

GO:0046982 : protein heterodimerization activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046982>)
GO:0038023 : signaling receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0038023>)
GO:0071723 : lipopeptide binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0071723>)
GO:0035663 : Toll-like receptor 2 binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035663>)

GO - Biological Process

GO:0006955 : immune response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006955>)
GO:0045087 : innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045087>)
GO:0007165 : signal transduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007165>)
GO:0006954 : inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)
GO:0001775 : cell activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0001775>)
GO:0002224 : toll-like receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002224>)
GO:0071727 : cellular response to triacyl bacterial lipopeptide
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071727>)
GO:0042495 : detection of triacyl bacterial lipopeptide
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042495>)
GO:0042116 : macrophage activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0042116>)
GO:0002755 : MyD88-dependent toll-like receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002755>)
GO:0045410 : positive regulation of interleukin-6 biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045410>)
GO:2000484 : positive regulation of interleukin-8 secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000484>)
GO:0034137 : positive regulation of toll-like receptor 2 signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034137>)
GO:0042535 : positive regulation of tumor necrosis factor biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042535>)
GO:0034130 : toll-like receptor 1 signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034130>)
GO:0038123 : toll-like receptor TLR1:TLR2 signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0038123>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0045121 : membrane raft (<https://www.ebi.ac.uk/QuickGO/term/GO:0045121>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0030670 : phagocytic vesicle membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030670>)
GO:0035354 : Toll-like receptor 1-Toll-like receptor 2 protein complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035354>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Unknown~#gephebase-summary-title>)

Aberration Type

Complex Change (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Complex Change~#gephebase-summary-title>)

Molecular Details of the Mutation

Several Complex Haplotypes under positive selection - evidence on Adaptive Introgression from Neanderthal (2 haplotypes) and Denisova (1 haplotype)

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping~#gephebase-summary-title>)

Main Reference

Convergent evolution in European and Rroma populations reveals pressure exerted by plague on Toll-like receptors. (2014) (<https://pubmed.ncbi.nlm.nih.gov/24550294>)

Authors

Laayouni H; Oosting M; Luisi P; Ioana M; Alonso S; RicaÑ±o-Ponce I; Trynka G; Zhernakova A; Plantinga TS; Cheng SC; van der Meer JW; Popp R; Sood A; Thelma BK; Wijmenga C; Joosten LA; Bertranpetit J; Netea MG

Abstract

Recent historical periods in Europe have been characterized by severe epidemic events such as plague, smallpox, or influenza that shaped the immune system of modern populations. This study aims to identify signals of convergent evolution of the immune system, based on the peculiar demographic history in which two populations with different genetic ancestry, Europeans and Rroma (Gypsies), have lived in the same geographic area and have been exposed to similar environments, including infections, during the last millennium. We identified several genes under evolutionary pressure in European/Romanian and Rroma/Gipsy populations, but not in a Northwest Indian population, the geographic origin of the Rroma. Genes in the immune system were highly represented among those under strong evolutionary pressures in Europeans, and infections are likely to have played an important role. For example, Toll-like receptor 1 (TLR1)/TLR6/TLR10 gene cluster showed a strong signal of adaptive selection. Their gene products are functional receptors for *Yersinia pestis*, the agent of plague, as shown by overexpression studies showing induction of proinflammatory cytokines such as TNF, IL-1 β , and IL-6 as one possible infection that may have exerted evolutionary pressures. Immunogenetic analysis showed that TLR1, TLR6, and TLR10 single-nucleotide polymorphisms modulate *Y. pestis*-induced cytokine responses. Other infections may also have played an important role. Thus, reconstruction of evolutionary history of European populations has identified several immune pathways, among them TLR1/TLR6/TLR10, as being shaped by convergent evolution in two human populations with different origins under the same infectious environment.

Additional References

Introgression of Neanderthal- and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. (2016) (<https://pubmed.ncbi.nlm.nih.gov/26748514>)

RELATED GEPHE

2 (IL4, interleukin-4) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^9606^/and+Trait=Immune response/and+groupHaplotypes=true#gephebase-summary-title>)

Related Genes

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@adaptive @Introgression @BalancingSelection multiple alleles (genetic heterogeneity) ; Positive and Balancing Selection