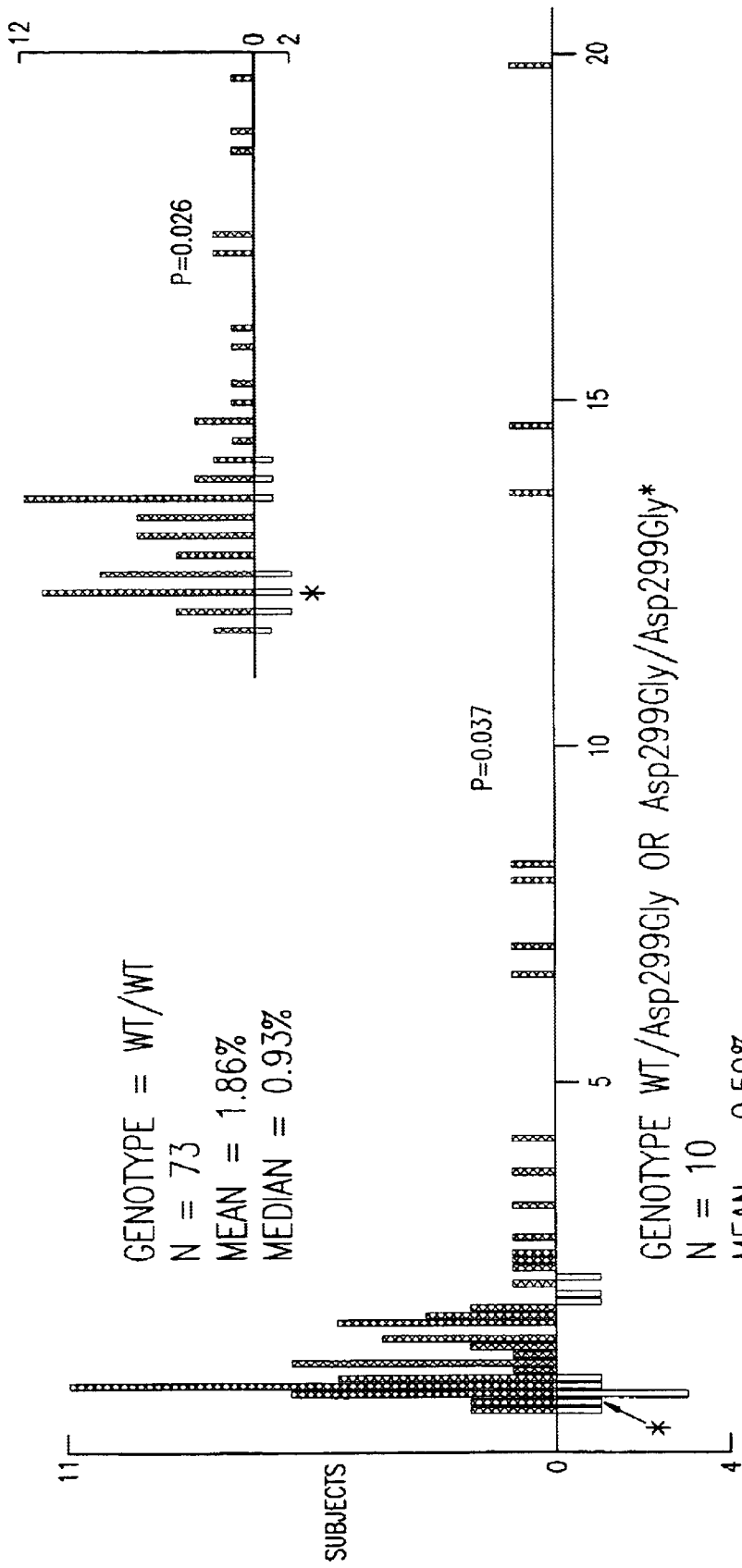


FIG. 5

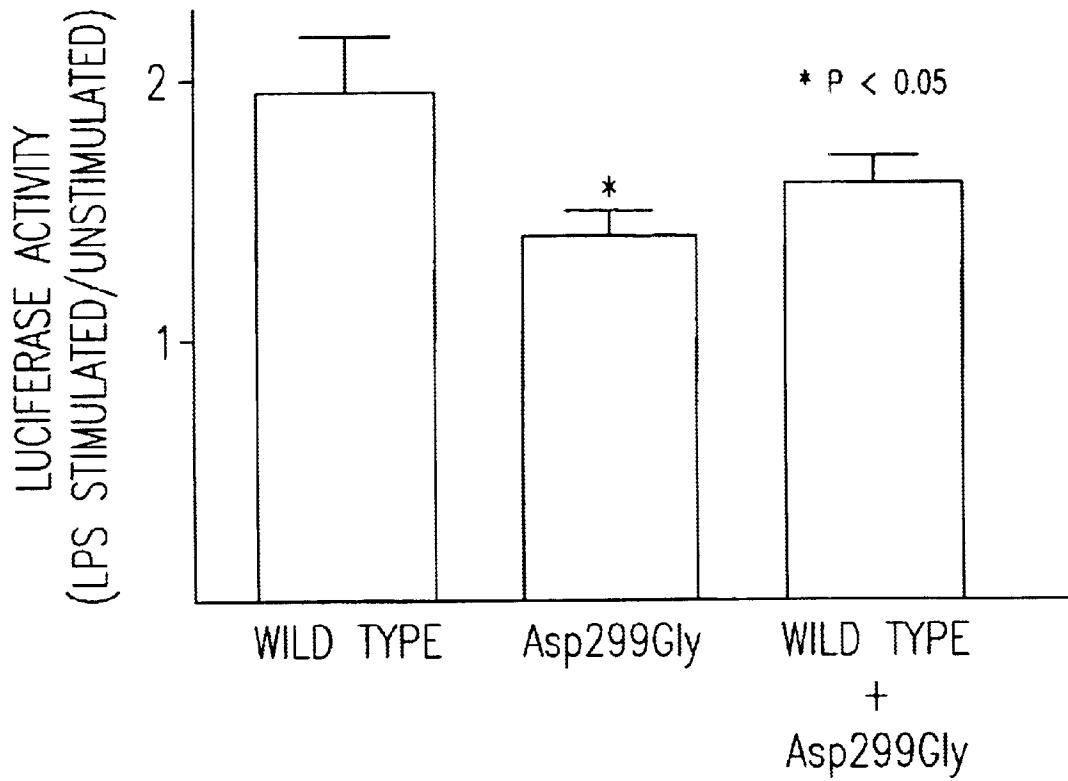


FIG. 6A

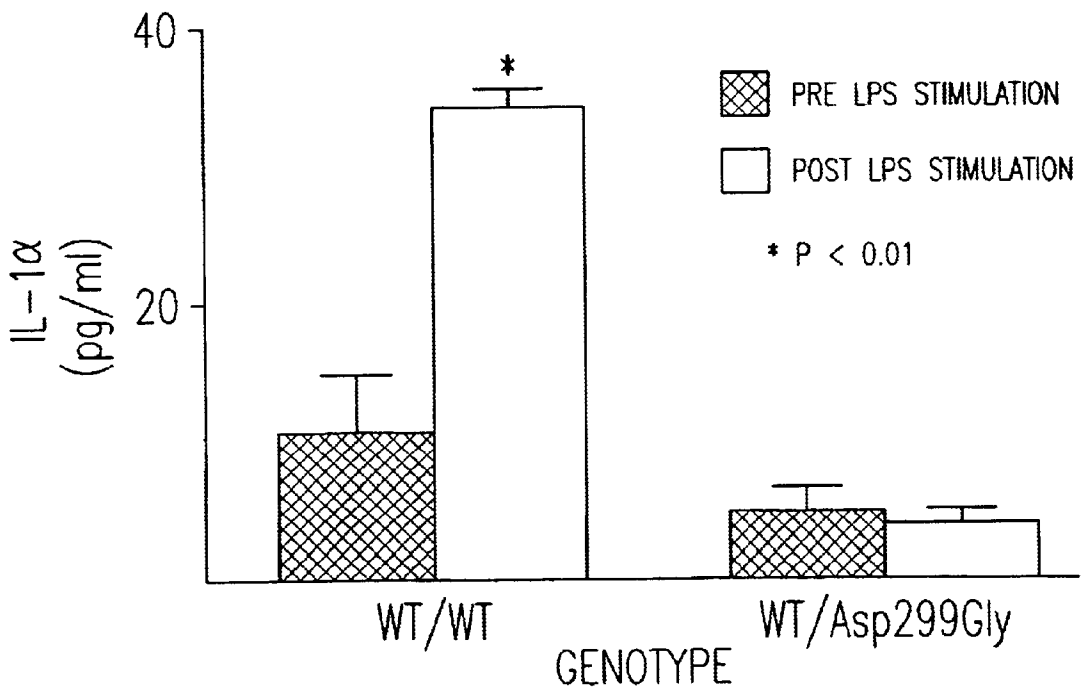


FIG. 6B

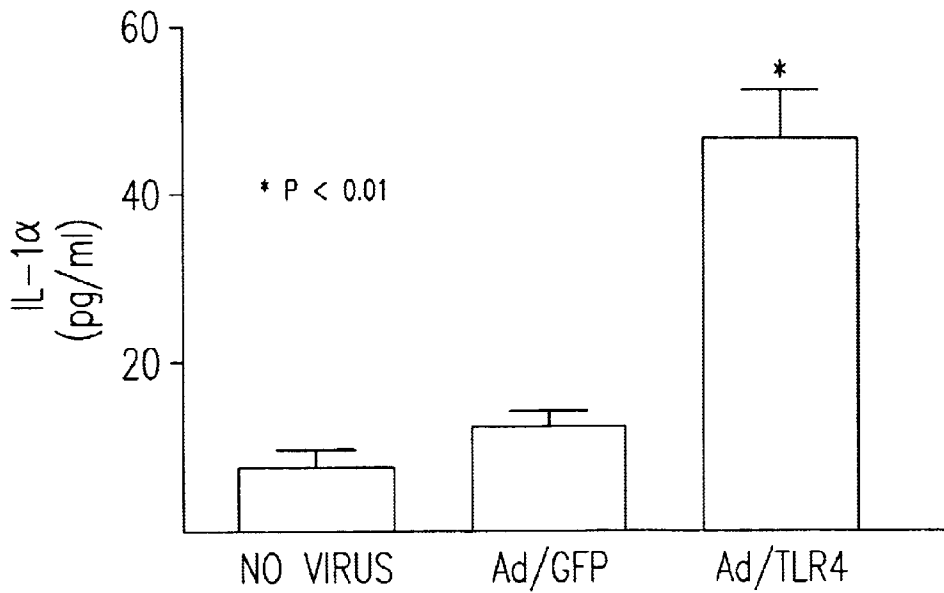


FIG. 6C

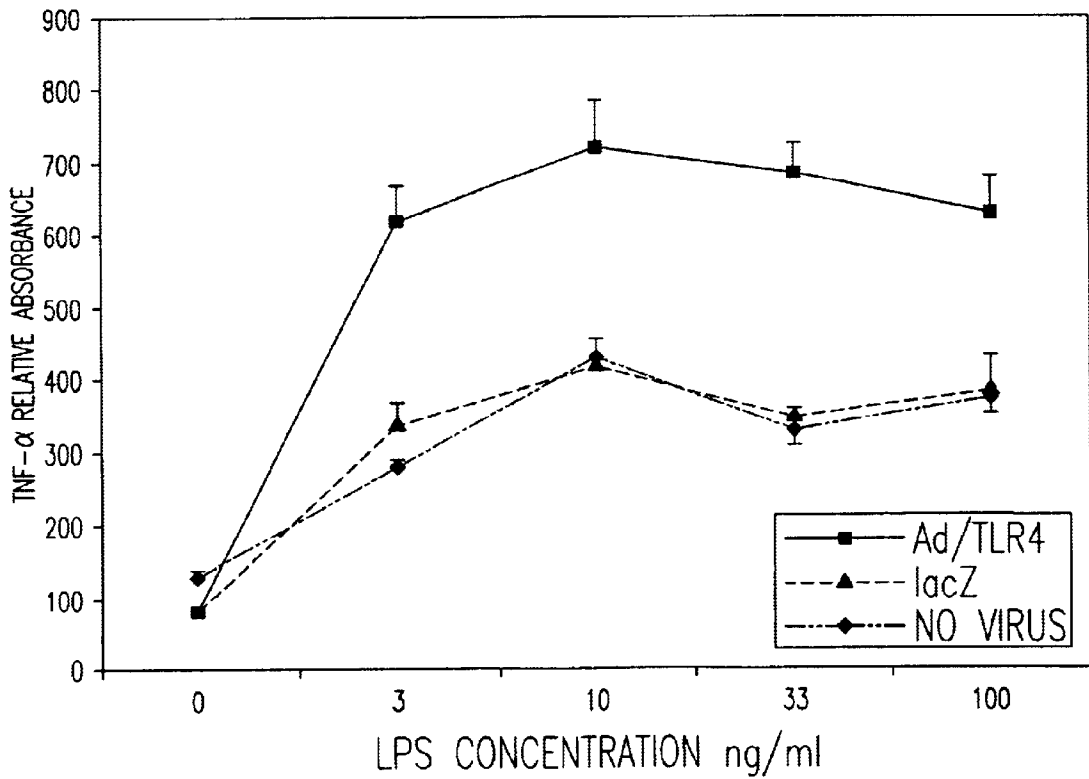


FIG. 6D



<u>Amino Acid</u>	<u>Codon</u>
Phe	UUU, UUC
Ser	UCU, UCC, UCA, UCG, AGU, AGC
Tyr	UAU, UAC
Cys	UGU, UGC
Leu	UUA, UUG, CUU, CUC, CUA, CUG
Trp	UGG
Pro	CCU, CCC, CCA, CCG
His	CAU, CAC
Arg	CGU, CGC, CGA, CGG, AGA, AGG
Gln	CAA, CAG
Ile	AUU, AUC, AUA
Thr	ACU, ACC, ACA, ACG
Asn	AAU, AAC
Lys	AAA, AAG
Met	AUG
Val	GUU, GUC, GUA, GUG
Ala	GCU, GCC, GCA, GCG
Asp	GAU, GAC
Gly	GGU, GGC, GGA, GGG
Glu	GAA, GAG

FIG. 7

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro	pro
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala	leu
Pro (P)	gly	gly
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

FIG. 8

**HUMAN TLR4 GENOMIC SEQUENCE**

AAAATACTCC CTTGCCTCAA AAACGTGCTCG GTCAAACGGT  
 GATAGCAAAC CACGCATTCA CAGGGCCACT GCTGCTCACA  
 AAACCAGTGA GGATGATGCC AGGATGATGT CTGCCCTCGCG  
 CCTGGCTGGG ACTCTGATCC CAGCCATGGC CTTCCCTCTCC  
 TGCCTGAGAC CAGAAAGCTG GGAGCCCTGC GTGGAGGTAT  
 GTGGCTGGAG TCAGCTCCTC TGAACCTTCC CTCACTTCTG  
 CCCAGAACTT CTCACTGTGT GCCCTGGTTT GTTTATTTTT  
 GCAAAAAAAA AAAGAGTTAA ATTACCTTAA AGACTCAAGA  
 AGCCACAGAG ATCAAATAAT TCATTGTTAC AGGGCACTAG  
 AGGCAGCCAT TGGGGGTTTG TTCCATTTGG AAATTTTGAG  
 TGCTAACAGG GGCATGAGAT AACATAGATC TGCTTAAGGT  
 CCCTGCTCTG CTACCTTGTG GCTCTGTGAA GAAATTATCA  
 AACCTGTCTG AGACTAGTTT TCGCATCTGT AAGAGAATTA  
 TAATACCTTC TTCACTAGAG AGTAAGCAGA CTGCTTCAGT  
 GTCATTTCTT CCCACTGGTG GTCTTTACAC TCAGCTTCAA  
 GCAGTCACCC TGCTCCTTTC AATCTCAGGA AAAAGATGGC  
 TTTGTGTGTG TGTCTCT : A : G : AGAAAGAA CTTTCTAAGT  
 TGGTGCAGA CTTCTGTATG CAGTAATATA GTTTAGTCCA  
 GAGGATGAAA AAAATAAGAG A : ATGAAAAA GGAAAAGAGA  
 GAGAGAGA : G AAGAAAAAAG CAAGAGGGAA AT : ATGTATA  
 ATGTCAGCTA ATGCAAC : AG TTTCTTTCTT AGTGAATAC  
 CAATCAGCTG : GTTG : GTAA TCTT : ATTCA TGATGGATCT  
 CTTTTGTTTT TCCCCTGCGC AGACTTC : AC AGTTGCTTTA  
 GAAACCCATA GTAGAGCCGA A : CAGCTAAG AAAATGATTT  
 ACAGTGAGGC AGGGTCAGAA ACTCAAGAGA GAAAAAGCCA  
 GCTGCAGTC : CTGAAGT : TG AGGATATAGG : AGAAAATCA  
 AGTAATATTT AGCAAAGACT AATTCATTAT CTTGAAGCCA  
 TCCCTTCCCT CAATTCCCTG CCCATAGTCC TCCTCCTTGT  
 CCTCTTCTCT GNA : TCCCTC TGCTGTTAGG TTA : ATGG : A  
 GATAGATTTT CTAATTANGC TCACTGCGAG ATAAAACCCA  
 GCCCATGTTT CTATTAGNCA ATATTGTCTT TGAGGCTCCA  
 TGGCTTGCAN CATTTAAGCA GACATACGAA TGAAGATCTG  
 CATGTTTGAA CTCTGACTTT GCGCATATTA CTTCATTCT  
 TTGAATTTCC ATTTTCCTCA TCTTTAAATG CTTATTTGAA  
 GATTAAGTGA AAGTATATAA CAAACAAGAA CTATGCAGGC  
 GTATGGTAAG GGATTAATGA TAGATGATAA TAATTAATGT  
 TGACATCTAT TGATCACTTA TACTGTAGCG GGCTTTTAAA  
 TAAACTCTTT AAACACCTTA TCTCATTTAA TCCTTCAAAC  
 ATTCTATTGG TTTCAAACAA CAGAAAATA CAATTAGCTG  
 GCTTCTGCAA GGAATTTTGT TGGAGGAAAT GAGAGCATTC  
 AGAAATTAGA TGGGAGCGTT AGAGAATTAG GCTTACAAAG  
 AATGTGGGAA AGTAGGCTAG AAAGCAGTGT AAAAACAAAG  
 ACAGCATAAA GCACTTGACC TTATTTACTA GGTTCACCA  
 TGGGAATCCA TGCCTCTAA AGATTTCCCC CTATTTCTAC  
 ATCACTTTGC TCAAGGGTCA ATGAGCCAAG GAAAAGAATG

**FIG. 9A**

CAGTTGTCAA AATCTGGGCC ATGACTAAGG AAGGTCTGGA  
CATCTTGACT GCCAGACAGT CTCCCCAATG ATATGGAGTA  
TTTAGAATGA TACTGGATAT TTTATTTATT TTTTGTATTT  
TCAACTTTTA AGTTCAGAGG CACATGTGCA GAGCATGCAG  
GTTTATTACA TAAGTAAATG TGTGCCATGG TGATTTGCTG  
CATAGATCAT GAAAATATGG AACGCATCAT GGATTTGTGT  
GTCATCCTTG TGCAGGGGCC ATGCTCATCT TCTCTGTATC  
CTTCCAATTT TAGTATATGT GCTACTGCAG CAAGCACGAT  
ATTGGATATT TTATTACCTA CATTTTACAT ATGATAAAAT  
GAGGCTCACT GAGGTTTTTC TTTTGTTTCGT TTTATTTTGT  
TTTGTTTTTA AAGACTTGGC CCTAAACCAC ACAGAAGAGC  
TGGCATGAAA CCCAGAGCTT TCAGACTCCG GAGCCTCAGC  
CCTTCACCCC GATTCCATTG CTTCTTGCTA AATGCTGCCG  
TTTTATCNCG GAGGTTAGAA TGCTGAGCAC GTAGTAGGTG  
CTCTTACTT TCTAATCTAG AGTAAGACAA TTTATAAGCA  
TGAATTGAGT GAATGGATGG ATGGATATAT GGATGGAAGG  
ATGGACAGAT GGATGAAAGG TTGACTGAAT TTTGTGCTTG  
CACAAAAGA GGCCCTCTC CACCATCTCT GGTCTAGGAG  
AGGGGAGTTG GGAGACCATG CAGTAAAGAT ACTTCATGTC  
ATGTGTAATC ATTGCAGGTG GTTCCTAATA TTACTIONTCA  
ATGCATGGAG CTGAATTTCT ACAAATCCC CGACAACCTC  
CCCTTCTCAA CCAAGAACCT GGACCTGAGC TTTAATCCCC  
TGAGGCATTT AGGCAGCTAT AGCTTCTTCA GTTTCCAGA  
ACTGCAGGTG CTGGATTTAT CCAGGTAATG AATCCACTTT  
TACATACTGC ACAAGGTGAG GTGTTTATTG TCCTATCATT  
TCATTATTGG ACTGGAAAGC TTGGTTTGTG GAGTCTCATC  
TTCATTCACT TATTCATTCA TACAACAGAT GTCTTATTAA  
CTATATAACC TTGAGCAAGC TACCTCTATT CTCCAGGTCT  
CAGTTTTCTA ATCTGTGAAG TAGGCAGTTG GCTGAGACAG  
CTTCTAAGGG CAATTCCTAAT TTTAGGTTTT CTTTTAAGAC  
AGGAGAGAAA ATTAGCTTAA ATTCTTTCAT AAGCAGCTAT  
TTATTGACTA CTTGCTATAT GTTGTACACT CTGCAAGAAG  
ACAGGCATAT ATTGATATAT AACACACAGC CCCTGTTGTT  
AAGGAGGCAT ATCTTCTTGA AAGAGTTAAT ACCTTAAAGT  
CCTGGGTATG GTCCTGGGTA CATAGTATAT AGTCAACACA  
TTTTAATTAT GATTTTTTGG ATCTGGAAC TGATATAAAG  
ATAGCGACAT ATAACAGTAG GTGATAAATT ATGTTTTAAAC  
TAAAGGTAAC TAATTGTATT TTTCAGAAGA GGGGCCCTCT  
CTGTGGTGGG TAGTCAAGAA AGATTCATGA ACTGCATAAG  
ATTCAAAACA TGTCTAGAAT ATTAAAATA GTGGTGGCAG  
GTGAAATGTC ATCTTGATAT TTTAGGGGAA CCAAATCTA  
AAAGGGTTTT CATCATCGGG GCCTTATTTG CAAATCGAAC  
TAGATAATGG ATCATGTTCT CTGCAATGGT TTGTAACAACA  
TTTCAAAAACA TTTTACATAT TTTTTATTAT AGAAATTATT  
GATAAAGACT AAGGTCACAG TATAAAAATC CTTTTTAGAG  
CAGACATTTT TGTAGAAGAG TGAACATATG ACCTATTATA  
CTCTAATTTG GATATAGATA GGATGTAACA AAGGAGTAAT

FIG. 9B

GGGAACAATT CAAAGGCAGT GGTATAGTGC ATANAGTCCT  
GTTGGGGTCA GAAGACCTGA GCCCAAGTTT ACCCCCAACA  
TTTATAACCC ATGTAACCTT AGCATATTAC TTCATCTCCC  
TTAATCCTTA GTTTCATATC TGATCAATGG AAATGATGAA  
ACTTATTCTG CTGGATTAAA TGTGATAATA AATATTAATA  
TGCTGTATAT ATTTAAATTT TTATAAAATA TATTTTATAA  
GCATAAAGTA TTCTTACAGA ATTTCATTAG GTTTTTAAAA  
TAATTTCAAC TTTTATTTTT GATTCAGGGA TTTACATGGT  
TATATTGCGT AATGCTGAGG TGTAGGGTAC AATCGATACC  
ATCACTCAGG TAGTGAGCAT AGTACCCAAT AGTTAGTTTT  
TCAACCCTTG CTGCTTTCTC TCTATCCCCT CTCTAGTAAT  
CCCCAGGGTC TATTTTTGTC ATCTTTATGT CCATGTGTAC  
TCCATGTTTG GATCCTACTT ATAAAGTGAG AACTCATGGT  
ATTTGGCTTT CTGTNCCTTT GTTNGCTAAT TTGCTTAGGA  
TAATGGCTAC TAGCTGCATC TATGCCATTA TGTTCTAAAT  
TTCANTTNCC TGCATGAAAA TTTTGTCAAG TACTCTATTA  
AGGTAGACCA CCTCTCCCTT TTTTTTCAA ACAAGAAGTA  
GNTTTTCCCA AACAAATGCC TTATGGAATT NATCTTCAAT  
CCNNGGATAC CCAATAACTT GCCCAAANC CTTAATCTGN  
CTTACAGAGA GGCCACCTC CTTCTGTAAC CCATAGGAGA  
TTTGGATTGG TAAGAATGCT TTGTGATAGC CCAGCAGCCT  
TCTTCCCTT ATAGAAATAT ATATATANTC TTTTATAGG  
TGAGGAACTG AAGCTTGAAT AATTTAAATG ACTTATATAC  
ATNATCATTG CTTGTTAGCC ACAGACCAGA GATTTAAGTT  
CNCATCTCCA GAATCCAAC TAAATGTTTT CTTTGTCTTA  
ATACTCTACT TCTCTAAAGT GATTATCACC AATGTAATGA  
TATAGAGNCA CAGCAAGACC CTTTCCTTCT CACCTAATGT  
ATAGAGCAAT GCAGAGATAG AATGATGGGC TATAACAATC  
ATATAATTGA AAGAAAGAAC TTCAAAAATA ATCAAGTTCA  
GCTGTTTGAT TTATAAATGT GATAACTAAA ACCTAGAGAG  
GAAAAGAGGT ACTCAAGATC ACACAGTAGG AGAGGACTGC  
AGAAACACCA AACCCAAGCT CTTTGTCCA CTCTCCAGC  
GTTCTTTCTA CTATACTGCC TATCCTTTAT CTAGTTACCA  
ATAAATAACA AAAGCTTGGA CCACAATGCT TTTATTGTCT  
AGGAAACTCC TGAAGAAGCT AAATAAAATG GGTGGGGAAT  
ATTGTAAATG TAATTCAGGC TGGATTAAGA AAGAACTTAT  
TTGACATTGT AACTGACAAG CACCTGCAAT GCTGAAAGGA  
ATTTTTCATT GGCNTGCTGT TTGCTGGGCT GCATCAAAGC  
CCTGTCTCTA GGACATGTCT CTGAACATTG TGTGTAGCAT  
GGCTTTCATT TCTTTTAGGA TAAAATTCAA AACCTTTTAT  
CTGGTTGGTA AACCTCTGCC TAATTGGGAA CCTTCTTTCT  
CCACAACCTC ATATTGTACA CTCCAATTC ATCTCTGTTC  
TCCAACCATG GAAGCTATTT GTCATGATTC CTCCTTGIGT  
CATTTTTTTT CTGTCAACCT TGGGGCTTTT GTGTTTGCTG  
TTCACCTCAC CTCCTTTTAT TGTTAACTTC TACTCATCTT  
TCAATTTTCA ACTTAAGTGT TCTCAGAGAA ACCTACTTTG  
ATTTTCTTGG TCCANAACGG TTCTCTGGAT GTGAACTCTT

FIG. 9C

ATAGCACATA ATTTTCACTT TTTTCCACAA AACTCGCTCC  
 TATCACCTGT TACAAGCATT TACCTCTGAT AACAGAAGT  
 TTCAAATATC TAGCTGTCAT GTAAGCACTT TTCATAAACA  
 TTAAGAGTAT CTGTGACACT TATGTGTAAT GTTTCGTATC  
 TCTGAAATTG ATATTTACCA GTCATTTATC TTGGCTACCA  
 ACTAACAACT ATCCATATTA TCTGTACCAA TCAGATGTAT  
 AATCACAATT TTGTGTGACA GAAAATGGCT AAACCTTGATC  
 CAAGGCTATT ACATGCTTT : ATCAACTGCA CAATCTTTAT  
 ATATGTCAAT TATTGATCTT TAACTGATTT CCTTCTTATG  
 : GATTTTCTC CTCTGCTTAT CATGTATGCC TAACAT : GAC  
 AAAAAAG : AG CCTA : TCATT GCAGCCAGTA TGATAATACT  
 CA : GTCTGTG GGGCTTCTTA TTTGCTTAT : TCCATCATCA  
 TCTGTCCTGC TTGATGTCTT TGCCTATGCA CAATCATATG  
 : ACCCATCAC ATCTGTATGA AGAGC : TGGA TGACTIONGAT  
 TAATATTCT : AT : : TTTAG GTTCTTATT : CAGCAGAAAT  
 ATTAGATAA : TCAATGTCTT TTTATTCTG TAGGTGTGAA  
 ATCCAGACAA TTGAAGATGG GGCATATCAG AGCCT : AAGC  
 CACCTCTCTA CCTTAATATT GACAGGAAAC CCCATCCAGA  
 GTTTAGCCCT GGGAGCCTTT TCTGGACTAT CAAGTTTACA  
 GAAGCTGGTG GCTGTGGAGA CAAATCTAGC ATCTCTAGAG  
 AACTTCCCCA TTGGACATCT CAAAACCTTG AAAGAACTTA  
 ATGTGGCTCA CAATCTTATC CAATCTTCA AATTACCTGA  
 GTATTTTTCT AATCTGACCA ATCTAGAGCA CTTGGACCTT  
 TCCAGCAACA AGATTCAAAG TATTTATTGC ACAGACTTGC  
 GGGTTCTACA TCAAATGCC CTACTIONATC TCTCTTAGA  
 CCTGTCCCTG AACCTATGA ACTTTATCCA ACCAGGTGCA  
 TTTAAAGAAA TTAGGCTTCA TAAGCTGACT TTAAGAAATA  
 ATTTTGATAG TTTAAATGTA ATGAAAACCT GTATTCAAGG  
 TCTGGCTGGT TTAGAAGTCC ATCGTTTGGT TCTGGGAGAA  
 TTTAGAAATG AAGGAAACTT GGAAAAGTTT GACAAATCTG  
 CTCTAGAGGG CCTGTGCAAT TTGACCATTG AAGAATTCCC  
 GATTAGCATA CTTAGACTAC TACCTCGATG ATATTATTGA  
 CTTATTTAAT TGGTTGACAA ATGGTTCTTC ATTTTCCCTG  
 GTGAGTGTGA CTATTGAAAG GGTAAGAAC TTTTCTTATA  
 ATTTCCGATG GCAACATTTA GAATTAGTTA ACTGTAAATT  
 TGGACAGTTT CCCACATTGA AACTCAAATC TCTCAAAGG  
 CTTACTTTCA CTCCAACAA AGGTGGGAAT GCTTTTTCAG  
 AAGTTGATCT ACCAAGCCTT GAGTTTCTAG ATCTCAGTAG  
 AAATGGCTTG AGTTTCAAAG GTTCTGTTT TCAAAGTGAT  
 TTTGGGACAA CCA : GCCT : A AAGTATTTAG ATCTGAGCTT  
 CAATGGTGTT A : TTACCATG AGTTCAAAC TCTTGGGCTT  
 AGAACA : ACT AGAACATCTG GATTTCCAGC ATTCCAATTT  
 GAAACA : AAT GAGTGAGTTT TCAGTATTCC TA : TCACTCA  
 GAAA : CCT : C ATTTACCTTG ACATTTCTCA TACTCACACC  
 AGAGTTGCTT TCAATGGCAT CTTCAATGGC TTGTCCAGTC  
 TCGAAGTCTT GAAAATGGCT GGCAATTCTT TCCAGGAAAA  
 CTTCTTCCA GATATCTTCA CAGAGCTGAG AAACCTTGACC

FIG. 9D

TTCCTGGACC TCTCTCAGTG TCAACTGGAG CAGTTGTCTC  
CAACAGCATT TAACTCACTC TCCAGTCTTC AGGFACTAAA  
TATGAGCCAC AACAACTTCT TTTTATTGGA TACGTTTCCT  
TATAAGTGTC TGAACTCCCT CCAGGTTCTT GATTACAGTC  
TCAATCACAT AATGACTTCC AAAAAACAGG AACTACAGCA  
TTTTCCAAGT AGTCTAGCTT TCTTAAATCT TACTCAGAAT  
GACTTTGCTT GTACTTGTGA ACACCAGAGT TTCCTGCAAT  
GGATCAAGGA CCAGAGGCAG CTCTTGGTGG AAGTTGAACG  
AATGGAATGT GCAACACCTT CAGATAAGCA GGGCATGCCT  
GTGCTGAGTT TGAATATCAC CTGTCAGATG AATAAGACCA  
TCATTGGTGT GTCGGTCCTC AGTGTGCTTG TAGTATCTGT  
TGTAGCAGTT CTGGTCTATA AGTTCTATTT TCACCTGATG  
CTTCTTGCTG GCTGCATAAA GTATGGTAGA GGTGAAAACA  
TCTATGATGC CTTTGTATC TACTCAAGCC AGGATGAGGA  
CTGGGTAAGG AATGAGCTAG TAAAGAATTT AGAAGAAGGG  
GTGCCTCCAT TTCAGCTCTG CCTTCACTAC AGAGACTTTA  
TTCCCGGTGT GGCCATTGCT GCCAACATCA TCCATGAAGG  
TTCCATAAA AGCCGAAAGG TGATTGTTGT GGTGTCCCAG  
CACTTCATCC AGAGCCGCTG GTGTATCTTT GAATATGAGA  
TTGCTCAGAC CTGGCAGTTT CTGAGCAGTC GTGCTGGTAT  
CATCTTCATT GTCCTGCAGA AGGTGGAGAA GACCCTGCTC  
AGGCAGCAGG TGGAGCTGTA CCGCCTTCTC AGCAGGAACA  
CTTACCTGGA GTGGGAGGAC AGTGTCTCTG GCGGCACAT  
CTTCTGGAGA CGACTCAGAA AAGCCCTGCT GGATGGTAAA  
TCATGGAATC CAGAAGGAAC AGTGGGTACA GGATGCAATT  
GGCAGGAAGC AACATCTATC TGAAGAGGAA AAATAAAAAC  
CTCCTGAGGC ATTTCTTGCC CAGCTGGGTC CAACACTTGT  
TCAGTTAATA AGTATTAAT GCTGCCACAT GTCAGGCCTT  
ATGCTAAGGG TGAGTAATTC CATGGTGCAC TAGATATGCA  
GGGCTGCTAA TCTCAAGGAG CTTCCAGTGC AGAGGGAATA  
AATGCTAGAC TAAAATACAG AGTCTTCCAG GTGGGCATTT  
CAACCACTC AGTCAAGGAA CCCATGACAA AGAAAGTCAT  
TTCAACTCTT ACCTCATCAA GTTGAATAAA GACAGAGAAA  
ACAGAAAGAG ACATTGTTCT TTTCTGAGT CTTTTGAATG  
GAAATTGTAT TATGTTATAG CCATCATAAA ACCATTTTGG  
TAGTTTTGAC TGAACTGGGT GTTCACTTTT TCCTTTTTGA  
TTGAATACAA TTTAAATTCT ACTTGATGAC TGCAGTCGTC  
AAGGGGCTCC TGATGCAAGA TGCCCCTCC ATTTTAAGTC  
TGCTCCTTA CAGAGGTTAA AGTCTAGTGG CTAATTCCTA  
AGGAAACCTG ATTAACACAT GCTCACAACC ATCCTGGTCA  
TTCTCGAGCA TGTTCTATTT TTTAACTAAT CACCCCTGAT  
ATATTTTTAT TTTTATATAT CCAGTTTTCA TTTTTTTACG  
TCTTGCTTAT AAGCTAATAT CATAAATAAG GTTGTTTAAG  
ACGTGCTTCA AATATCCATA TTAACCACTA TTTTTCAAGG  
AAGTATGGAA AAGTACACTC TGTCACCTTG TCACTCGATG  
TCATTCCAAA GTTATTGCCT ACTAAGTAAT GACTGTCAATG  
AAAGCAGCAT TGAATAAATT TGTTAAAGG GGGCACTCTT

FIG. 9E

TTAAACGGGA	AGAAAATTTT	CGCTTCCTGG	TCTTATCATG
GACAATTTGG	GCTATAGGCA	TGAAGGAAGT	GGGATTACCT
CAGGAAGTCA	CCTTTTCTTG	ATTCCAGAAA	CATATGGGCT
GATAAACCCG	GGGTGACCTC	ATGAAATGAG	TTGCAGCAGA
TGTTTATTTT	TTTCAGAACA	AGTGATGTTT	GATGGACCTA
TGAATCTATT	TAGGGAGACA	CAGATGGCTG	GGATCCCTCC
CCTGTACCCT	TCTCACTGCC	AGGAGAACTA	CGTGTGAAGG
TATTC AAGGC	AGGGAGTATA	CATTGCTGTT	TCCTGTTGGG
CAATGCTCCT	TGACCACATT	TTGGGAAGAG	TGGATGTTAT
CATTGAGAAA	ACAATGTGTC	TGGAATTAAT	GGGGTTCTTA
TAAAGAAGGT	TCCCAGAAAA	GAATGTTCAT	TCCAGCTTCT
TCAGGAAACA	GGAACATTCA	AGGAAAAGGA	CAATCAGGAT
GTCATCAGGG	AAATGAAAAT	AAAAACCACA	ATGAGATATC
ACCTTATACC	AGGTAGATGG	CTACTATAAA	AAAATGAAGT
GTCATCAAGG	ATATAGAGAA	ATTGGAACCC	TTCTTCACTG
CTGGAGGGAA	TGGAAAATGG	TGTAGCCGTT	ATGAAAAACA
GTACGGAGGT	TTCTCAAAAA	TTAAAAATAG	AACTGCTATA
TGATCCAGCA	ATCTCACTTC	TGTATATATA	CCCAAAATAA
TTGAAATCAG	AATTTCAAGA	AAATATTTAC	ACTCCCATGT
TCATTGTGGC	ACTCTTCACA	ATCACTGTTT	CCAAAGTTAT
GGAAACAACC	CAAATTTCCA	TTGGAAAATA	AATGGACAAA
GGAAATGTGC	ATATAACGTA	CAATGGGGAT	ATTATTCAGC
CTAAAAAAG	GGGGGATCCT	GTTATTTATG	ACAACATGAA
TAAACCCGGA	GGCCATTATG	CTATGTAAAA	TGAGCAAGTA
ACAGAAAGAC	AAATACTGCC	TGATTTTCATT	TATATGAGGT
TCTAAAATAG	TCAAATCAT	AGAAGCAGAG	AATAGAACAG
TGGTTCCTAG	GGAAAAGGAG	GAAGGGAGAA	ATGAGGAAAT
AGGGAGTTGT	CTAATTGGTA	TAAAATTATA	GTATGCAAGA
TGAATTAGCT	CTAAAGATCA	GCTGTATAGC	AGAGTTCGTA
TAATGAACAA	TACTGTATTA	TGCACTTAAC	ATTTTGTTAA
GAGGGTACCT	CTCATGTTAA	GTGTTCTTAC	CATATACATA
TACACAAGGA	AGCTTTTGGG	GGTGATGGAT	ATATTTATTA
CCTTGATTGT	GGTGATGGTT	TGACAGGTAT	GTGACTATGT
CTAAATCAT	CAAATGTAT	ACATTAAATA	TATGCAGTTT
TATAATATCA	AAAAAAAAAA	AAAAAAAAAA	

FIG. 9F



## VARIANT TLR4 NUCLEIC ACID AND USES THEREOF

### STATEMENT OF GOVERNMENT RIGHT

This invention was made at least in part with a grant from the Government of the United States of America (grants ES06537, ES07498, and ES05605 from the National Institute of Environmental Sciences, grant HL62628 from the National Heart and Lung Institute, and grant RR00059 from the General Clinical Research Centers Program). The Government may have certain rights in the invention.

### BACKGROUND OF THE INVENTION

Endotoxin or lipopolysaccharide (LPS), released from the cell wall of bacteria, plays a central role in a broad spectrum of human disease. The pathogenic importance of LPS in gram-negative sepsis is well established. Intravenous LPS induces all of the clinical features of gram-negative sepsis, including fever, shock, leukopenia followed by leukocytosis, and disseminated intravascular coagulation (Favorite et al., 1942). Higher concentrations of circulating levels of endotoxin have been associated with manifestations of systemic inflammatory response syndrome (Wang et al., 1995) and the development of acute respiratory distress syndrome following sepsis (Brigham et al., 1986). Inhaled endotoxin can induce airflow obstruction in naive or previously unexposed subjects (Michel et al., 1992) and is the most important occupational exposure associated with the development Schwartz et al., 1995a), and progression (Schwartz et al., 1995b), of airway disease among exposed workers. The concentration of endotoxin in the domestic setting appears to be associated with the clinical severity of asthma (Michel et al., 1996). Moreover, recent studies have shown that endotoxin is a contaminant of particulate matter in air pollution and may play a role in the pathophysiologic consequences of air pollution (Bonner et al., 1998). Thus, endotoxin is an important cause of morbidity and mortality.

The ability of the host to respond to endotoxin may play an important role in determining the severity of the physiologic and biologic response to this frequently encountered toxin. In mice, genetic differences in susceptibility to LPS have been established. LPS hyporesponsiveness arose spontaneously and was first identified in the C3H/HeJ strain. This strain had an LD<sub>50</sub> for LPS at least 20 times that observed in A/HeJ mice (Sultzzer et al., 1968). In addition to C3H/HeJ, two other mouse strains, C57BL10/ScCR (Coutinho et al., 1978) and its progenitor strain, C57BL/10ScN, (Vogel et al., 1979), are hyporesponsive to LPS.

Moreover, several reports suggest that humans may also respond differently to LPS. A patient with recurrent bacterial infections has been reported to be refractory to the in vivo and in vitro effects of LPS (Kuhns et al., 1997). Following challenge with intravenous LPS, this patient had no systemic increase in IL6 or G-CSF and had a minimal rise in the concentration of leukocytes, TNF- $\alpha$ , and IL-8. Inter-individual differences have also been reported in the release and synthesis of cytokines by monocytes stimulated with LPS in vitro (Santamaria et al., 1989).

LPS is thought to cause much of its morbidity and mortality by activating kinases (DeFranco et al., 1998) that control the function of transcription factors (nuclear factor- $\kappa$ B and AP-1) and ultimately lead to production of pro-inflammatory cytokines and co-stimulatory molecules (Wright, 1999). Several lines of evidence suggest that the toll receptor (TLR) family, and specifically TLR4 and TLR2 regulate the interaction between LPS and intracellular

kinases and may serve as a proximal target to interrupt LPS signaling (Wright, 1998; Medzhitov et al., 1997). Both TLR4 and TLR2 activate signaling through NF- $\kappa$ B and AP-1 in transfected human cell lines (Medzhitov et al., 1997; Yang et al., 1998), and TLR4 mediates LPS induced signal transduction (Chow et al., 1999). CD14, a glycosylphosphatidyl inositol-linked receptor that binds LPS (Poltorak et al., 1998a) enhances LPS induced TLR2 (Yanget al., 1998) and TLR4 (Chow et al., 1998) signaling, suggesting that the toll receptors interact with CD14 to initiate the cellular response to LPS. Studies in mice indicate that 1) the TLR4 gene maps to the critical region in LPS hyporesponsive mice (Poltorak et al., 1998), 2) mutations in the TLR4 gene (Poltorak et al., 1998; Qureshi et al., 1999) are found in mouse strains (C3H/HeJ and C57BL10/ScCr) that are defective in their response to LPS, and 3) disruption of the TLR4 gene results in a LPS hyporesponsive phenotype (Hoshino et al., 1999).

Thus, there is need to determine whether the human TLR4 gene is polymorphic, and whether any particular polymorphism is associated with disease, e.g., LPS hyporesponsiveness.

### SUMMARY OF THE INVENTION

The invention provides a method to identify a mammal, e.g., a human, at risk of, or having, an indication associated with altered innate immunity, e.g., to bacterial infection. The method comprises contacting an amount of DNA obtained from a human physiological sample with an amount of at least one TLR4-specific oligonucleotide under conditions effective to amplify the DNA so as to yield amplified DNA. Then it is determined whether the amplified DNA comprises a nucleotide substitution, e.g., one that results in an amino acid substitution, i.e., the TLR4 DNA of the human encodes a variant TLR4. Thus, the invention is useful to detect polymorphisms in the TLR4 gene.

Normal healthy, non-asthmatic subjects demonstrate a reproducible airway response to an incremental LPS inhalation challenge test, with some subjects developing airflow obstruction when challenged with low concentrations of LPS and others virtually unaffected by high concentrations of inhaled LPS. These findings suggest that the spectrum of LPS responsiveness in humans is quite variable from one individual to the next (but reproducible within an individual), and that a substantial portion of the population may be hyporesponsive to inhaled LPS. As described hereinbelow, an incremental LPS inhalation challenge test was employed to reliably phenotype individuals as either responsive (at least a 20% decline in the forced expiratory volume in one second (FEV<sub>1</sub>) after inhaling up to 41.5  $\mu$ g LPS) or hyporesponsive (FEV<sub>1</sub> >80% of their baseline after inhaling 41.5  $\mu$ g of LPS) to inhaled LPS. Fifty-two (63%) of these individuals were responsive to inhaled LPS and 31 (37%) were hyporesponsive to inhaled LPS.

These results were employed to determine the relationship between polymorphisms in the TLR4 gene and the airway response to inhaled LPS in the 83 normal healthy, non-asthmatic subjects. Using single stranded conformational variant (SSCV) analysis and direct sequencing, a missense mutation (A896G) was identified in the fourth exon of the TLR4 gene that results in replacement of a conserved aspartic acid residue with glycine at position 299 in the extracellular domain of the TLR4 receptor. The Asp299Gly sequence variant occurred in 3 LPS responsive (5.8%) and 7 LPS hyporesponsive (22.6%) study subjects (p=0.03). Among the subjects with the common TLR4 allele (N=73),

the dose-response slope (percent decline  $FEV_1$ /cumulative dose of inhaled LPS) averaged a 1.86% decline in  $FEV_1/\mu\text{g}$  inhaled LPS (range 0.01%–19.78%), while the dose-response slope for the subjects with the Asp299Gly allele (N=10) was significantly less ( $p=0.007$ ), averaging 0.59% decline in  $FEV_1/\mu\text{g}$  inhaled LPS (range 0.00%–1.59%). Thus, a sequence polymorphism in the TLR4 gene, i.e., a missense mutation (Asp299Gly) in the fourth exon of the TLR4 gene, occurs in a substantial portion of the population, add frequency in other population Iowa, French and is associated with an airway hyporesponsive in humans challenged with inhaled LPS. The allelic frequency of the A896G substitution was 6.6% in the study population, 7.9% in a normal control population from Iowa (Lidral et al., 1998), and 3.3% in the parental chromosomes in of the CEPH population (NIH-CEPH, 1992).

The invention also provides an isolated and purified nucleic acid molecule comprising a nucleic acid segment, e.g., genomic DNA or cDNA, encoding TLR4, such as a variant TLR4. Also provided are primers, oligonucleotides and probes comprising the isolated nucleic acid sequences of the invention. The nucleic acid molecules of the invention may be single stranded or double stranded.

Transfection of CHO cells with either the wild-type or the mutant (Asp299Gly) allele of the TLR4 gene demonstrated that this mutation interrupts TLR4-mediated LPS signaling. Moreover, the wild-type allele of TLR4 rescues the LPS hyporesponsive phenotype in either airway epithelial cells or alveolar macrophages obtained from individuals with the TLR4 mutation. Thus, these results provide the first genetic evidence that a common mutation causes differences in LPS responsiveness that may contribute to several disease states in humans.

Therefore, the invention further provides an expression cassette comprising a nucleic acid molecule of the invention, a host cell transformed with the expression cassette, and TLR4 polypeptides isolated therefrom. The transformed host cells, or isolated TLR4 polypeptides, may be useful in identifying agents that modulate, i.e., enhance or inhibit, TLR4 activity. Thus, the invention also provides a method to treat an individual at risk of, or having, an indication associated with altered innate immunity, in which an agent that alters TLR4 activity is administered to the individual.

#### BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Genomic structure for the human TLR4 gene (exons are represented by boxes and introns are represented by lines). The coding sequence is in black and the nucleotides encoding the transmembrane domain (TM) are shaded. The positions of the introns in the published TLR4 cDNA sequence (Rock et al., 1998; Genbank Accession No. U88880) are listed. The exon (caps) and intron (lower case) sequences at each of the splice junctions is shown (sequences at 5' and 3' splice junctions for intron 1, SEQ ID NO:1 and SEQ ID NO:63, respectively; for intron 2, SEQ ID NO:2 and SEQ ID NO:64, respectively; and for intron 3, SEQ ID NO:3 and SEQ ID NO:65, respectively).

FIG. 2. The human TLR4 gene is alternatively spliced. Photographs are of agarose gels containing the products amplified from a multi-tissue cDNA panel from human adult (panel a; Clontech #K1420-1, Palo Alto, Calif.), and human fetal (panel b; Clontech #K1425-1, Palo Alto, Calif.) cDNA. The tissues included brain (B), heart (H), kidney (K), liver (Li), lung (Lu), pancreas (Pa), placenta (PI), skeletal muscle (Sk), spleen (Sp), and thymus (T). The first lane of each gel included a 100 bp molecular weight standard (MW). The

forward and reverse PCR primers were derived from exons 1 and 4, respectively (see panel c) and amplified three products of 453, 333, and 167 bp. The DNA sequence for these bands showed that both exons 2 and 3 were present in the 453 bp band, that exon 2 was absent in the 333 bp product, and that both exons 2 and 3 were absent in the 167 bp band. The 453 bp and 333 bp sequences are identical to previously published sequences for the human TLR cDNA (Medzhitov et al., 1997; Rock et al., 1998). The open, closed, and shaded boxes indicate the untranslated, translated, and transmembrane domain portions of the TLR4 exons, respectively. The ends of the cDNAs were arbitrarily terminated at the stop codon (STP).

FIG. 3. Mutations in the human TLR4 gene. The SSCV and sequence analysis were performed blinded to the LPS response phenotype of the study subjects. The SSCV gel in panel a contains the products amplified from two samples that are homozygous for the 1060A allele (lanes 1 and 3), a heterozygous sample (lane 2) with both the 896A and 896G alleles, and a homozygous sample (lane 4) with only the 896G allele. The SSCV gel in panel b contains the products amplified from a sample that is homozygous for the T allele at position -11 and the T allele at position 315 (lane 1), and from a sample that is heterozygous with a T and a deletion at position -11 and a T and a C allele at position 315. The nucleotide numbers are based on the previously published TLR4 cDNA sequence (Rock et al., 1998).

FIG. 4. The aspartic acid residue at position 299 is conserved. A portion of the predicted amino acid sequence is aligned for the TLR4 genes from human (Rock et al., 1998; SEQ ID NO:4), mouse (Poitorak et al., 1998; SEQ ID NO:5), rat (Genbank Accession No. AF057025; SEQ ID NO:6), and hamster (D. Golenbock, SEQ ID NO:7). The position of the first amino acid in each sequence is given. The aspartic acid at position 299 is indicated with an arrow. Conserved amino acids are shaded.

FIG. 5. Frequency distribution histogram of the dose-response slope (% decline in  $FEV_1/\mu\text{g}$  LPS). The % decline in  $FEV_1/\mu\text{g}$  LPS was calculated following administration of the cumulative LPS dose that either resulted in at least a 20% decline in  $FEV_1$  or the decline in  $FEV_1$  following a cumulative inhaled dose of 41.5  $\mu\text{g}$  LPS. Subjects above the x-axis (solid bars) are homozygous for the 896A allele (WT/WT); subjects below the x-axis (open bars) are either heterozygous or homozygous (\*) for the missense Asp299Gly allele. The data is replotted in the inset after the values on the x-axis were log normalized. P values are presented for the comparison of the % decline in  $FEV_1/\mu\text{g}$  LPS between subjects with the WT/WT genotype (N=73) and those with at least one Asp299Gly allele (N=10) using absolute values (P=0.37) and log normalized values (P=0.26). Since the distribution of the dose-response slope (% decline  $FEV_1$ /cumulative dose of inhaled LPS) was highly skewed, the two-sample Monte-Carlo permutation test based on 10,000 permutations was used to calculate P values (Fisher et al., 1993) the missense mutation (N=10) using absolute values (p=0.04) and the log normalized values (p=0.04) and the log normalized values (p=0.025).

FIG. 6. A) CHO/CD-14 cells that express the CD-14 receptor (generous gift of Doug Golenbock) were transfected with a wild-type or mutant TLR4 allele, and then exposed to LPS. Cells were co-transfected with a luciferase reporter construct. B) IL-1 $\alpha$  levels from airway epithelial cells of individuals which had been genotyped for TLR4. IL-1 $\alpha$  levels before and after LPS exposure are shown. C) IL-1 $\alpha$  levels from airway epithelial cells from a TLR4 heterozygote (WT/Asp299Gly). The cells were transduced

with a recombinant adenovirus which expresses TLR4 (Rock et al., 1998), or a recombinant adenovirus which expresses green fluorescent protein (GFP), and then exposed to LPS. D) TNF- $\alpha$  levels from alveolar macrophage from a TLR4 homozygote (Asp299Gly/Asp299Gly). The cells were transduced with a recombinant adenovirus which expresses TLR4 (Rock et al., 1998), and then exposed to LPS.

FIG. 7. Codons

FIG. 8. Exemplary amino acid substitutions.

FIG. 9. Partial nucleotide sequence of genomic human TLR4 DNA (SEQ ID NO:62).

#### DETAILED DESCRIPTION OF THE INVENTION

As used herein, the terms "isolated and/or purified" refer to in vitro preparation, isolation and/or purification of a nucleic acid molecule or polypeptide, so that it is not associated with in vivo substances. Thus, with respect to an "isolated nucleic acid molecule", which includes a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, the "isolated nucleic acid molecule" (1) is not associated with all or a portion of a polynucleotide in which the "isolated nucleic acid molecule" is found in nature, (2) is operably linked to a polynucleotide which it is not linked to in nature, or (3) does not occur in nature as part of a larger sequence. An isolated nucleic acid molecule means a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide. The term includes single and double stranded forms of DNA. The term "oligonucleotide" referred to herein includes naturally occurring, and modified nucleotides linked together by naturally occurring, and non-naturally occurring oligonucleotide linkages. Oligonucleotides are a polynucleotide subset with 200 bases or fewer in length. Preferably, oligonucleotides are 10 to 60 bases in length and most preferably 12, 13, 14, 15, 16, 17, 18, 19, or 20 to 40 bases in length. Oligonucleotides are usually single stranded, e.g., for primers or probes; although oligonucleotides may be double stranded, e.g., for use in the construction of a variant. Oligonucleotides of the invention can be either sense or antisense oligonucleotides. The term "naturally occurring nucleotides" referred to herein includes deoxyribonucleotides and ribonucleotides. The term "modified nucleotides" referred to herein includes nucleotides with modified or substituted sugar groups and the like. The term "oligonucleotide linkages" referred to herein includes oligonucleotide linkages such as phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoranilothioate, phosphoraniladate, phosphorbamidate, and the like. An oligonucleotide can include a label for detection, if desired.

The term "isolated polypeptide" means a polypeptide encoded by genomic DNA, cDNA or recombinant RNA, or is synthetic origin, or some combination thereof, which isolated polypeptide (1) is not associated with proteins found in nature, (2) is free of other proteins from the same source, e.g., free of human proteins, (3) is expressed by a cell from a different species, or (4) does not occur in nature.

The term "sequence homology" means the proportion of base matches between two nucleic acid sequences or the proportion amino acid matches between two amino acid sequences. When sequence homology is expressed as a percentage, e.g., 50%, the percentage denotes the proportion of matches over the length of sequence from one TLR4

allele that is compared to another TLR4 allele. Gaps (in either of the two sequences) are permitted to maximize matching; gap lengths of 15 bases or less are usually used, 6 bases or less are preferred with 2 bases or less more preferred. When using oligonucleotides as probes or treatments, the sequence homology between the target nucleic acid and the oligonucleotide sequence is generally not less than 17 target base matches out of 20 possible oligonucleotide base pair matches (85%); preferably not less than 9 matches out of 10 possible base pair matches (90%), and more preferably not less than 19 matches out of 20 possible base pair matches (95%).

The term "selectively hybridize" means to detectably and specifically bind. Polynucleotides, oligonucleotides and fragments of the invention selectively hybridize to nucleic acid strands under hybridization and wash conditions that minimize appreciable amounts of detectable binding to nonspecific nucleic acids. High stringency conditions can be used to achieve selective hybridization conditions as known in the art and discussed herein. Generally, the nucleic acid sequence homology between the polynucleotides, oligonucleotides, and fragments of the invention and a nucleic acid sequence of interest is at least 65%, and more typically with preferably increasing homologies of at least about 70%, about 90%, about 95%, about 98%, and 100%.

Two amino acid sequences are homologous if there is a partial or complete identity between their sequences. For example, 85% homology means that 85% of the amino acids are identical when the two sequences are aligned for maximum matching. Gaps (in either of the two sequences being matched) are allowed in maximizing matching; gap lengths of 5 or less are preferred with 2 or less being more preferred. Alternatively and preferably, two protein sequences (or polypeptide sequences derived from them of at least 30 amino acids in length) are homologous, as this term is used herein, if they have an alignment score of at more than 5 (in standard deviation units) using the program ALIGN with the mutation data matrix and a gap penalty of 6 or greater. See Dayhoff, M. O., in Atlas of Protein Sequence and Structure, 1972, volume 5, National Biomedical Research Foundation, pp. 101-110, and Supplement 2 to this volume, pp. 1-10. The two sequences or parts thereof are more preferably homologous if their amino acids are greater than or equal to 50% identical when optimally aligned using the ALIGN program.

The term "corresponds to" is used herein to mean that a polynucleotide sequence is homologous (i.e., is identical, not strictly evolutionarily related) to all or a portion of a reference polynucleotide sequence, or that a polypeptide sequence is identical to a reference polypeptide sequence. In contradistinction, the term "complementary to" is used herein to mean that the complementary sequence is homologous to all or a portion of a reference polynucleotide sequence. For illustration, the nucleotide sequence "TATAC" corresponds to a reference sequence "TATAC" and is complementary to a reference sequence "GTATA".

The following terms are used to describe the sequence relationships between two or more polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a complete cDNA or gene sequence. Generally, a reference sequence is at least 20 nucleotides in length, frequently at least 25 nucleotides in

length, and often at least 50 nucleotides in length. Since two polynucleotides may each (1) comprise a sequence (i.e., a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) may further comprise a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity.

A "comparison window", as used herein, refers to a conceptual segment of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math.* 2: 482, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 2: 443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. (U.S.A.)* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by inspection, and the best alignment (i.e., resulting in the highest percentage of homology over the comparison window) generated by the various methods is selected.

The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The terms "substantial identity" as used herein denote a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 20-50 nucleotides, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison.

As applied to polypeptides, the term "substantial identity" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least about 80 percent sequence identity, preferably at least about 90 percent sequence identity, more preferably at least about 95 percent sequence identity, and most preferably at least about 99 percent sequence identity.

As used herein, "substantially pure" means an object species is the predominant species present (i.e., on a molar basis it is more abundant than any other individual species

in the composition), and preferably a substantially purified fraction is a composition wherein the object species comprises at least about 50 percent (on a molar basis) of all macromolecular species present. Generally, a substantially pure composition will comprise more than about 80 percent of all macromolecular species present in the composition, more preferably more than about 85%, about 90%, about 95%, and about 99%. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

An isolated "variant" TLR4 polypeptide has at least 50%, preferably at least about 80%, and more preferably at least about 90%, but less than 100%, contiguous amino acid sequence homology or identity to the amino acid sequence of a reference (wild-type) TLR4 polypeptide. Preferably, the TLR4 polypeptides of the invention are biologically active. Biologically active polypeptides include those that induce an immune response when administered to an organism, are bound by antibodies specific for TLR4, activate signaling through NF-KB and AP-1, interact with CD14, or induce cytokine release following LPS stimulation. While it is preferred that a variant TLR4 has at least about 0.1%, preferably at least about 1%, and more preferably at least about 10%, of the activity of wild-type TLR4, the invention includes variant TLR4 polypeptides having no detectable biological activity. Likewise, a "variant" TLR4 nucleic acid molecule has at least about 80%, preferably at least about 90% and more preferably at least about 95% but less than 100% contiguous nucleic acid sequence homology or identity to the nucleic acid sequence of a wild-type TLR4 gene.

As used herein, an "indication or condition associated with aberrant, modified or altered innate immunity" includes, but is not limited to, hyporesponsiveness to LPS, susceptibility to infection with gram-negative bacteria, susceptibility to sepsis by gram-negative bacteria, susceptibility to chronic airway disease, susceptibility to asthma, susceptibility to arthritis, susceptibility to pyelonephritis, susceptibility to gall bladder disease, susceptibility to pneumonia, susceptibility to bronchitis, susceptibility to chronic obstructive pulmonary disease, severity of cystic fibrosis, and susceptibility to local and systemic inflammatory conditions, e.g., systemic inflammatory response syndrome (SIRS), local gram negative bacterial infection, or acute respiratory distress syndrome (ARDS).

#### A Nucleic Acid Molecule of the Invention

1. Sources of the Nucleic Acid Molecules of the Invention  
Sources of nucleic acid molecules from which the present nucleic acid molecules encoding TLR4, a portion (fragment) thereof, a variant thereof or the nucleic acid complement thereof, include total or polyA<sup>+</sup> RNA from any mammalian, preferably human, cellular source from which cDNAs can be derived by methods known in the art. Other sources of the DNA molecules of the invention include genomic libraries derived from any mammalian cellular source. Moreover, the present DNA molecules may be prepared in vitro, e.g., by synthesizing an oligonucleotide of about 100, preferably about 75, more preferably about 50, and even more preferably about 40, nucleotides in length, or by subcloning a portion of a DNA segment that encodes a particular TLR4.

#### 2. Isolation of a Gene Encoding TLR4

A nucleic acid molecule encoding TLR4 can be identified and isolated using standard methods, as described by Sambrook et al., *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor, N.Y. (1989). For example, reverse-

transcriptase PCR (RT-PCR) can be employed to isolate and clone TLR4 cDNAs. Oligo-dT can be employed as a primer in a reverse transcriptase reaction to prepare first-strand cDNAs from isolated RNA which contains RNA sequences of interest, e.g., total RNA isolated from human tissue. RNA can be isolated by methods known to the art, e.g., using TRIZOL™ reagent (GIBCO-BRL/Life Technologies, Gaithersburg, Md.). Resultant first-strand cDNAs are then amplified in PCR reactions.

“Polymerase chain reaction” or “PCR” refers to a procedure or technique in which amounts of a preselected fragment of nucleic acid, RNA and/or DNA, are amplified as described in U.S. Pat. No. 4,683,195. Generally, sequence information from the ends of the region of interest or beyond is employed to design oligonucleotide primers comprising at least 7–8 nucleotides. These primers will be identical or similar in sequence to opposite strands of the template to be amplified. PCR can be used to amplify specific RNA sequences, specific DNA sequences from total genomic DNA, and cDNA transcribed from total cellular RNA, bacteriophage or plasmid sequences, and the like. See generally Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51, 263 (1987); Erlich, ed., *PCR Technology*, (Stockton Press, N.Y., 1989). Thus, PCR-based cloning approaches rely upon conserved sequences deduced from alignments of related gene or polypeptide sequences.

Primers are made to correspond to highly conserved regions of polypeptides or nucleotide sequences which were identified and compared to generate the primers, e.g., by a sequence comparison of other mammalian TLR4. One primer is prepared which is predicted to anneal to the antisense strand, and another primer prepared which is predicted to anneal to the sense strand, of a DNA molecule which encodes TLR4.

The products of each PCR reaction are separated via an agarose gel and all consistently amplified products are gel-purified and cloned directly into a suitable vector, such as a known plasmid vector. The resultant plasmids are subjected to restriction endonuclease and dideoxy sequencing of double-stranded plasmid DNAs.

Another approach to identify, isolate and clone cDNAs which encode TLR4 is to screen a cDNA or genomic library. Screening for DNA fragments that encode all or a portion of a DNA encoding TLR4 can be accomplished by probing the library with a probe which has sequences that are highly conserved between genes believed to be related to TLR4, e.g., the homolog of a particular TLR4 from a different species, or by screening of plaques for binding to antibodies that specifically recognize TLR4. DNA fragments that bind to a probe having sequences which are related to TLR4, or which are immunoreactive with antibodies to TLR4, can be subcloned into a suitable vector and sequenced and/or used as probes to identify other cDNAs encoding all or a portion of TLR4.

Thus, “isolated and/or purified TLR4” nucleic acid refers to in vitro isolation of a nucleic acid molecule from its natural cellular environment, and from association with other components of the cell, such as nucleic acid or polypeptide, so that it can be sequenced, replicated, and/or expressed. For example, “isolated TLR4 nucleic acid” is RNA or DNA containing greater than 9, preferably 36, and more preferably 45 or more, sequential nucleotide bases that encode at least a portion of TLR4, a variant thereof, RNA or DNA complementary thereto, or which hybridizes to, RNA or DNA comprising TLR4 sequences, and remains stably bound under stringent conditions, as defined by methods well known in the art e.g., in Sambrook et al., supra. Thus,

the RNA or DNA is “isolated” in that it is free from at least one contaminating nucleic acid with which it is normally associated in the natural source of the RNA or DNA and is preferably substantially free of any other mammalian RNA or DNA. The phrase “free from at least one contaminating source nucleic acid with which it is normally associated” includes the case where the nucleic acid is reintroduced into the source or natural cell but is in a different chromosomal location or is otherwise flanked by nucleic acid sequences not normally found in the source cell.

As used herein, the term “recombinant nucleic acid”, e.g., “recombinant DNA sequence or segment”, refers to a nucleic acid, e.g., to DNA, that has been derived or isolated from any appropriate tissue source, that may be subsequently chemically altered in vitro, so that its sequence is not naturally occurring, or corresponds to naturally occurring sequences that are not positioned as they would be positioned in a genome which has not been transformed with exogenous DNA. An example of DNA “derived” from a source, would be a DNA sequence that is identified as a useful fragment within a given organism, and which is then chemically synthesized in essentially pure form. An example of such DNA “isolated” from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering.

Thus, recovery or isolation of a given fragment of DNA from a restriction digest can employ separation of the digest on polyacrylamide or agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of the gel from DNA. See Lawn et al., *Nucleic Acids Res.*, 9, 6103 (1981), and Goeddel et al., *Nucleic Acids Res.*, 8, 4057 (1980). Therefore, “isolated DNA” includes completely synthetic DNA sequences, semi-synthetic DNA sequences, DNA sequences isolated from biological sources, and DNA sequences derived from RNA, as well as mixtures thereof.

As used herein, the term “derived” with respect to a RNA molecule means that the RNA molecule has complementary sequence identity to a particular DNA molecule.

3. Variant of the Nucleic Acid Molecules of the Invention  
Nucleic acid molecules encoding amino acid sequence variants of TLR4 are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of TLR4 nucleic acid.

Oligonucleotide-mediated mutagenesis is a preferred method for preparing amino acid substitution variants of TLR4. This technique is well known in the art as described by Adelman et al., *DNA*, 2, 183 (1983). Briefly, TLR4 DNA is altered by hybridizing an oligonucleotide encoding the desired mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of TLR4. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the TLR4 DNA.

Generally, oligonucleotides of at least 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to

15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al., *Proc. Natl. Acad. Sci. U.S.A.*, 75, 5765 (1978).

The DNA template can be generated by those vectors that are either derived from bacteriophage M13 vectors (the commercially available M13 mp 18 and M13 mp 19 vectors are suitable), or those vectors that contain a single-stranded phage origin of replication as described by Viera et al., *Meth. Enzymol.*, 153, 3 (1987). Thus, the DNA that is to be mutated may be inserted into one of these vectors to generate single-stranded template. Production of the single-stranded template is described in Sections 4.21–4.41 of Sambrook et al., *Molecular Cloning A Laboratory Manual* (Cold Spring Harbor Laboratory Press, N.Y. 1989).

Alternatively, single-stranded DNA template may be generated by denaturing double-stranded plasmid (or other) DNA using standard techniques.

For alteration of the native DNA sequence (to generate amino acid sequence variants, for example), the oligonucleotide is hybridized to the single-stranded template under suitable hybridization conditions. A DNA polymerizing enzyme, usually the Klenow fragment of DNA polymerase I, is then added to synthesize the complementary strand of the template using the oligonucleotide as a primer for synthesis. A heteroduplex molecule is thus formed such that one strand of DNA encodes the mutated form of TLR4, and the other strand (the original template) encodes the native, unaltered sequence of TLR4. This heteroduplex molecule is then transformed into a suitable host cell, usually a prokaryote such as *E. coli* JM101. After the cells are grown, they are plated onto agarose plates and screened using the oligonucleotide primer radiolabeled with 32-phosphate to identify the bacterial colonies that contain the mutated DNA. The mutated region is then removed and placed in an appropriate vector for peptide or polypeptide production, generally an expression vector of the type typically employed for transformation of an appropriate host.

The method described immediately above may be modified such that a homoduplex molecule is created wherein both strands of the plasmid contain the mutations(s). The modifications are as follows: The single-stranded oligonucleotide is annealed to the single-stranded template as described above. A mixture of three deoxyribonucleotides, deoxyriboadenosine (dATP), deoxyriboguanosine (dGTP), and deoxyribothymidine (dTTP), is combined with a modified thiodeoxyribocytosine called dCTP-( $\alpha$ S) (which can be obtained from the Amersham Corporation). This mixture is added to the template-oligonucleotide complex. Upon addition of DNA polymerase to this mixture, a strand of DNA identical to the template except for the mutated bases is generated. In addition, this new strand of DNA will contain dCTP-( $\alpha$ S) instead of dCTP, which serves to protect it from restriction endonuclease digestion.

After the template strand of the double-stranded heteroduplex is nicked with an appropriate restriction enzyme, the template strand can be digested with ExoIII nuclease or another appropriate nuclease past the region that contains the site(s) to be mutagenized. The reaction is then stopped to leave a molecule that is only partially single-stranded. A complete double-stranded DNA homoduplex is then formed using DNA polymerase in the presence of all four deoxyribonucleotide triphosphates, ATP, and DNA ligase. This homoduplex molecule can then be transformed into a suitable host cell such as *E. coli* JM101.

For example, a preferred embodiment of the invention is an isolated and purified DNA molecule comprising a human DNA segment encoding a variant TLR4 having a nucleotide substitution at position 896 (A896G) which encodes an amino acid substitution (Asp299Gly). Other nucleotide substitutions which result in silent mutations, missense mutations, or a nonsense mutations, can be ascertained by reference to FIG. 7, FIG. 8 and page D1 in Appendix D in Sambrook et al., *Molecular Cloning: A laboratory Manual* (1989).

## B. Chimeric Expression Cassettes

To prepare expression cassettes for transformation herein, the recombinant DNA sequence or segment may be circular or linear, double-stranded or single-stranded. A DNA sequence which encodes an RNA sequence that is substantially complementary to a mRNA sequence encoding TLR4 is typically a “sense” DNA sequence cloned into a cassette in the opposite orientation (i.e., 3' to 5' rather than 5' to 3'). Generally, the DNA sequence or segment is in the form of chimeric DNA, such as plasmid DNA, that can also contain coding regions flanked by control sequences which promote the expression of the DNA present in the resultant cell line.

As used herein, “chimeric” means that a vector comprises DNA from at least two different species, or comprises DNA from the same species, which is linked or associated in a manner which does not occur in the “native” or wild type of the species.

Aside from DNA sequences that serve as transcription units for TLR4, or portions thereof, a portion of the recombinant DNA may be untranscribed, serving a regulatory or a structural function. For example, the DNA may itself comprise a promoter that is active in mammalian cells, or may utilize a promoter already present in the genome that is the transformation target. Such promoters include the CMV promoter, as well as the SV40 late promoter and retroviral LTRs (long terminal repeat elements), although many other promoter elements well known to the art may be employed in the practice of the invention.

Other elements functional in the host cells, such as introns, enhancers, polyadenylation sequences and the like, may also be a part of the DNA. Such elements may or may not be necessary for the function of the DNA, but may provide improved expression of the DNA by affecting transcription, stability of the mRNA, or the like. Such elements may be included in the DNA as desired to obtain the optimal performance of the transforming DNA in the cell.

“Control sequences” is defined to mean DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotic cells, for example, include a promoter, and optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

“Operably linked” is defined to mean that the nucleic acids are placed in a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a peptide or polypeptide if it is expressed as a preprotein that participates in the secretion of the peptide or polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation.

Generally, “operably linked” means that the DNA sequences being linked are contiguous and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accord with conventional practice.

The DNA to be introduced into the cells further will generally contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of transformed cells from the population of cells sought to be transformed. Alternatively, the selectable marker may be carried on a separate piece of DNA and used in a co-transformation procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to enable expression in the host cells. Useful selectable markers are well known in the art and include, for example, antibiotic and herbicide-resistance genes, such as neo, hpt, dhfr, bar, aroA, dapA and the like. See also, the genes listed on Table 1 of Lundquist et al. (U.S. Pat. No. 5,848,956).

Reporter genes are used for identifying potentially transformed cells and for evaluating the functionality of regulatory sequences. Reporter genes which encode for easily assayable proteins are well known in the art. In general, a reporter gene is a gene which is not present in or expressed by the recipient organism or tissue and which encodes a protein whose expression is manifested by some easily detectable property, e.g., enzymatic activity. Preferred genes include the chloramphenicol acetyl transferase gene (cat) from Tn9 of *E. coli*, the beta-glucuronidase gene (gus) of the uidA locus of *E. coli*, and the luciferase luc gene from firefly *Photinus pyralis*. Expression of the reporter gene is assayed at a suitable time after the DNA has been introduced into the recipient cells.

The general methods for constructing recombinant DNA which can transform target cells are well known to those skilled in the art, and the same compositions and methods of construction may be utilized to produce the DNA useful herein. For example, J. Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press (2d ed., 1989), provides suitable methods of construction.

### C. Transformation Into Host Cells

The recombinant DNA can be readily introduced into the host cells, e.g., mammalian, bacterial, yeast or insect cells by transfection with an expression vector comprising DNA encoding TLR4 or its complement, by any procedure useful for the introduction into a particular cell, e.g., physical or biological methods, to yield a transformed cell having the recombinant DNA stably integrated into its genome, so that the DNA molecules, sequences, or segments, of the present invention are expressed by the host cell.

Physical methods to introduce a DNA into a host cell include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, and the like. Biological methods to introduce the DNA of interest into a host cell include the use of DNA and RNA viral vectors. The main advantage of physical methods is that they are not associated with pathological or oncogenic processes of viruses. However, they are less precise, often resulting in multiple copy insertions, random integration, disruption of foreign and endogenous gene sequences, and unpredictable expression. Viral vectors, useful to introduce genes to mammalian cells include, but are not limited to, poxvirus vectors, herpes simplex virus I vectors, adenovirus vectors, adeno-associated virus vectors, and the like.

As used herein, the term “cell line” or “host cell” is intended to refer to well-characterized homogenous, biologically pure populations of cells. These cells may be eukaryotic cells that are neoplastic or which have been “immortalized” in vitro by methods known in the art, as well as primary cells, or prokaryotic cells. The cell line or host cell is preferably of mammalian origin, but cell lines or host cells of non-mammalian origin may be employed, including plant, insect, yeast, fungal or as “bacterial sources. Generally, the DNA sequence is related to a DNA sequence which is resident in the genome of the host cell but is not expressed, or not highly expressed; or, alternatively, over-expressed.

“Transfected” or “transformed” is used herein to include any host cell or cell line, the genome of which has been altered or augmented by the presence of at least one DNA sequence, which DNA is also referred to in the art of genetic engineering as “heterologous DNA,” recombinant DNA,” “exogenous DNA,” “genetically engineered,” “non-native,” or “foreign DNA,” wherein said DNA was isolated and introduced into the genome of the host cell or cell line by the process of genetic engineering. The host cells of the present invention are typically produced by transfection with a DNA sequence in a plasmid expression vector, a viral expression vector, or as an isolated linear DNA sequence.

To confirm the presence of the DNA sequence in the host cell, a variety of assays may be performed. Such assays include, for example, “molecular biological” assays well known to those of skill in the art such as Southern and Northern blotting, RT-PCR and PCR; “biochemical” assays, such as detecting the presence or absence of a particular TLR4, e.g., by immunological means (ELISAs and Western blots) or by assays described herein.

To detect and quantitate RNA produced from introduced DNA segments, RT-PCR may be employed. In this application of PCR, it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique demonstrates the presence of an RNA species and gives information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern in hybridizations. These techniques are modifications of Northern blotting and only demonstrate the presence or absence of an RNA species.

While Southern blotting and PCR may be used to detect the DNA segment in question, they do not provide information as to whether the DNA segment is being expressed. Expression may be evaluated by specifically identifying the polypeptide products of the introduced DNA sequences or evaluating the phenotypic changes brought about by the expression of the introduced DNA segment in the host cell.

### TLR4 Polypeptides, Variant, and Derivatives Thereof

The present isolated, purified TLR4 polypeptides, variants or derivatives thereof, can be synthesized in vitro, e.g., by the solid phase peptide synthetic method or by recombinant DNA approaches (see above). The solid phase peptide synthetic method is an established and widely used method, which is described in the following references: Stewart et al., *Solid Phase Peptide Synthesis*, W. H. Freeman Co., San Francisco (1969); Merrifield, *J. Am. Chem. Soc.*, 85 2149

(1963); Meienhofer in "Hormonal Proteins and Peptides," ed; C. H. Li, Vol. 2 (Academic Press, 1973), pp. 48-267; Bavaay and Merrifield, "The Peptides," eds. E. Gross and F. Meienhofer, Vol. 2 (Academic Press, 1980) pp. 3-285; and Clark-Lewis et al., *Meth. Enzymol.*, 287, 233 (1997). These peptides can be further purified by fractionation on immunoaffinity or ion-exchange columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on an anion-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; or ligand affinity chromatography.

Once isolated and characterized, derivatives, e.g., chemically derived derivatives, of a given TLR4 can be readily prepared. For example, amides of the TLR4 or TLR4 variants of the present invention may also be prepared by techniques well known in the art for converting a carboxylic acid group or precursor, to an amide. A preferred method for amide formation at the C-terminal carboxyl group is to cleave the peptide from a solid support with an appropriate amine, or to cleave in the presence of an alcohol, yielding an ester, followed by aminolysis with the desired amine.

Salts of carboxyl groups of a peptide or peptide variant of the invention may be prepared in the usual manner by contacting the peptide with one or more equivalents of a desired base such as, for example, a metallic hydroxide base, e.g., sodium hydroxide; a metal carbonate or bicarbonate base such as, for example, sodium carbonate or sodium bicarbonate; or an amine base such as, for example, triethylamine, triethanolamine, and the like.

N-acyl derivatives of an amino group of the TLR4 or variant thereof may be prepared by utilizing an N-acyl protected amino acid for the final condensation, or by acylating a protected or unprotected peptide. O-acyl derivatives may be prepared, for example, by acylation of a free hydroxy peptide or peptide resin. Either acylation may be carried out using standard acylating reagents such as acyl halides, anhydrides, acyl imidazoles, and the like. Both N- and O-acylation may be carried out together, if desired.

Formyl-methionine, pyroglutamine and trimethyl-alanine may be substituted at the N-terminal residue of the peptide or peptide variant. Other amino-terminal modifications include aminoxyepentane modifications (see Simmons et al., *Science*, 276, 276 (1997)).

In addition, the amino acid sequence of TLR4 can be modified so as to result in a variant TLR4. The modification includes the substitution of at least one amino acid residue in the polypeptide for another amino acid residue, including substitutions which utilize the D rather than L form, as well as other well known amino acid analogs, e.g., unnatural amino acids such as  $\alpha$ ,  $\alpha$ -disubstituted amino acids, N-alkyl amino acids, lactic acid, and the like. These analogs include phosphoserine, phosphothreonine, phosphotyrosine, hydroxyproline, gamma-carboxyglutamate; hippuric acid, octahydroindole-2-carboxylic acid, staling, 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid, penicillamine, ornithine, citrulline,  $\alpha$ -methyl-alanine, para-benzoyl-phenylalanine, phenylglycine, propargylglycine, sarcosine,  $\epsilon$ -N,N,N-trimethyllysine,  $\epsilon$ -N-acetyllysine, acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine,  $\omega$ -N-methylarginine, and other similar amino acids and imino acids and tert-butylglycine.

Conservative amino acid substitutions include aspartic-glutamic as acidic in amino acids; lysine/arginine/histidine as basic amino acids; leucine/isoleucine, methionine/valine, alanine/valine as hydrophobic amino acids; serine/glycine/

alanine/threonine as hydrophilic amino acids. Conservative amino acid substitution also includes groupings based on side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. For example, it is reasonable to expect that replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the properties of the resulting variant polypeptide. Whether an amino acid change results in a functional polypeptide can readily be determined by assaying the activity of the polypeptide variant. Such assays are described herein.

Conservative substitutions are shown in FIG. 8 under the heading of exemplary substitutions. More preferred substitutions are under the heading of preferred substitutions. After the substitutions are introduced, the variants are screened for biological activity.

Amino acid substitutions falling within the scope of the invention, are, in general, accomplished by selecting substitutions that do not differ significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic; cys, ser, thr;
- (3) acidic: asp, glu;
- (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic; trp, tyr, phe.

The invention also envisions polypeptide variants with non-conservative substitutions. Non-conservative substitutions entail exchanging a member of one of the classes described above for another.

Acid addition salts of the polypeptide or variant polypeptide or of amino residues of the polypeptide or variant polypeptide may be prepared by contacting the polypeptide or amine with one or more equivalents of the desired inorganic or organic acid, such as, for example, hydrochloric acid. Esters of carboxyl groups of the polypeptides may also be prepared by any of the usual methods known in the art.

#### E. Methods of the Invention

The invention provides a method to diagnose individuals who are at a greater risk of deleterious consequences due to bacterial infection, e.g., the individuals may be more susceptible to infection by gram-negative bacteria, e.g., local gram-negative infection, more susceptible to sepsis induced by gram-negative bacteria, more susceptible to chronic airway disease, more susceptible to asthma, more susceptible to gall bladder disease, more susceptible to pyelonephritis, more susceptible to pneumonia, more susceptible to bronchitis, more susceptible to chronic obstructive pulmonary disease, more susceptible to arthritis, at higher risk for severe cystic fibrosis, and more susceptible to



local and systemic inflammatory conditions such as systemic inflammatory response syndrome (SIRS), and acute respiratory distress syndrome (ARDS). The invention is also useful in the development of drugs that target the TLR4 gene product, e.g., increase or decrease the function of TLR4, especially the extracellular domain. These agents may thus be useful to prevent or ameliorate infection by gram-negative bacteria, prevent or ameliorate sepsis induced by gram-negative bacteria, prevent or ameliorate LPS-induced chronic airway disease in normal, cystic fibrosis and asthmatic populations, prevent or ameliorate arthritis, and prevent or ameliorate local and systemic inflammatory conditions such as SIRS and ARDS, particularly in individuals at risk for these indications or conditions.

The invention will be further described by the following non-limiting

#### EXAMPLE 1

##### Methods

**Study Subjects.** The study population consisted of 83 healthy adult volunteers (31 men, 52 women) aged 18–50. Exclusion criteria included any history of allergies, tobacco use, cardiac or pulmonary disease. After written informed consent was obtained, all subjects were screened with spirometry, inhalation challenge with histamine, skin testing for common aeroallergens, chest x-ray, and electrocardiogram. All participants had normal screening studies (including histamine  $PC_{20} > 32$  mg/ml), were on no medications (except birth control), and had no significant acute or chronic cardiopulmonary disease or occupational exposures. **Inhalation Challenge Protocol.** All subjects were exposed by inhalation challenge to buffered sterile saline (HBSS) followed by increasing concentrations of LPS. The solutions were delivered via a DeVilbiss 646 nebulizer powered by compressed air at 30 psi (DeVilbiss Co., Somerset, Pa.) and a Rosenthal dosimeter (Laboratory for Applied Immunology, Baltimore, Md.). After the HBSS, subsequent inhalations delivered in increasing doses of LPS according to the following schedule: 0.5  $\mu$ g, 1.0  $\mu$ g, 2.0  $\mu$ g, 3.0  $\mu$ g, 5.0  $\mu$ g, 10  $\mu$ g, and 20  $\mu$ g. Thus, the entire protocol delivered a total of 41.5  $\mu$ g of LPS.

**Incremental LPS inhalation challenge.** The incremental LPS inhalation challenge was performed as follows. The % decline in  $FEV_1/\mu$ g LPS was calculated following administration of the cumulative LPS dose that either resulted in at least a 20% decline in:  $FEV_1$  or the decline in  $FEV_1$  following a cumulative inhaled dose of 41.5  $\mu$ g of LPS. Subjects above the x-axis (solid bars in FIG. 5) are homozygous for the wild type allele (WT/WT); subjects below the x-axis (open bars in FIG. 5) are either heterozygous or homozygous (\*) for the missense Asp299Gly allele. The data is replotted in the inset after the values for the dose-response slope were log normalized. P values are presented for the comparison of the % decline in  $FEV_1/\mu$ g LPS between subjects with the WT/WT genotype (N=73) and those with at least one Asp299Gly allele (N=10) using absolute values (P=0.037) and log normalized values (p=0.026). Since the distribution of the dose-response slope (% decline  $FEV_1$ /cumulative dose of inhaled LPS) was highly skewed, the two-sample Monte-Carlo permutation test based on 10,000 permutations was used to calculate P values (Fisher et al., 1993). To assess the allelic frequency of TLR4 sequence variants, a well-characterized Iowa population (Lidral et al., 1998) and the Centre d'Etude du Polymorphisme Humain (CEPH) population (NIH-CEPIT, 1992) were screened for specific sequence variants identified in the 83 study subjects.

**Endotoxin.** Solutions of endotoxin for inhalation were prepared according to a standard protocol using lyophilized

*Escherichia coli* (serotype 0111:B4, Sigma Chemical Co., St. Louis, Mo.) LPS. These solutions of LPS were resuspended in sterile Hank's balanced salt solution (without calcium or magnesium) at a pH of 7.0 and filter sterilized.

All solutions used for inhalation were tested for sterility (bacteria and fungi) and LPS content (*Limulus ameobocyte* lysate assay, QCL-1000; Whittaker Bioproducts, Walkersville, Md.) prior to separation into individual aliquots. These aliquots were stored immediately after preparation at  $-70^\circ$  C. until used.

**Physiologic Measurements.** A Spirotech (Atlanta, Ga.) S600 spirometer was used to assess pulmonary function; spirometry was performed using standards established by the American Thoracic Society. Subjects were positioned upright in a chair and were using noseclips. Baseline spirometry was recorded after inhalation of saline, and then 1, 10, 20, and 30 minutes following inhalation of each dose of LPS, and compared with the post-saline baseline spirometry. If the study subject's  $FEV_1$  was greater than 80% of the baseline measurement at the final assessment (30 minutes post-saline), the inhalation challenge was continued and the next does of LPS was administered. The challenge test was terminated when any of the following criteria had been met: 1) the subject did not wish to continue for any reason; 2) the subject's FEV, decreased 20% or greater from baseline; or 3) a cumulative dose of 41.5  $\mu$ g had been achieved. Of 84 subjects enrolled in the study, 1 subject withdrew prior to completion of the LPS inhalation challenge test, 52 subjects had at least a 20% decline in the FEV, during the LPS inhalation challenge test, and 31 subjects inhaled a cumulative dose of 41.5  $\mu$ g of LPS and did not decrease their  $FEV_1$  by 20%.

**Assignment of Phenotype.** Study subjects were categorized as either "Responsive" or "hypo-responsive" to inhaled LPS. In the course of previous investigations, a large number of study subjects have been exposed to inhaled LPS (Jagiell *et al.*, 1996; Deetz *et al.*, 1997). In general, most healthy non-asthmatic study subjects develop airflow obstruction ( $FEV_1 \leq 80\%$  of the pre-exposure value) when challenged with approximately 40  $\mu$ g of LPS. Based on this and a standard approach to the definition of airway hyperreactivity ( $FEV_1$  decline of 20% from pre-exposure values) (Chai *et al.*, 1975), subjects were categorized as "LPS responsive" if they decreased their  $FEV_1$  by at least 20% at any point during the LPS inhalation challenge, or "hypo-responsive" if they had <20% decline in their  $FEV_1$  after inhaling a cumulative dose of 41.5  $\mu$ g of LPS. **Isolation of Genomic Clone.** A human bacterial artificial chromosomal (SAC) library (Research Genetics; Huntsville, Ala.) was screened with two sets of primers (1F: 5' ATGGGGCATATCAGAGCCTA 3; SEQ ED NO:8, IR: 5' GTCCAATGGGGAAGTTCTCT 3; SEQ ID NO:9, 2F: 5' TCATTGTCCTGCAGAAGGTG 3; SEQ ID NO:10, and 2R: 5' CAGGGCTTTTCTGAGTCGTC3; SEQ ID NO:11) derived from the human TLR4 gene (Genbank Accession Nos. U88880 and U93091). These sets of primers amplified a 160 bp and 140 bp product, respectively. PCR reactions were prepared by combining the following components: 1  $\mu$ l of PCR 10 $\times$  buffer (100 mM Tris-HCl, pH 8.3, 500 mM KCl), 200  $\mu$ M each of dCTP, dGTP, dATP, and dTTP, 0.25  $\mu$ M of each primer, 0.2 U of AmpliTaq DNA polymerase (Perkin Elmer; Norwalk, Conn.) and 1  $\mu$ l of the library sample in a final volume of 10  $\mu$ l. Thermal cycling was performed with an initial denaturation at 94 $^\circ$  C. for 3 minutes followed by 35 cycles comprising 94 $^\circ$  C., 55 $^\circ$  C., and 72 $^\circ$  C. steps of 30 seconds each and a final extension of 72 $^\circ$  C. for 5 minutes. PCR products were separated by electrophoresis on 2%

agarose gels, stained with ethidium bromide and visualized under UV light.

Mutation Detection. Genomic DNA was isolated from whole blood obtained from the study subjects using a rapid salt isolation procedure (Laitinen et al., 1994). Overlapping primer sets were designed across the coding sequence such that products did not exceed 250 bp (Table 1). Primers were derived from flanking intronic sequences to include all splice sites. PCR reactions were prepared as described above except that 10–20 ng of genomic DNA was used at template. Amplification products were separated on non-denaturing, fan-cooled gels containing 5% acrylamide/bis (19:1), 0.5× TBE, and 2.5% glycerol for 3 hours at 20 W. A subset of

PCR products were also run on MDE gels. The gels were subjected to silver staining and aberrant bands extracted from the gel, reamplified, and sequenced in both directions. To verify the sequence of the aberrant band, the same primers were used to amplify and sequence genomic DNA from each subject. At least one individual without the aberrant band was also sequenced for comparison. Amplification products derived from the extracted DNA were purified using spin columns (Qiagen, Santa Clarita, Calif.) and DNA concentration determined by spectrophotometry. The DNA sequence was determined with a Model 377 automated DNA sequencer (Perkin Elmer; Norwalk, Conn.).

TABLE 1

Primers for amplification of TLR4 coding region.					
Exon	5' NT <sup>a</sup>	FORWARD PRIMER (5'-3')	5' NT <sup>a</sup>	REVERSE PRIMER (5'-3')	SIZE (bp)
1	24	CTGCTCGGTCAAACGGTGAAT <sup>1</sup>	+33	AGTCAGCTCCTCTGAACITTC <sup>2</sup>	206
2	-106	CAGCAAGCAGCATATTTGGAT <sup>3,b</sup>	+18	CGTGCTCAGCAITCTAACCT <sup>4,b</sup>	244
3	-53	GAGTTGGGAGACCATGTCAGT <sup>5</sup>	+41	GAACACCTCACCTTGTGCAG <sup>6</sup>	262
4	-52	GGTTCATATTCAGCAGAAAT <sup>7</sup>	483	CTTGATAGTCCAGAAAAGGCT <sup>8</sup>	172
4	496	GGTGGCTGTGGAGACAAATC <sup>9</sup>	691	CCGCAAGTCTGTGCAATAAA <sup>10</sup>	195
4	639	ACTTGGACCTTCCAGCAAC <sup>11</sup>	798	GTCAGCTTATGAAGCCTAATTTCT <sup>12</sup>	159
4	751	CTTTATCCAACCAGGTGCA <sup>13</sup>	952	CAAATGACACAGGCCCTCTAGA <sup>14</sup>	201
4	882	TGGGAGAATTTAGAAATGAAGGA <sup>15</sup>	1080	AAAGTCTTTTACCCTTTCAATAGTCA <sup>16</sup>	198
4	1032	TTTCTTCATTTCCCTGGTGA <sup>17</sup>	1161	AGAGATTTGAGTTTCAATGTGGG <sup>18</sup>	129
4	1129	TGGACAGTTTCCACATGTA <sup>19</sup>	1309	CTTTAGGCTGGTTGTCCCAA <sup>20</sup>	180
4	1262	TTCAAAGGTTGCTGTTCTCAA <sup>21</sup>	1426	TGAAAACCTCACTCAITTTGTTTCAA <sup>22</sup>	164
4	1349	TCAAACCTCTTGGGCTTAGAACA <sup>23</sup>	1526	CTTCGAGACTGGACAAGCCA <sup>24</sup>	177
4	1480	CAGAGTTGCTTTCATGCGCA <sup>25</sup>	1614	GAGAGGTCCAGGAAGGTCAA <sup>26</sup>	134
4	1551	TCCAGGAAAACITCCITCCA <sup>27</sup>	1746	ACCTGGAGGGAGTTCAGACA <sup>28</sup>	195
4	1702	TTCATGGATACGTTTCC <sup>29</sup>	1905	AAGAGCTGCCTCTGGTCTT <sup>30</sup>	203
4	1863	ACCAGAGTTTCTGCAATGG <sup>31</sup>	2032	TACAAGCACACTGAGGACCG <sup>32</sup>	169
4	1956	TGCCGTGCTGAGTTTGAAT <sup>33</sup>	2100	TATATGCAGCCAGCAAGAAG <sup>34</sup>	144
4	2013	CGGTCTCAGTGTGCTTGTAA <sup>35</sup>	2208	GGAGGCACCCCTTCTCTAA <sup>36</sup>	195
4	2149	CCAGGATGAGGACTGGGTAA <sup>37</sup>	2338	GCGGCTCTGGATGAAGTGTCT <sup>38</sup>	189
4	2290	AAGCCGAAAGGTGATTGTTG <sup>39</sup>	2442	CTGAGCAGGTCTTCTCCAC <sup>40</sup>	152
4	2398	TATCATCTTCAITGTCTGCAGA <sup>41</sup>	2617	AGATGTTGCTTCTGCCAAT <sup>42</sup>	219
4	2406	TCATTGCTCTGCAGAAAGGTG <sup>43</sup>	2548	CAGGGCTTTTCTGAGTCGTC <sup>44</sup>	142
4	2529	GACGACTCAGAAAAGCCCTG <sup>45</sup>	2683	TGAACAAGTGTGGACCCAG <sup>46</sup>	154
4	2597	AATTGGCAGGAAGCAACATC <sup>47</sup>	2772	GATTAGCAGCCCTGCATATCT <sup>48</sup>	175

<sup>1</sup>relative to published cDNA sequence of Medzhitov et al. (1997), Genbank accession #U93091

<sup>b</sup>relative to published cDNA sequence of Rock et al. (1997), Genbank Accession #U88880, since exon 2 is absent in #U93091. A “-” indicates primer is within intron on the 5' side of amplified exon; a “+” indicates primer is on the 3' side.

- <sup>1</sup>SEQ ID NO:12
- <sup>2</sup>SEQ ID NO:36
- <sup>3</sup>SEQ ID NO:13
- <sup>4</sup>SEQ ID NO:37
- <sup>5</sup>SEQ ID NO:14
- <sup>6</sup>SEQ ID NO:38
- <sup>7</sup>SEQ ID NO:15
- <sup>8</sup>SEQ ID NO:39
- <sup>9</sup>SEQ ID NO:16
- <sup>10</sup>SEQ ID NO:40
- <sup>11</sup>SEQ ID NO:17
- <sup>12</sup>SEQ ID NO:41
- <sup>13</sup>SEQ ID NO:18
- <sup>14</sup>SEQ ID NO:42
- <sup>15</sup>SEQ ID NO:19
- <sup>16</sup>SEQ ID NO:43
- <sup>17</sup>SEQ ID NO:20
- <sup>18</sup>SEQ ID NO:44
- <sup>19</sup>SEQ ID NO:21
- <sup>20</sup>SEQ ID NO:45
- <sup>21</sup>SEQ ID NO:22
- <sup>22</sup>SEQ ID NO:46
- <sup>23</sup>SEQ ID NO:23
- <sup>24</sup>SEQ ID NO:47
- <sup>25</sup>SEQ ID NO:24
- <sup>26</sup>SEQ ID NO:48
- <sup>27</sup>SEQ ID NO:25
- <sup>28</sup>SEQ ID NO:49
- <sup>29</sup>SEQ ID NO:26
- <sup>30</sup>SEQ ID NO:50

TABLE 1-continued

<u>Primers for amplification of TLR4 coding region.</u>				
Exon	5' NT <sup>a</sup>	FORWARD PRIMER (5'-3')	5' NT <sup>a</sup> REVERSE PRIMER (5'-3')	SIZE (bp)
		<sup>31</sup> SEQ ID NO:27		
		<sup>32</sup> SEQ ID NO:51		
		<sup>33</sup> SEQ ID NO:28		
		<sup>34</sup> SEQ ID NO:52		
		<sup>35</sup> SEQ ID NO:29		
		<sup>36</sup> SEQ ID NO:53		
		<sup>37</sup> SEQ ID NO:30		
		<sup>38</sup> SEQ ID NO:54		
		<sup>39</sup> SEQ ID NO:31		
		<sup>40</sup> SEQ ID NO:55		
		<sup>41</sup> SEQ ID NO:32		
		<sup>42</sup> SEQ ID NO:56		
		<sup>43</sup> SEQ ID NO:33		
		<sup>44</sup> SEQ ID NO:57		
		<sup>45</sup> SEQ ID NO:34		
		<sup>46</sup> SEQ ID NO:58		
		<sup>47</sup> SEQ ID NO:35		
		<sup>48</sup> SEQ ID NO:59		

Multi-tissue cDNA Expression Screen. Human adult (Clontech #K1420-1; Palo Alto, Calif.) and fetal (Clontech #K1425-1; Palo Alto, Calif.) multi-tissue cDNA panels were screened by PCR using primers derived from exon 1 (forward;

5' GCTCACAGAAGCAGTGAGGA 3'; SEQ ID NO:60) and exon 4 (reverse; 5' TAGGCTCTGATATGCCCAI3'; SEQ ID NO:61) of the human TLR4 gene. These PCR experiments were performed in 10  $\mu$ l reactions composed of 0.025 U/ $\mu$ l of DNA polymerase (BioXACT; BioLine; Reno, Nev.), 1.0  $\mu$ M of each primer, 200  $\mu$ M of each dNTP, 1  $\mu$ l of 10 $\times$  buffer supplied by the manufacturer, and 1  $\mu$ l of the cDNA sample. PCR conditions were: 95 $^{\circ}$  C. for 2 minutes; cycles of 0.5 minutes at 10 94 $^{\circ}$  C., 0.5 minutes at 55 $^{\circ}$  C., and 1 minute at 68 $^{\circ}$  C.; followed by a final extension step for 10 minutes at 68 $^{\circ}$  C. The amplified products were separated on a 2% agarose gel, stained with ethidium bromide, and visualized under UV light.

Statistical Analysis. The statistical analysis was designed to determine whether specific mutations in the TLR4 gene were associated with the airway hyporesponsiveness to inhaled LPS. A one-tailed test of statistical significance was employed (Fleiss, 1986). In a 2 $\times$ 2 analysis, a Fisher's one-tailed exact test was used to determine whether specific mutations of the TLR4 gene occurred more frequently in study subjects who were considered LPS hyporesponsive compared to those with a normal airway response to inhaled LPS. In addition, because of the nonparametric distribution of dose-response slope (percent decline FEV<sub>1</sub>/cumulative dose of inhaled LPS), this outcome log was transformed and the Student's one-tailed T test (assuming unequal variances) was used to determine whether the dose-response slope was significantly less in subjects with a specific mutation of TLR4 compared to subjects with the common TLR4 allele.

Biossays. Cells were maintained in F12 media supplemented with 10% fetal calf serum (Gibco, Rockville, Md.), 2 mM L-glutamine, and 10,000 units penicillin/streptomycin, with 1  $\mu$ g/ml of G418 as selective antibiotic. Cells were transfected with a mixture of 4  $\mu$ g of DNA and 10  $\mu$ l of Superfect (Qiagen, Valencia, Calif.) for a 35 mm<sup>2</sup> dish. The DNA mix consisted of 2  $\mu$ g of DNA and 10  $\mu$ g NF $\kappa$ B reporter plasmid encoding for the luciferase gene (Clontech, Palo Alto, Calif.) and 1  $\mu$ g of each TLR4 (Medzhitov et al., 1997; Genbank #U93091) expression plasmid (WT or Asp299Gly). If only one expression plasmid was used, empty vector pcDNA3.1<sup>+</sup> was added to keep the

DNA concentration constant. Twenty-four hours later the cells were stimulated with 100 ng/ml of LPS for 6 hours. Total luciferase activity was measured using a commercially available method (Tropix, Bedford, Mass.). Briefly, after rising with PBS, cells were removed from filters by incubation with 120  $\mu$ l lysis buffer (25 mM Tris-phosphate, pH 7.8; 2 mM DTT; 2 mM 1,2-diaminocyclohexane-N,N,N',N'-tetraacetic acid; 10% glycerol; and 1% Triton X-100) for 15 minutes. Light emission was quantified in a luminometer (Analytical Luminescence Laboratory, San Diego, Calif.).

Airway epithelial cells were obtained from trachea and bronchi of lungs removed for organ donation. Cell were genotyped for TLR4 and isolated by enzyme digestion as previously described (Zabner et al., 1996). Freshly isolated cells were seeded at a density of 5 $\times$ 10<sup>5</sup> cells/cm<sup>2</sup> onto collagen-coated, 0.6 cm<sup>2</sup> diameter millicell polycarbonate filters (Millipore Corp., Bedford, Mass.). The cells were maintained at 37 $^{\circ}$  C. in a humidified atmosphere of 5% CO<sub>2</sub> and air. Twenty-four hours after plating, the mucosal media was removed and the cells were allowed to grow at the air-liquid interface. The culture media consisted of a 1:1 mix of DMEM/Ham's F12, 5% Ultraser G (Biosera SA, Cedex, France), 100 U/ml penicillin, 100  $\mu$ g/ml streptomycin, 1% nonessential amino acids, and 0.12 U/mi insulin. Epithelia were tested for transepithelial resistance, and for morphology by scanning electron microscopy. Fourteen days after seeding, the basal release of IL-1 $\alpha$  was measured in WT/WT (12 specimens from 4 individuals) and WT/Asp299Gly (24 specimens from 4 individuals) epithelia by collecting the basolateral conditioned media after 24 hours (FIG. 6b). The epithelia were then exposed to: 100 ng/ml of LPS on the apical side for 6 hours, and the basolateral media was collected after 24 hours. IL-1 $\alpha$  was measured using a commercially available ELISA (R&D; Minneapolis, Minn.).

To rescue the LPS hyporesponsive phenotype, heterozygote (WT/Asp299Gly) airway epithelia (FIG. 6c) or homozygote (Asp299Gly/Asp299Gly) alveolar macrophages (FIG. 6d) were transfected with a recombinant adenovirus vector expressing TLR4 (Rock et al. 1998; Genbank #U88880) that was prepared as described previously (Dandson et al., 1994) by the University of Iowa Gene Transfer Vector Core at titers of about 10<sup>10</sup> infectious units (I.U.)/ml. Briefly TLR4 plasmid was blunt ended and cloned into the shuttle vector pAd5/CMV $\kappa$ -NpA using the EcoRV site. Fourteen days after seeding of the airway epithelia (20 specimens from 4 individuals), 50 MOI of the recombinant

viruses (Ad/TLR4 and Ad/eGFP in phosphate buffered saline) were added to the basolateral surface of the epithelia for 30 minutes (Walters et al., 1999). After infection, the epithelia were incubated at 37° C. for an additional 48 hours before the LPS stimulation assay. To assay for basal LPS response, the media was changed with fresh 500  $\mu$ l of Ultrosor G, and collected after 24 hours to measure the basal IL-1 $\alpha$  secretion to the basolateral side. After collecting the basal specimen, the epithelia were exposed to 100 ng/ml of LPS on the apical side for 6 hours, and the media was collected after 24 hours. To assay for gene transfer efficiency, the epithelia was associated with 0.05% trypsin and 0.53 mM EDTA. Fluorescence from 50,000 individual cells was analyzed using fluorescence-activated cell analysis (FACSscan, Lysys II software, Becton Dickinson, San Jose, Calif.). The percentage of GFP positive cells ranged between 52% and 76%. Human alveolar macrophages were collected by BAL from a homozygote (Asp299Gly/Asp299Gly) study subject as previously described (Deetz et al., 1967). Macrophages were seeded onto a 96 well plate at a density of 10<sup>5</sup> cells per well. The cells were infected after 4 hours with Ad/TLR4 in a CaPi coprecipitate (Iasbinder et al., 1998) at an MOI of 50, and a Ca<sup>++</sup> concentration of 16.8 mM. Sixteen hours after infection, the cells were exposed to LPS in 1% serum for 6 hours, and the media was collected. TNF- $\alpha$  was measured using a commercially available ELISA (R&D; Minneapolis, Minn.).

### Results

**Genomic Structure of the TLR4 Gene.** To determine the genomic structure of the TLR4 gene, a bacterial artificial chromosome (BAC) library was screened by PCR with primers derived from the 5' and 3' ends of the cDNA sequence. Human BAC clone 439F3 was identified with both sets of primers and sequenced to identify exon/intro splice sites using the two published cDNA sequences (Medzhitov et al., 1997; Rock et al., 1998). The TLR4 cDNA published by Medzhitov et al. (1997) (Genbank Accession No. U93091) was missing a 120 bp sequence beginning at nucleotide 136 of the other published cDNA (Rock et al., 1998) (Genbank Accession No. U88880). Assuming this missing sequence represented an alternatively spliced exon, DNA sequencing primers were designed to amplify across the predicted splice junctions. When the genomic sequence (FIG. 9) was compared to the cDNA sequences, the exon/intron junctions were revealed (FIG. 1). The human TLR4 gene is organized into 4 exons that span about 11 kb of genomic DNA. As predicted, the 120 bp sequence missing in the cDNA from Medzhitov et al. (1997) corresponds to exon 2.

To determine whether other exons may be revealed by additional splice forms, a panel of cDNAs from adult (FIG. 2a) and fetal (FIG. 2b) tissues were examined with PCR primers designed to amplify all nucleotides between exons 1 and 4. In all adult and fetal tissues, three products were amplified (453, 333, and 167 bp), although their relative amounts varied. In addition to the 3' end of exon 1 and the 5' end of exon 4, the 453 bp product contained both exons 2 and 3, the 333 bp product was missing exon 2, and the 167 bp product was missing both exons 2 and 3 (FIG. 2c). The 453 and 333 bp products are identical to the published cDNA sequences (Medzhitov et al., 1997; Rock et al., 1998), and confirm that no other exons are present for the human TLR4 gene. The 167 bp product depicts alternative splicing of exons 1 and 4, and represents a novel TLR4 product. The nucleotide position of alleles are relative to the TLR4 cDNA sequence published by Medzhitov et al. (1997).

**Mutation Analysis.** SSCV was employed to detect sequence variants across the entire coding region of TLR4 gene in the 83 unrelated probands who completed the incremental LPS inhalation challenge test. When band shifts were detected on SSCV analysis, the bands were sequenced to identify and confirm the sequence variants. The SSCV and sequence analysis were performed blinded to the LPS response phenotype of the study subjects. A band variant was detected by SSCV in 10 (12%) of the 83 subjects, and direct sequencing detected an A to G substitution at nucleotide 896 of the published TLR4 cDNA (FIG. 3a) (Genbank Accession No. U88880). To confirm these findings, the 83 unrelated probands were sequenced in the forward and reverse directions with primers designed to amplify the 896 nucleotide; the same 10 individuals were found to have the A896G substitution and the remaining individuals were confirmed to have the common TLR4 allele. Importantly, one of the 10 individuals with the A896G substitution was homozygous for this mutation and the remaining 9 had a single mutant allele. The allelic frequency of the A896G substitution was 6.6% in the study population, 7.9% in a normal control population from Iowa (Lidral et al., 1998), and 3.3% in the parental chromosomes of the CEPH population (NIH-CEPH, 1992).

The A896G substitution results in replacement of a conserved aspartic acid (A) residue with glycine (G) at amino acid 299 (FIG. 4). This missense mutation (Asp299Gly) is in the fourth exon of TLR4 and is present in the extracellular domain of this receptor. The region surrounding amino acid 299 appears to be in an alpha helical conformation (Gibrat et al., 1987). Replacement of the conserved aspartic acid with glycine at position 299 causes disruption of the alpha helical protein structure resulting in the formation of an extended beta strand (Gibrat et al., 1987).

Two other SSCV variants were identified in a single proband; a T to C change at nucleotide 479 (FIG. 3b) and a deletion of a thymine nucleotide at position -11 in the third intron. The T479C variant did not alter the amino acid composition and is therefore considered a silent mutation. The T-11 variant did not alter the acceptor splice site, so the significance of this deletion is unknown. The subject with these two sequence variants was responsive to inhaled LPS.

An additional missense mutation was identified within exon 4 of the TLR4 gene. This mutation results in the replacement of a threonine with an isoleucine residue at amino acid 399, which is on the 3' side of the previously identified Asp299Gly mutation. Both mutations are present within the extracellular domain of the TLR4 protein. When the genotypes were compared with the phenotypes associated with endotoxin responsiveness, one individual who carried the Asp299Gly mutation did not carry the Thr399Ile mutation. Likewise, one individual who had the Thr399Ile mutation did not have the Asp299Gly mutation. Nine of the 83 volunteers carry both mutations. There was a strong correlation between both of the TLR4 mutations and endotoxin hyporesponsiveness.

**Phenotype/Genotype Analysis.** Of the 83 unrelated study subjects who completed the LPS inhalation challenge test, 52 (63%) were responsive to inhaled LPS and 31 (37%) were hyporesponsive to inhaled LPS. When the genotypes of these individuals were examined, the Asp299Gly sequence variant occurred in 3 LPS responsive (5.8%) and 7 LPS hyporesponsive (22.6%) study subjects (C=0.029). Among the subjects with the common TLR4 allele (N=73), the dose-response slope (percent decline FEV<sub>1</sub>/cumulative dose of inhaled LPS) averaged 1.86% decline in FEV<sub>1</sub>/μg inhaled LPS (range 0.01%–19.78%), while the dose-response slope

for the subjects with the Asp299Gly allele (N=10) was significantly less (P=0.037), averaging 0.59% decline in FEV<sub>1</sub>/μg inhaled LPS (range 0.00%–1.59%) (FIG. 5). This group difference in the dose-response slope also exists on the log scale (P=0.026) where log (1+A FEV<sub>1</sub>) was used since one individual has a Δ FEV<sub>1</sub> of 0.0. The subject who was homozygous for the Asp299Gly allele was hyporesponsive to inhaled LPS with a 0.28% decline in FEV<sub>1</sub>/μg of inhaled LPS. This homozygote Asp299Gly subject is one of a monozygote twin pair, her twin sister was subsequently phenotyped and was also found to be hyporesponsive to inhaled LPS with a 0.34% decline in FEV<sub>1</sub>/μg of inhaled LPS.

The biological significance of the Asp299Gly mutation was evaluated in several ways. First, transfection of CHO cells with either the WT or the mutant TLR4 gene demonstrated that the mutant allele does not respond normally to LPS stimulation (FIG. 6a). Second, airway epithelia obtained from heterozygote (WT/Asp299Gly) individuals do not respond to LPS stimulation (FIG. 6b). Third, the wild-type allele of TLR4 clearly restored LPS responsiveness in either airway epithelial cells (FIG. 6c) or alveolar macrophages (FIG. 6d) obtained from individuals with the TLR4 mutation.

#### Discussion

The results described herein provide the first direct evidence to indicate that a sequence polymorphism in the TLR4 gene is associated with a hyporesponsive LPS phenotype in humans that interrupts LPS signaling. This conclusion is supported by the following findings: 1) unrelated subjects with the Asp299Gly substitution were significantly less responsive to inhaled LPS than those homozygous for the common TLR4 allele; 2) an individual who was homozygous for the Asp299Gly substitution was hyporesponsive to inhaled LPS; 3) a monozygous twin pair, homozygous for the Asp299Gly substitution, demonstrated a very similar response to inhaled LPS; and 4) in vitro studies demonstrate that mutant TLR4 does not respond to LPS stimulation. This conclusion is indirectly supported by the finding in C3H/HeJ mice where a point mutation in intracellular domain of Tlr4 is also associated with LPS hyporesponsiveness (Poltorak et al., 1998; Qureshi et al., 1999). The identified Asp299Gly missense mutation is in the fourth exon of the TLR4 gene and, unlike the C3H/HeJ mutation, is located in the extracellular domain of this receptor. The findings described herein suggest that a specific region in the extracellular domain of TLR4 may play an important role in receptor function and regulation of the innate immune response to LPS in humans.

This discovery may have important ramifications for a broad spectrum of human diseases. First, the Asp299Gly TLR4 substitution is a relatively common mutation, potentially affecting the responsiveness of a substantial portion of the population to LPS. The allelic frequency of the Asp299Gly TLR4 substitution in the three populations screened was between 3.3% and 7.9%, and homozygous individuals were identified in each of the populations. Second, the results described herein provide further support for the role of TLR4 in LPS signaling. A fundamental understanding of LPS signaling will undoubtedly alter approaches to gram-negative sepsis, as well as other diseases thought to be mediated by endotoxin, such as the systemic inflammatory response syndrome (Wang et al., 1995), acute respiratory distress syndrome (Brighan et al., 1986), and asthma or other forms of airway disease caused (Rylander et al., 1989; Schwartz et al., 1995) or exacerbated (Schwartz et

al., 1995; Michel et al., 1996) by endotoxin. Identification of the essential components of LPS signaling also provide new therapeutic targets for endotoxin mediated conditions. Third, the specific Asp299Gly TLR4 substitution may provide a simple screening mechanism to risk stratify a population. Identification of this mutation may lead to a better appreciation of the role of LPS responsiveness in a broad range of acquired and genetic disorders. For example, mutations of the TLR4 gene may explain why a minority of patients with gram-negative sepsis develop ARDS (Hudson et al., 1995) or why patients with cystic fibrosis and the identical CFTR mutation have different courses of disease (Veeze et al., 1994). Finally, it must be acknowledged that normal responsiveness to endotoxin is an important component of innate immunity, and the Asp299Gly TLR4 substitution may prove to be associated with negative clinical outcomes. In fact, the C3H/HeJ mouse is more susceptible to *Salmonella typhimurium* (O'Brien et al., 1980), despite its resistance to LPS (Sultzter et al., 1968). Although individuals with the Asp299Gly TLR4 substitution may be more resistant to localized forms of endotoxin-induced inflammation, these individuals may prove to be more susceptible to a systemic inflammatory response initiated or exacerbated by endotoxin.

The findings described herein demonstrate that a specific region in the extracellular domain of TLR4 plays an important role in receptor function and regulation of the innate immune response to LPS in humans. The sequence variants reported thus far for mammalian, i.e., murine, TLR4 are located in the cytoplasmic domain (Poltorak et al., 1998; Qureshi et al., 1999). While it is logical to hypothesize that mutations in the cytoplasmic domain of TLR4 disrupt the signaling pathway leading to activation of NF-κB and AP-1 (Medzhitov et al., 1998), the potential mechanisms that are altered by mutations in extracellular domain of TLR4 are less obvious.

TLR4 is a transmembrane protein and it is therefore not surprising to find a putative signal peptide at the N-terminus, presumably responsible for proper trafficking to the cell membrane (Medzhitov et al., 1997). This finding raises the possibility that sequence variants in the extracellular domain of TLR4 can disrupt trafficking of this receptor to the cell membrane and enhance proteolysis. There are several examples in the literature which show that the presence of a single point mutation at a conserved amino acid can disrupt protein folding and specifically affect protein trafficking (Jackson et al., 1998; DeFranco et al., 1998). Mutations of this kind could give rise to a range of phenotypes from almost normal to completely unresponsive, depending on the severity of the trafficking defect. Another possible mechanism that may explain the association between a mutation in the extracellular domain of TLR4 and LPS responsiveness is impairment of ligand binding to the extracellular domain. The extracellular domains of the toll proteins are clearly involved in the cellular response to LPS (Medzhitov et al., 1997; Yang et al., 1998). Yet, so far no convincing evidence has been found that the toll proteins are directly interacting with LPS (Wright, 1999). The discovery of an association between a mutation in the extracellular domain of TLR4 and a discernable LPS phenotype in humans should aid in clarifying whether the extracellular domain of this receptor is important for proper membrane localization of TLR4 and if LPS directly interacts with TLR4. A final possibility is that the missense mutation of TLR4 affects its interaction with either an extracellular ligand or an intracellular protein (Wright, 1999). The extracellular domain of TLR4, and specifically the Asp299Gly

amino acid change may provide a key therapeutic target to modulate LPS signaling.

TLR4 may be one of several factors that may regulate the airway response to inhaled LPS. Among the subjects with the Asp299Gly substitution, 7 were hyporesponsive to LPS and 3 developed airflow obstruction during the LPS inhalation challenge test. None of the subjects with this mutation were in the most sensitive quartile of the LPS responders. Although asthmatic patients were included because of their increased airway responsiveness to inhaled LPS (Michel et al., 1989), it remains possible that the 3 subjects with the Asp299Gly substitution who were responsive to inhaled LPS had some type of airway inflammation (e.g., early viral illness) that enhanced their response to inhaled LPS. Moreover, since 22.6% of the study subjects who were hyporesponsive to LPS had at least one copy of the Asp299Gly TLR4 allele, other genes (or possibly acquired conditions) may prove to play a role in modulating the biological response to LPS. For instance, TNF- $\alpha$  is one of the primary cytokines that mediates the toxic effects of LPS (Beutler et al., 1985). A polymorphism at -308 in the TNF- $\alpha$  promoter region results in higher constitutive and inducible levels of TNF- $\alpha$  (Wilson et al., 1997), and this polymorphism has been shown to result in a worse outcome in children with either meningococcal disease (Nadel et al., 1996) or cerebral malaria (McGuire et al., 1994). Likewise, allelic variants of TLR4 receptors and their ligands appear to delay the progression of disease in patients with HIV infection (Mummidi et al., 1995). Thus, TLR4 appears to represent only one of a number of genetic variants that may modulate the pathophysiologic response to LPS.

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All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification, this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details herein may be varied considerably without departing from the basic principles of the invention.

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What is claimed is:

1. A method of identifying a human at risk of, or having, an indication associated with altered innate immunity, comprising:
  - a) contacting an amount of a nucleic acid sample obtained from a human physiological sample with an amount of at least one Toll-like receptor-4 (TLR4)-specific oligo-

- nucleotide under conditions effective to amplify TLR4 DNA having SEQ ID NO: 62, the complement thereof, or a portion thereof, so as to yield amplified TLR4 DNA which includes DNA encoding amino acid residue 299 of TLR4; and
- b) detecting or determining whether the amplified DNA encodes a TLR4 polypeptide having an amino acid

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substitution at residue 299, thereby identifying whether the human is at risk of or has an indication associated with innate immunity.

2. The method of claim 1 wherein the nucleic acid sample comprises genomic DNA.

3. The method of claim 1 wherein the nucleic acid sample is cDNA.

4. The method of claim 1 wherein the amplified DNA is subjected to electrophoresis in step b).

5. A method to detect a polymorphism in a human Toll-like receptor-4 (TLR4) gene, comprising:

detecting or determining whether amplified TLR4 DNA obtained from a human nucleic acid sample comprises nucleic acid encoding a TLR4 polypeptide having an amino acid substitution at residue 299 of TLR4, wherein the amplified TLR4 DNA is obtained by contacting an amount of the nucleic acid sample with an amount of at least one TLR4-specific oligonucleotide under conditions effective to amplify TLR4 DNA having SEQ ID NO: 62, the complement thereof, or a portion thereof.

6. The method of claim 5, wherein the nucleic acid sample comprises genomic DNA.

7. The method of claim 5, wherein the nucleic acid sample is cDNA.

8. The method of claim 5, wherein the amplified DNA is subjected to electrophoresis.

9. The method of claim 1 or 5, wherein the sample has nucleic acid which encodes an amino acid substitution at residue 299.

10. The method of claim 1 or 5, wherein the substitution at residue 299 is glycine for aspartic acid.

11. The method of claim 1 or 5, further comprising detecting or determining whether the amplified DNA encodes a TLR4 polypeptide having an amino acid substitution at residue 399.

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12. The method of claim 11, wherein the amino acid substitution at residue 399 is isoleucine for threonine.

13. The method of claim 1 or 5, wherein the TLR4-specific oligonucleotide is SEQ ID NO:19 or SEQ ID NO:43, or the complement thereof.

14. The method of claim 1 or 5, wherein the TLR4-specific oligonucleotide is SEQ ID NO:22 or SEQ ID NO:46, or the complement thereof.

15. The method of claim 1 or 5, wherein at least two TLR4 specific oligonucleotides are contacted with the sample.

16. The method of claim 15, wherein the two TLR4 specific oligonucleotides are SEQ ID NO:19 and SEQ ID NO:22, or the complement thereof.

17. The method of claim 15, wherein the two TLR4 specific oligonucleotides are SEQ ID NO:43 and SEQ ID NO:46, or the complement thereof.

18. The method of claim 1 or 5, wherein the TLR4 specific oligonucleotide is SEQ ID NO:12, SEQ ID NO:18, SEQ ID NO:24, SEQ ID NO:30, SEQ ID NO:36, SEQ ID NO:42, SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:13, SEQ ID NO:19, SEQ ID NO:25, SEQ ID NO:31, SEQ ID NO:37, SEQ ID NO:43, SEQ ID NO:49, SEQ ID NO:55, SEQ ID NO:14, SEQ ID NO:20, SEQ ID NO:26, SEQ ID NO:32, SEQ ID NO:38, SEQ ID NO:44, SEQ ID NO:50, SEQ ID NO:56, SEQ ID NO:15, SEQ ID NO:21, SEQ ID NO:27, SEQ ID NO:33, SEQ ID NO:39, SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57, SEQ ID NO: 16, SEQ ID NO:22, SEQ ID NO:28, SEQ ID NO:34, SEQ ID NO:40, SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58, SEQ ID NO:17, SEQ ID NO:23, SEQ ID NO:29, SEQ ID NO:35, SEQ ID NO:41, SEQ ID NO:47, SEQ ID NO:53, SEQ ID NO:59, or the complement thereof.

\* \* \* \* \*

UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION**

PATENT NO. : 6,740,487 B1  
DATED : May 25, 2004  
INVENTOR(S) : Schwartz et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 55,

Line 15, delete "reside 299" and insert -- residue 299 --.

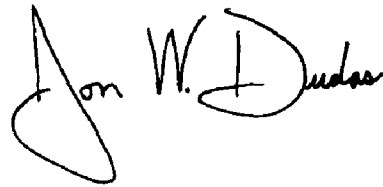
Column 56,

Line 3, delete "TLR4specific" and insert -- TLR4-specific --, therefor.

Line 32, delete "NO59" and insert -- NO:59 --, therefor.

Signed and Sealed this

Sixteenth Day of November, 2004

A handwritten signature in black ink that reads "Jon W. Dudas". The signature is written in a cursive style with a large, looped initial "J".

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JON W. DUDAS  
*Director of the United States Patent and Trademark Office*