

evolution of host resistance and tolerance

7 March 2022

Definitions/questions

- **resistance**: host's ability to resist or minimize infection
- **tolerance**: host's ability to support parasite infection without losing fitness
- **competence**: host's ability to support *and transmit* parasites (especially vector-borne)
- encounter and compatibility filters: avoiding parasites vs killing vs tolerating them

Mechanisms

- active defense (*plastic* or *facultative* defenses): **recognition systems** and **effectors**
 - recognition systems are the *qualitative* component of host defense: does the host recognize that the parasite (specifically, a parasite **antigen**) is present? These will typically evolve by Red Queen dynamics (i.e., via an inverse matching allele model). In vertebrates: **antibodies**
 - must be **specific** (self/non-self recognition), trigger proportionate response
 - coded by the **major histocompatibility complex** (self/non-self recognition), **somatic recombination**, deletion of host-specific antigens (Borghans, Beltman, and De Boer 2004; Acevedo-Whitehouse and Cunningham 2006; Rauch, Kalbe, and Reusch 2006; Spurgin and Richardson 2010)
 - *effectors*: what does the host do once the parasite is detected?
- passive/always-on defense (*constitutive* defenses)
 - changing cell surface receptors (e.g. CCR5-Δ32 (HIV, Hummel et al. (2005)); matching-allele model
- parasite countermeasures (immune evasion [trypanosomes], immune suppression [measles, anthrax, ...]) (Schmid-Hempel 2009)

Costs and tradeoffs

What are the **costs** of resistance and tolerance? (= Why aren't all hosts tolerant/resistant to all parasites?)

(Klemme, Hyvärinen, and Karvonen 2020)

- cost of maintaining recognition mechanisms

- cost of choosing different habitats
- tradeoffs (RQ-related or ?)

Population-level evolution (eco-evolution)

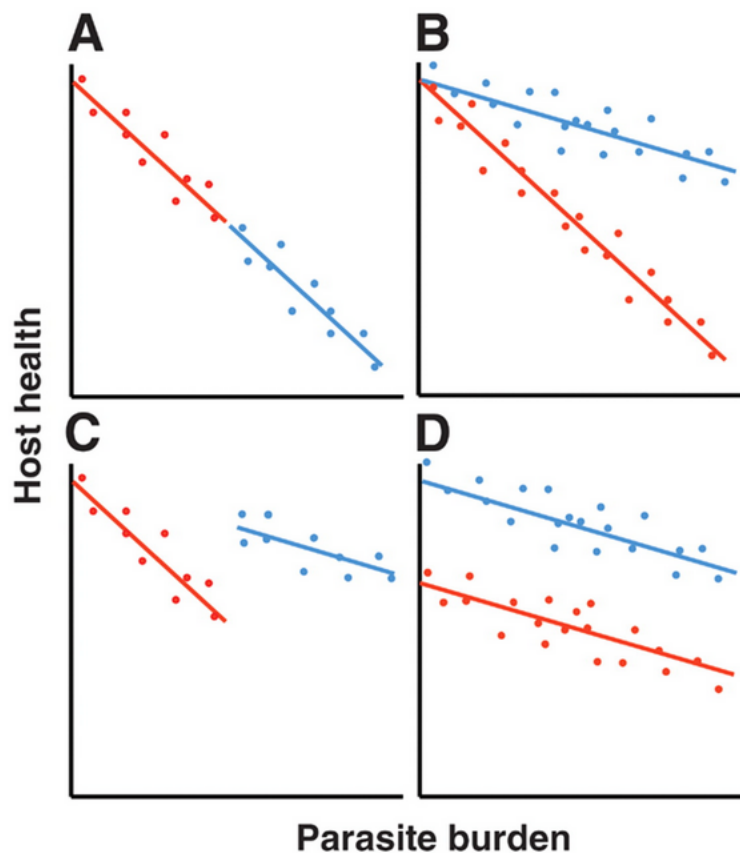
Stahl et al. (1999); Roy and Kirchner (2000)

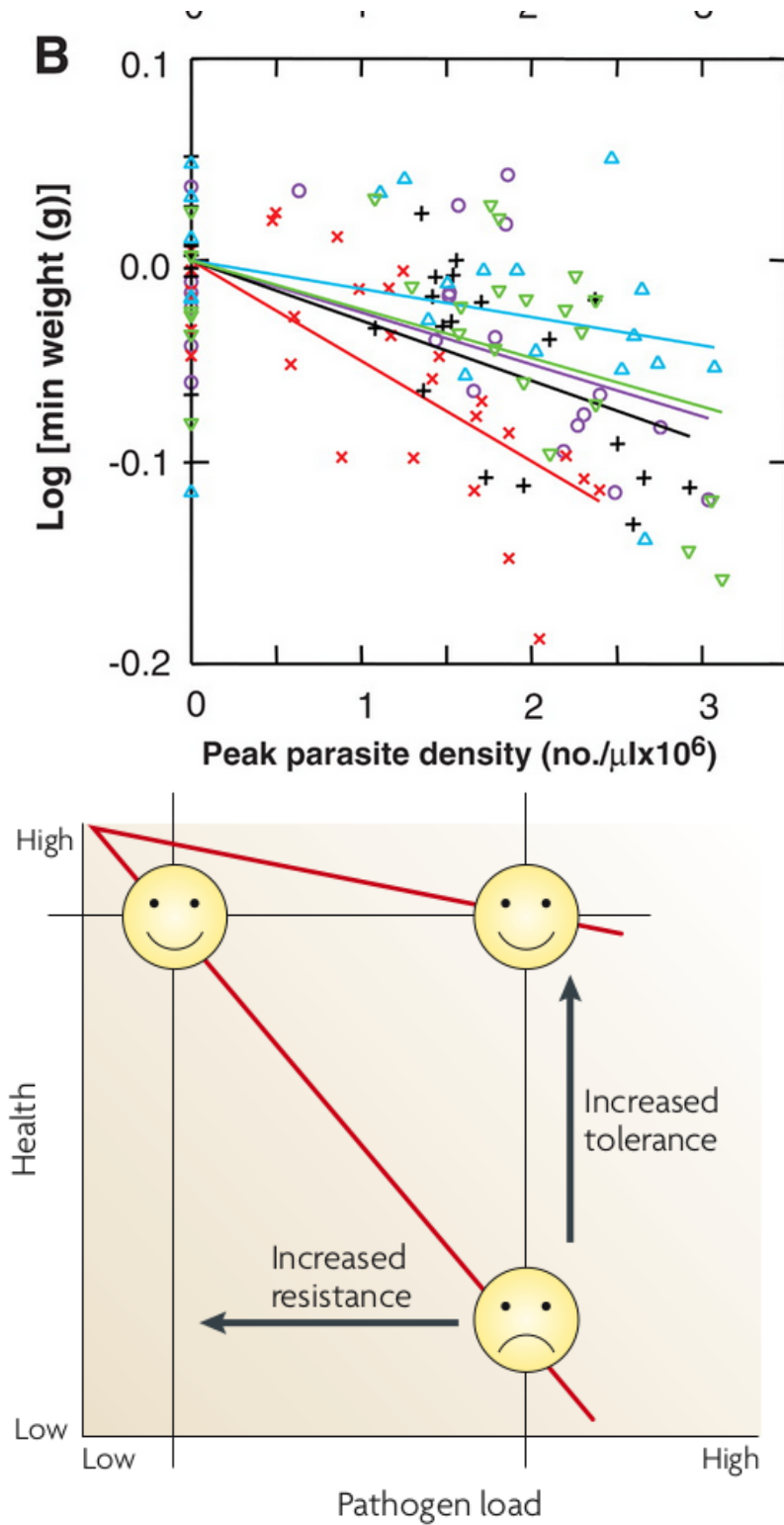
- resistance lowers prevalence - selects against itself; expect *polymorphism*
- tolerance increases prevalence - selects for itself (*apparent competition* with non-tolerant genotypes); expect *fixation*. (Is tolerance evolution-proof? (Schneider and Ayres 2008))

Measuring quantitative resistance/tolerance

- tolerance: loss of fitness **per unit parasite load**
- resistance: level of parasite load

(Raberg, Sim, and Read 2007; Råberg, Graham, and Read 2009)





Disentangling the history/origin of deleterious recessive Mendelian alleles

- Genetic *polymorphisms* are interesting; why haven't they been eliminated or fixed?

hypotheses

- genetic drift (null)
 - historic size of populations? (historical records, population genetics [*coalescents*])
 - strength of selection/maintenance in large populations?
- heterozygote advantage
- frequency-dependent selection (RQ vs. arms race)

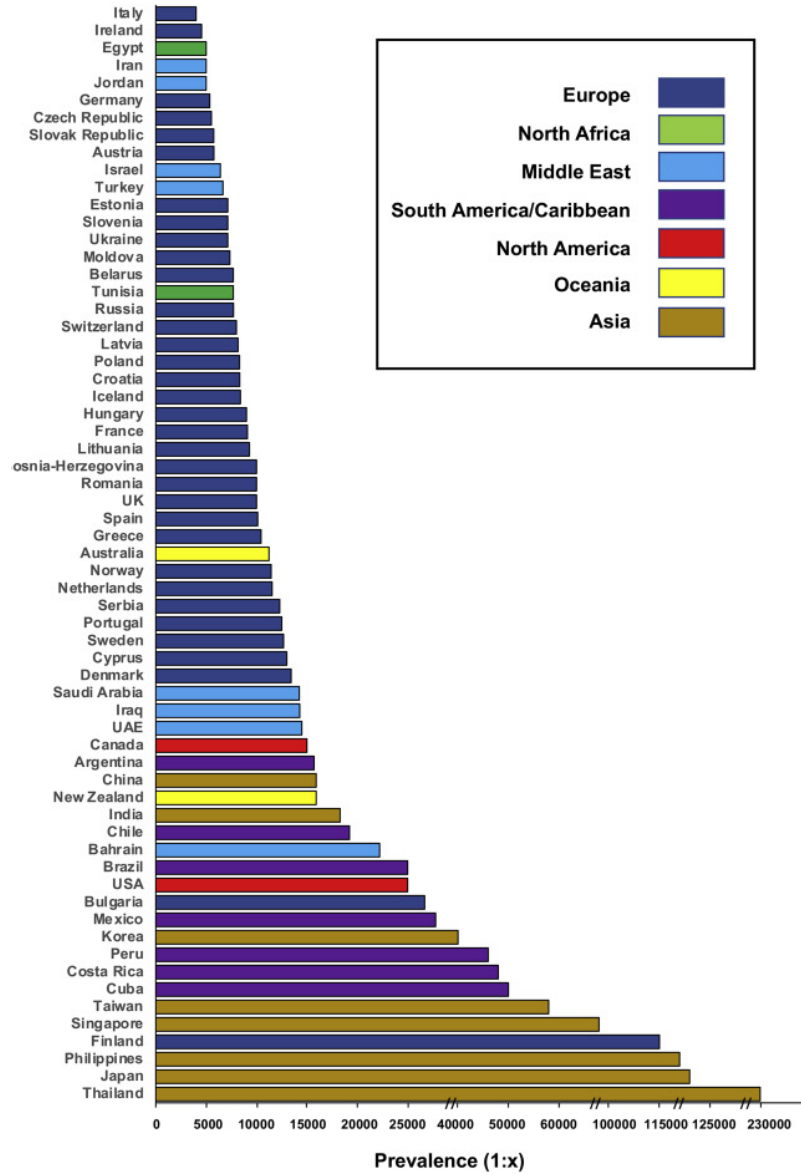
Tay-Sachs disease

- Lethal abnormality in hexosaminidase A (lipid metabolism); early (infant/toddler) death
- Mendelian, recessive lethal ($s = 1$)
- allele frequency $\approx 1/300$ in US population, $1/30$ in Ashkenazi (E. European) Jews: also high in French Canadians, Cajuns, Pennsylvania Dutch ...
- Population-genetic evidence suggests drift
- (Terrible!) speculation about **overdominance** or **heterozygote advantage**: Tb resistance, intelligence: ???
(Spyropoulos 1988; Frost 2012; Frisch et al. 2004)

phenylketonuria (PKU)

- metabolic disorder (phenylalanine)
- many different mutations
- homozygous PKU historically lethal (**selection coefficient** = 1)
- PKU alleles are old

PKU incidence (Hillert et al. 2020)



PKU genetics

why not drift? (Krawczak and Zschocke 2003)

- many different mutations
- present across many populations
- populations without history of being small
 - e.g. Irish gene pool from ≈ 2500 BC
 - population size was 100K-200K
 - current expected frequency 0.6% is twice as high as expected

PKU genetics: conclusion

- calculation from genetic models
- heterozygote advantage probably $\approx 1.5\%$
- hard to measure directly!
- probably due to higher phenylalanine levels in heterozygotes
- phenotypic effects?
 - higher birth weight
 - mycotoxin resistance?
 - starvation resistance?

Sickle-cell

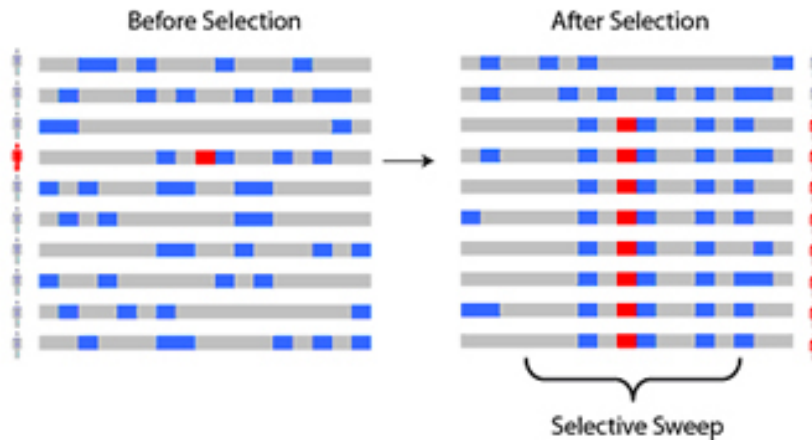
- overdominance
(heterozygote advantage)
- selection for *falciparum* malaria resistance
- geographic patterns;
consistency with malaria distribution
- mechanistic basis for protection
- evidence for positive selection (age??)

Balanced polymorphisms

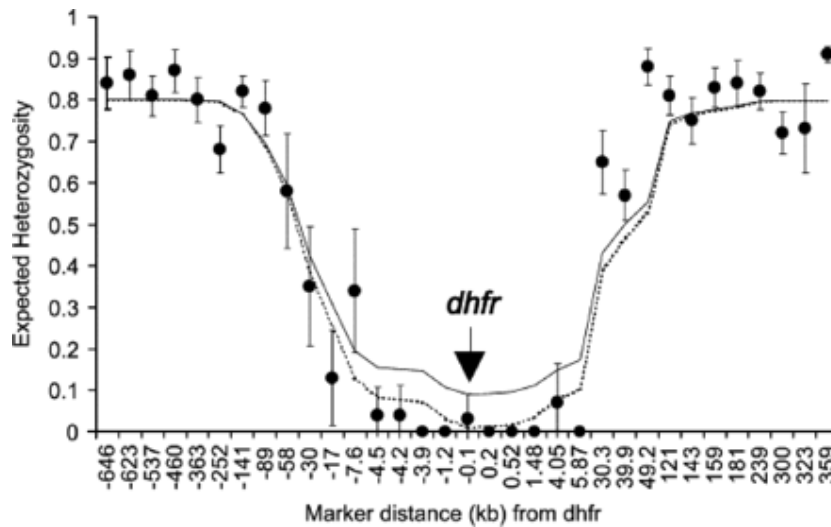
- Sickle-cell (and all cases of overdominance) depends on genetic makeup of the *population*
- chance of mating with a carrier is higher when allele is more common
- easier to do the math at the level of alleles

Selective sweeps

- strong selection on an allele
- individuals carrying that allele have high fitness
- lower (gene-specific) **effective population size**
- neighbouring loci carried along as **haplotypes: hitchhiking**
- haplotypes gradually erode (narrow) by recombination
- e.g. MHC class I variability in chimpanzees decreased $\sim 2-3$ mya (Groot et al. 2002)



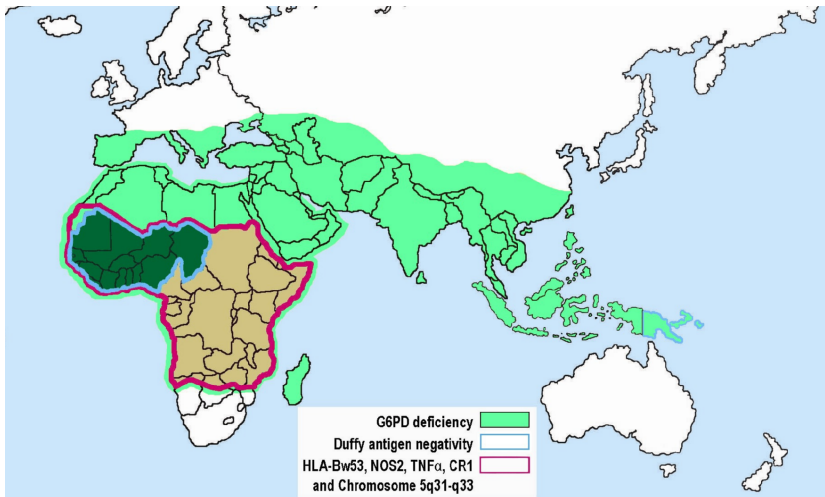
Selective sweep: chromosome pattern



(Nair et al. 2003)

Other malaria-protective variation

- hemoglobin variants:
 - blood groups, Rh-negativity (older than malaria)
 - thalassemia
- enzyme variants:
 - GP6D deficiency/favism
 - * Mediterranean populations
 - * X-linked
 - * arose 5-10K years ago: agriculture?
- Duffy antigens (protection against *vivax* malaria)



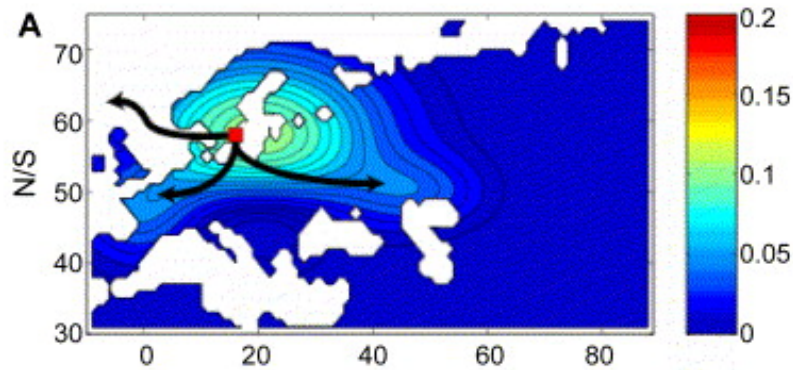
Wikipedia

Cystic fibrosis

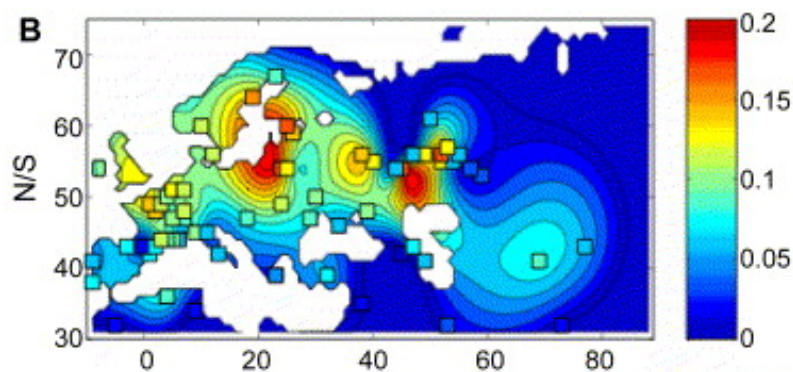
- Lethal lung disease: mucus build-up
(1/4 chance of death before 30, previously much higher)
- 4% carriers in European whites (1/2500 diseased: $2pq = 0.04 \rightarrow q^2 = 0.0004$)
- Mutated *cftr* gene, changes chloride metabolism;
age approx. 50 KYA
- Protection from cholera? (First European cholera epidemic 1817)
Dehydrating intestinal diseases? Typhoid?
- **Pleiotropy** (multiple effects from one gene)

HIV

From Galvani and Novembre (2005):



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- where does CCR5-Δ32 come from?
- homozygous individuals are healthy ...
- at least 5000 years old; Hummel et al. (2005); Novembre, Galvani, and Slatkin (2005); Galvani and Novembre (2005); Lidén, Linderholm, and Götherström (2006)
 - “If Δ32 were neutral, population genetics theory predicts it would have to be much older given its frequency.”
- high dispersal, sustained strong selection ($s > 0.1$); what selective agent? plague? smallpox?

Summary: variation in Mendelian traits

- (relatively) simple inheritance
 - recessive/dominant, autosomal/X/Y-linked
- mechanisms
 - drift
 - heterozygote advantage

- balancing selection/tradeoffs; gene \times environment interaction
- evidence
 - ancient DNA
 - phylogenetic patterns/*coalescent* methods to estimate origin times/places
 - biogeography/history of disease/environment
 - mechanism
 - population history

more examples

Domínguez-Andrés and Netea (2019)

Pathogen or disease	Gene or gene variants	Effect association	Refs
<i>Plasmodium falciparum</i>	<i>HBB</i> , <i>HBC</i> , <i>HBA1</i> , <i>HBA2</i> <i>FCGR2B</i>	Protection (associated with hemoglobinopathies) Protection (associated with SLE ^a)	[9,13,102] [69]
<i>Plasmodium vivax</i>	<i>DARC</i> , <i>HLA-DRB1*</i> and <i>HLA-DQB1*</i>	Protection	[11,12,103]
Bacterial sepsis	<i>CASP12</i> (T ¹²⁵ C)	Protection	[14]
<i>Mycobacterium tuberculosis</i>	<i>VDR</i> , <i>SLC11A1</i> , <i>TIRAP</i> , <i>HLA</i> , <i>CCL2</i> , <i>IL12A</i> <i>IFNG</i> (874T/A)	Protection Detrimental	[17,18,104] [40]
Lassa virus	<i>IL21</i> and <i>LARGE</i>	Protection	[20]
<i>Trypanosoma brucei</i>	<i>APOL1</i>	Protection (associated with SLE)	[68]
Viral infections (e.g., HSV type 2, influenza, papillomavirus)	<i>HLA-DQ2</i> and <i>HLA-DQ8</i>	Protection (associated with SLE)	[105,106]
Bacterial products (<i>Escherichia coli</i> LPS and muramyl dipeptide)	<i>SH2B3</i> rs3184504*A	Protection (detrimental for CD)	[72]
Gram-negative bacterial infections and parasitic infections	<i>NOD2</i> and <i>TLR4/CD14</i>	Protection (detrimental for IBD)	[74,107,108,109]
HIV-1	<i>CCR5Δ32</i>	Protection	[98]

^a

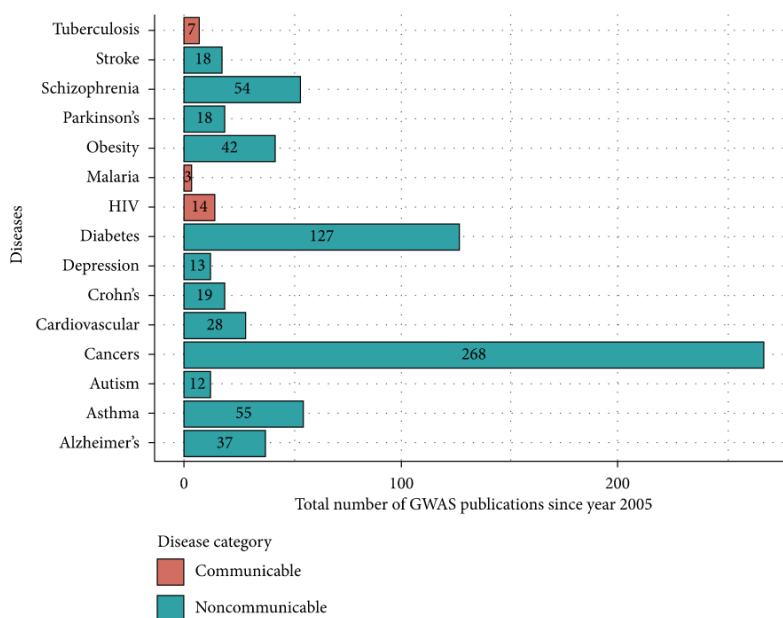
Abbreviations: CD, Crohn's disease; HSV, herpes simplex virus; IBD, inflammatory bowel

GWAS

Mboowa et al. (2018)

Figure 2

Comparison of selected communicable and noncommunicable disease GWASs since 2005.



References

- Acevedo-Whitehouse, K., and A. A Cunningham. 2006. "Is MHC Enough for Understanding Wildlife Immunogenetics?" *Trends in Ecology & Evolution* 21 (8): 433–38.
- Borghans, J. A. M, J. B Beltman, and R. J De Boer. 2004. "MHC Polymorphism Under Host-Pathogen Coevolution." *Immunogenetics* 55 (11): 732–39.
- Domínguez-Andrés, Jorge, and Mihai G. Netea. 2019. "Impact of Historic Migrations and Evolutionary Processes on Human Immunity." *Trends in Immunology* 40 (12): 1105–19. <https://doi.org/10.1016/j.it.2019.10.001>.
- Frisch, Amos, Roberto Colombo, Elena Michaelovsky, Mazal Karpati, Boleslaw Goldman, and Leah Peleg. 2004. "Origin and Spread of the 1278insTATC Mutation Causing Tay-Sachs Disease in Ashkenazi Jews: Genetic Drift as a Robust and Parsimonious Hypothesis." *Human Genetics* 114 (4): 366–76. <https://doi.org/10.1007/s00439-003-1072-8>.
- Frost, Peter. 2012. "Tay-Sachs and French Canadians: A Case of Gene-Culture Co-Evolution?" *Advances in Anthropology* 02 (03): 132–38. <https://doi.org/10.4236/aa.2012.23016>.
- Galvani, Alison P., and John Novembre. 2005. "The Evolutionary

- History of the CCR5- Δ 32 HIV-Resistance Mutation." *Microbes and Infection* 7 (2): 302–9. <https://doi.org/10.1016/j.micinf.2004.12.006>.
- Groot, Natasja G. de, Nel Otting, Gaby G. M. Doxiadis, Sunita S. Balla-Jhagjhoorsingh, Jonathan L. Heeney, Jon J. van Rood, Pascal Gagneux, and Ronald E. Bontrop. 2002. "Evidence for an Ancient Selective Sweep in the MHC Class I Gene Repertoire of Chimpanzees." *Proceedings of the National Academy of Sciences* 99 (18): 11748–53. <https://doi.org/10.1073/pnas.182420799>.
- Hillert, Alicia, Yair Anikster, Amaya Belanger-Quintana, Alberto Burlina, Barbara K. Burton, Carla Carducci, Ana E. Chiesa, et al. 2020. "The Genetic Landscape and Epidemiology of Phenylketonuria." *The American Journal of Human Genetics* 107 (2): 234–50. <https://doi.org/10.1016/j.ajhg.2020.06.006>.
- Hummel, S., D. Schmidt, B. Kremeyer, B. Herrmann, and M. Oppermann. 2005. "Detection of the CCR5- Δ 32 HIV Resistance Gene in Bronze Age Skeletons." *Genes & Immunity* 6 (4): 371–74. <https://doi.org/10.1038/sj.gene.6364172>.
- Klemme, Ines, Pekka Hyvärinen, and Anssi Karvonen. 2020. "Negative Associations Between Parasite Avoidance, Resistance and Tolerance Predict Host Health in Salmonid Fish Populations." *Proceedings of the Royal Society B: Biological Sciences* 287 (1925): 20200388. <https://doi.org/10.1098/rspb.2020.0388>.
- Krawczak, Michael, and Johannes Zschocke. 2003. "A Role for Overdominant Selection in Phenylketonuria? Evidence from Molecular Data." *Human Mutation* 21 (4): 394–97. <https://doi.org/10.1002/humu.10205>.
- Lidén, Kerstin, Anna Linderholm, and Anders Götherström. 2006. "Pushing It Back. Dating the CCR5–32 Bp Deletion to the Mesolithic in Sweden and Its Implications for the Meso\Neo Transition." *Documenta Praehistorica* 33 (December): 29–37. <https://doi.org/10.4312/dp.33.5>.
- Mboowa, Gerald, Ivan Sserwadda, Marion Amujal, and Norah Namatovu. 2018. "Human Genomic Loci Important in Common Infectious Diseases: Role of High-Throughput Sequencing and Genome-Wide Association Studies." *Canadian Journal of Infectious Diseases and Medical Microbiology* 2018 (March): e1875217. <https://doi.org/10.1155/2018/1875217>.
- Nair, Shalini, Jeff T. Williams, Alan Brockman, Lucy Paiphun, Mayfong Mayxay, Paul N. Newton, Jean-Paul Guthmann, et al. 2003. "A Selective Sweep Driven by Pyrimethamine Treatment in Southeast Asian Malaria Parasites." *Molecular Biology and Evolution* 20 (9): 1526–36. <https://doi.org/10.1093/molbev/msg162>.
- Novembre, John, Alison P. Galvani, and Montgomery Slatkin. 2005.

- "The Geographic Spread of the CCR5 Δ 32 HIV-Resistance Allele." *PLOS Biology* 3 (11): e339. <https://doi.org/10.1371/journal.pbio.0030339>.
- Råberg, Lars, Andrea L Graham, and Andrew F Read. 2009. "Decomposing Health: Tolerance and Resistance to Parasites in Animals." *Philosophical Transactions of the Royal Society B: Biological Sciences* 364 (1513): 37–49. <https://doi.org/10.1098/rstb.2008.0184>.
- Raberg, Lars, Derek Sim, and Andrew F. Read. 2007. "Disentangling Genetic Variation for Resistance and Tolerance to Infectious Diseases in Animals." *Science* 318 (5851): 812–14. <https://doi.org/10.1126/science.1148526>.
- Rauch, G., M. Kalbe, and T. B. H Reusch. 2006. "Relative Importance of MHC and Genetic Background for Parasite Load in a Field Experiment." *Evolutionary Ecology Research* 8 (2): 373–86.
- Roy, B. A., and J. W. Kirchner. 2000. "Evolutionary Dynamics of Pathogen Resistance and Tolerance." *Evolution* 54 (1): 51–63. <https://doi.org/10.1111/j.0014-3820.2000.tb00007.x>.
- Schmid-Hempel, Paul. 2009. "Immune Defence, Parasite Evasion Strategies and Their Relevance for 'Macroscopic Phenomena' Such as Virulence." *Philosophical Transactions of the Royal Society B: Biological Sciences* 364 (1513): 85–98. <https://doi.org/10.1098/rstb.2008.0157>.
- Schneider, David S., and Janelle S. Ayres. 2008. "Two Ways to Survive Infection: What Resistance and Tolerance Can Teach Us About Treating Infectious Diseases." *Nature Reviews Immunology* 8 (11): 889–95. <https://doi.org/10.1038/nri2432>.
- Spurgin, Lewis G., and David S. Richardson. 2010. "How Pathogens Drive Genetic Diversity: MHC, Mechanisms and Misunderstandings." *Proceedings of the Royal Society B: Biological Sciences* 277 (1684): 979–88. <https://doi.org/10.1098/rspb.2009.2084>.
- Spyropoulos, B. 1988. "Tay-Sachs Carriers and Tuberculosis Resistance." *Nature* 331 (6158): 666. <https://doi.org/10.1038/331666a0>.
- Stahl, Eli A., Greg Dwyer, Rodney Mauricio, Martin Kreitman, and Joy Bergelson. 1999. "Dynamics of Disease Resistance Polymorphism at the Rpm1 Locus of Arabidopsis." *Nature* 400 (6745): 667–71. <https://doi.org/10.1038/23260>.