Ancient Trans-Species Polymorphism at the Major Histocompatibility Complex in Primates

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Abstract

Classical genes within the Major Histocompatibility Complex (MHC) are responsible for peptide presentation to T cells, thus playing a central role in immune defense against pathogens. These genes are subject to strong selective pressures including both balancing and directional selection, resulting in exceptional genetic diversity—thousands of alleles per gene. Moreover, some alleles appear to be shared between primate species, a phenomenon known as *trans-species polymorphism (TSP)* or *incomplete lineage sorting*, which is rare in the genome overall. However, despite the clinical and evolutionary importance of MHC diversity, we currently lack a full picture of primate MHC evolution. To start addressing this gap, we used Bayesian phylogenetic methods to determine the extent of TSP at six classical MHC genes. We find strong support for TSP in all six genes, including between humans and old-world monkeys in HLA-DRB1 and even—remarkably—between humans and new-world monkeys in HLA-DQB1. Despite the long-term persistence of ancient lineages, we additionally observe rapid evolution at amino acids within the peptide-binding domain. The most rapidly-evolving positions are also strongly enriched for autoimmune and infectious disease associations. Together, these results suggest complex selective forces arising from differential peptide binding, which drive short-term allelic turnover within lineages while also maintaining deeply divergent lineages for at least 45 million years.

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Introduction

The Major Histocompatibility Complex (MHC) is a large immunity locus shared among the jawed vertebrates (Figure 1A)[1]. In humans, the MHC is also known as the HLA (Human Leukocyte Antigen) region; it spans about 5 MB on Chromosome 6 and contains 412 total genes[2,3]. This includes the "classical" MHC genes that are responsible for presenting protein fragments for inspection by T cells. MHC peptide presentation allows T cells to monitor the body for the presence of foreign peptides, which might indicate infection or cancer; this is crucial for vertebrate immune surveillance[4].

The MHC locus is extraordinarily polymorphic, with thousands of distinct alleles (i.e., haplotypes) observed at the classical genes[5–7]. Different alleles are functionally diverse, with distinct peptide-binding affinities and, consequently, allelic differences in pathogen detection[4]. Given this huge diversity of functionally distinct alleles, the MHC is by far the most important locus in the genome for inter-individual variation in both infectious and autoimmune disease risk, with thousands of GWAS hits[8]. Here, we aim to understand the evolution of the MHC by characterizing trans-species polymorphism in six classical genes, HLA-A, -B, -C, -DPB1, -DQB1 and -DRB1, and exploring the functional consequences.

Historically, the MHC provided some of the first clear examples of positive selection in early studies of molecular evolution. By the 1980s and 1990s, researchers had noted an excess of missense variants (i.e., $dN/dS > 1$) in the peptide-binding regions of classical MHC genes[9,10], alleles shared across species[11,12], and high nucleotide diversity across the region[13,14] in rodents and primates. Indeed, modern data show that nucleotide diversity in the human MHC exceeds 70-times the genome-wide average near the classical genes, suggesting ancient balancing selection (Figure 1A-C). Meanwhile, the MHC also features prominently in genome-wide scans for short-term directional selection[15–20].

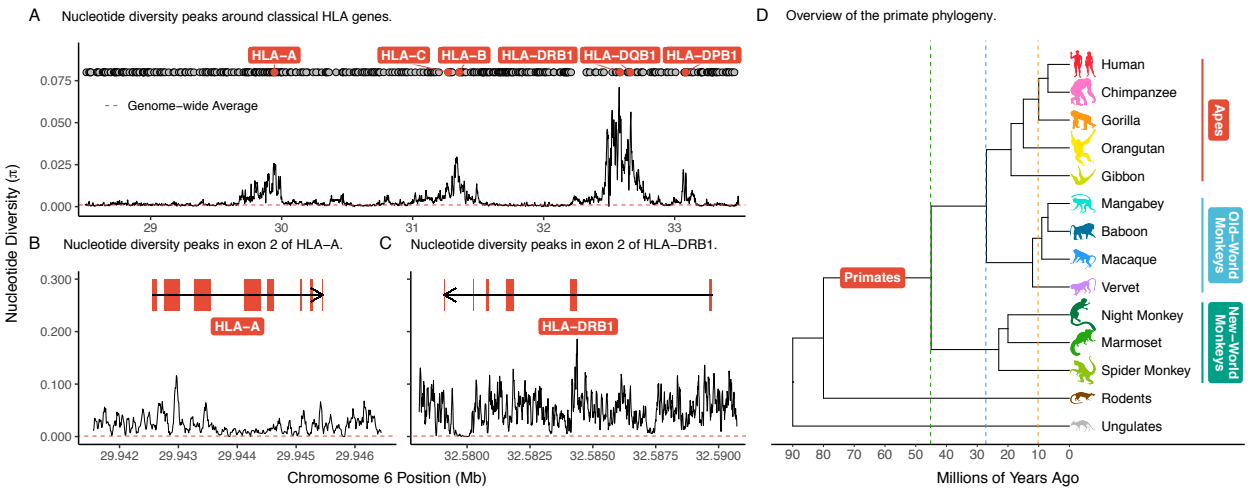

Figure 1: **The classical MHC region. A)** Each point at top represents the location of a gene, including the Class I HLA genes A, C, and B, and Class II HLA genes DRB1, DQB1, and DPB1 that are the focus of this paper. The black line shows nucleotide diversity (Nei and Li's π) across the region, while the red dotted line shows the genomewide average nucleotide diversity ($\pi \approx 0.001$)[21]. **B)** Nucleotide diversity around HLA-A, with exon structure shown. **C)** Nucleotide diversity around HLA-DRB1, with exon structure shown. Zoomed-in views of nucleotide diversity for the other genes is shown in Supplementary Figure S1. **D)** Species tree showing the phylogenetic relationships among selected primates from this study. The orange dashed line indicates the split of the human/chimpanzee lineage from gorilla, approximately 10 million years ago (Mya). The blue dashed line indicates the split of the ape lineage from OWM, approximately 27 Mya. The green line indicates the split of the Catarrhine lineage (apes and OWM) from NWM, approximately 45 Mya. References for divergence times are listed in Supplementary Table S1.

Selection at the MHC is believed to reflect the dynamics of host-pathogen evolution[1,22]. The MHC system

provides constant surveillance against a diverse and ever-changing array of pathogens, all while avoiding detection of self-peptides, which can lead to autoimmune disease. However, the precise mode of selection has not been fully resolved, and several models can explain salient features of the MHC. Under *heterozygote advantage*, individuals with different MHC alleles at each classical locus could defend against a wider range of pathogens than homozygotes. This would drive selection in favor of new alleles (as these would nearly always be heterozygous), and select against common alleles. The *divergent allele advantage* model extends the heterozygote advantage model by noting that heterozygotes with functionally divergent alleles may have better immune surveillance than heterozygotes with similar alleles[1,23]. Other models emphasize the role of pathogen evolution. In the *rare allele advantage/frequency dependent selection* models, pathogens adapt to avoid detection by the most frequent MHC alleles, meaning novel alleles enjoy fitness advantages[1,24]. Lastly, in *fluctuating selection*, pathogen pressures vary across time and space. Specific MHC alleles could become advantageous during epidemics, resulting in frequency shifts over time or across geographical areas[1]. In all of these modes, high diversity and long-term maintenance of alleles are inextricably linked.

In the present paper, we explore a particularly striking feature of the selection signals at MHC, namely the evidence for extremely deep coalescence structure. Some alleles (haplotypes) are more closely related to corresponding alleles from another species than they are to distinct alleles from their own species. This phenomenon is referred to as *trans-species polymorphism* (TSP).

TSP is rare overall in humans. Across most of the genome, human alleles coalesce to a common ancestor well within the human lineage, typically around 2 million years ago[25]. Indeed, only ∼100 loci genome-wide show compelling evidence for sharing of ancestral alleles between humans and our closest relatives, chimpanzees[26]. TSP among humans and more distantly-related species is even rarer; besides MHC, the only other clear example of deep TSP is at the ABO locus[27]. At this locus, both the A and B alleles are shared by descent throughout the apes, implying that the A and B lineages date back to at least the divergence-point of humans and gibbons ∼20 million years ago[28]. Such deep coalescence is extraordinarily unlikely under a neutral model, and instead points to some form of balancing selection.

Meanwhile, TSP is evident at multiple MHC genes, and in many different phylogenetic clades. TSP was first proposed in the 1980s on the basis of unusual sequence similarity between mice and rats[11,13,29–32], and between humans and chimpanzees[12,33]. Later work has reported likely TSP between humans and apes[34–37] and humans and old world monkeys[38–48,48–50] (see Supplement for more details); deep TSP is also consistent with the high levels of genetic diversity within the MHC. Such ancient TSP would make the MHC unique compared to any other locus in the genome. However, most previous work has not fully accounted for the inherent uncertainty in phylogenetic inference, especially given the potential for convergent evolution at functional sites. Although there is clear evidence for TSP, its exact depth at each gene is still uncertain.

Thus, despite the long history of evolutionary studies of the MHC, we still lack a full description of key aspects of variation in the classical MHC genes. In particular, while the high within-species diversity and between-species allele sharing have been well-known for 30 years, we still do not know precisely how ancient these lineages are, how this varies across genes, how to interpret the evidence for ancient lineages alongside the evidence for rapid evolution at specific sites, or how these evolutionary features relate to protein function and disease associations.

To address these questions, we used data from the IPD-MHC/HLA database, a large repository for MHC allele sequences from humans, non-human primates, and other vertebrates[5–7]. The thousands of full-length allele sequences deposited here provide a snapshot of MHC diversity across a wide range of species and allow us to answer questions at a larger scale than previously (Figure 1D). We account for the uncertainty in phylogenetic inference using a Bayesian MCMC approach (*BEAST2*) that samples from the posterior distribution of trees, allowing us to perform formal model-testing for shared ancestral lineages. *BEAST2* also permits evolutionary rates to vary across sites, thus allowing us to minimize the influence of rapidly-evolving, potentially-convergent positions. Lastly, we integrated this analysis with protein structural information and disease associations.

We find conclusive support for TSP among the great apes for HLA-B and -DPB1, and between humans and OWM in HLA-DRB1. Remarkably, we observe TSP in HLA-DQB1 going back to the common ancestor of humans and NWM, implying that alleles have been maintained by balancing selection for at least 45 million years. We also find that most rapidly-evolving sites in all six classical genes are located in the critical peptide-binding regions; moreover, the most rapidly-evolving sites are also the most frequently associated with immune phenotypes and diseases in the literature, connecting our evolutionary findings with their functional consequences. These results highlight the contrasting roles of ancient balancing selection and short-term directional selection within the peptide-binding regions of these genes, and motivate further evolutionary and functional studies to better understand this unique system.

Results

Data. We collated sequence data for six classical MHC genes from existing databases. The IPD-IMGT/HLA database contains over 32,800 human alleles[51], while the IPD-MHC database contains over 11,400 alleles across 77 species, including 55 non-human primates[52]. Most alleles belong to the highly polymorphic classical MHC genes, and most are partial sequences covering exons 2 and 3 (which contain the peptide binding region), while the rest span the entire coding regions of genes. A handful of alleles also include the introns, although such full sequences are limited to only a few species. We compiled alleles of six highly polymorphic classical genes, HLA-A, -B, -C, -DPB1, -DQB1, and -DRB1, for which the entire coding sequence (all exons) was available in the database (details in Methods). Because phylogenetic inference is computationally intensive, we reduced each set to a representative collection of alleles spanning the species' allelic diversity, according to the alleles' two-digit designations. The final data set consisted of 149 alleles for HLA-A, 197 for HLA-B, 61 for HLA-C, 100 alleles for HLA-DPB1, 122 alleles for HLA-DQB1, and 122 alleles for HLA-DRB1 (available as Supplementary Files).

Phylogenetic Inference. To assess the evidence for ancient TSP, we first reconstructed the phylogenetic relationships between alleles. This task is potentially challenging for several reasons: (i) phylogenetic inference is subject to considerable uncertainty, and it can be difficult to quantify (and visualize) the uncertainty in tree reconstruction; (ii) adaptive evolution of missense variants in the peptide-binding regions could make divergent alleles appear similar due to convergent evolution; (iii) recombination means that different regions of a gene have different ancestral histories, thus not conforming to standard phylogenetic assumptions.

To address these challenges, we used a method for Bayesian evolutionary analysis, *BEAST2*, to estimate allele trees[53,54]. Previous MHC work has mostly relied on either summary trees or rudimentary assessments of tree confidence such as bootstrap clade support, which do not naturally allow for hypothesis testing. As an MCMC method, *BEAST2* produces a large set of phylogenies, drawn from the posterior distribution, that we could use for formal model-testing. Second, to account for rapidly-evolving sites, we allowed evolutionary rates to vary among nucleotide sites. The package *SubstBMA*[55] allows *BEAST2* to estimate partitions among sites with different evolutionary rates for each partition, thereby preventing rapidly-evolving sites from disproportionately shaping the final phylogeny. The Bayesian framework also allowed us to incorporate priors, average over models, and quantify uncertainty. Third, to minimize the impact of recombination, we mainly describe the analysis of short regions—a single exon in most cases—even though this may increase uncertainty due to the smaller numbers of sites. We note that, if anything, recombination should bias the data *away* from observing TSP since recombination homogenizes haplotypes within species but not between. Nonetheless, we additionally support our main conclusions with an analysis of synonymous divergence distances that is independent of the phylogenetic analyses.

Trans-Species Polymorphism is Widespread. We considered six classical genes and five different subsets of each gene: exon 2 alone, exon 3 alone, exons 2 and 3 together (PBR), the non-PBR exons to-

gether (Other Exons), and all exons together (CDS). Because few intron sequences were available for non-human species, we did not include them in our analyses. For all six genes, the summary trees suggest deep sharing of ancient lineages among species.

Two of these trees are shown in Figure 2, corresponding to the second exons of HLA-DRB1 and HLA-DQB1, respectively (the other exons and genes are in Supplementary Figures S2-S7). Each image shows a single phylogeny that maximizes the product of posterior clade probabilities[56]. Each tip represents an IPD-MHC/HLA allele, named according to the standard hierarchical naming scheme[57] and with color and shape indicating the species. Clade labels were chosen somewhat arbitrarily to make it easier to indicate key interpretative features of the trees. Outgroup and single-species clades are collapsed for clarity.

Critically, we observe that, at both genes, the alleles fail to cluster together according to species, as indicated by the mixed-color clades throughout the trees. At HLA-DRB1, the human alleles (in red) are

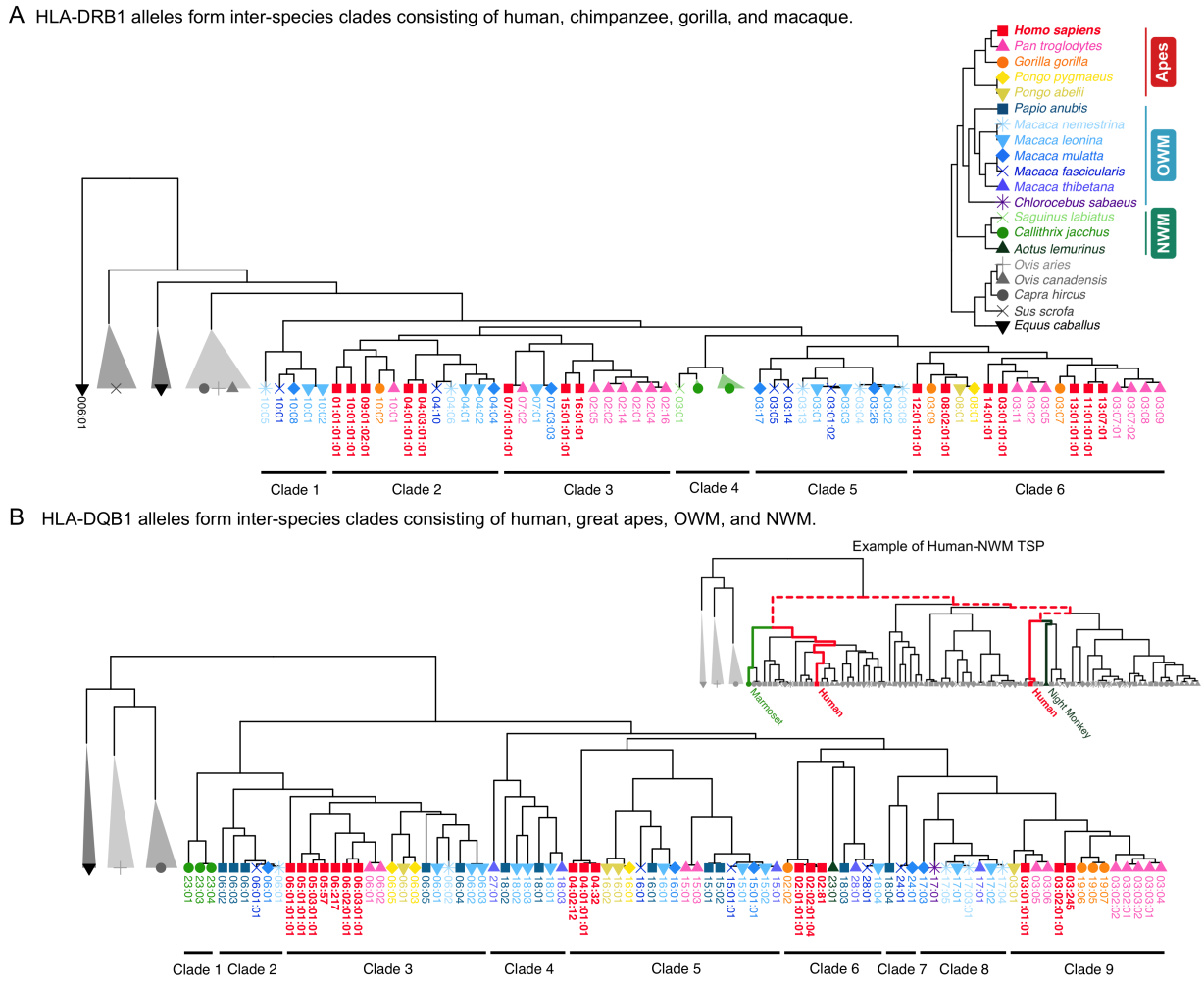

Figure 2: **BEAST2 allele summary trees using sequences from exon 2. A)** HLA-DRB1 and **B)** HLA-DQB1. Each tip represents an allele, with color and shape representing the species. Human alleles (red squares) are also bolded for emphasis. Outgroup and single-species clades are collapsed for clarity. The color/shape key (upper right) also depicts the species tree. The smaller inset tree in panel B highlights the relationships between two human alleles (red) and two NWM alleles (green). The indicated human and NWM lineages coalesce more recently between groups than within each group. This particular example of ancient TSP has extremely strong statistical support (Bayes factor > 7000).

spread across the tree, appearing in Clades 2, 3, and 6. Chimpanzee alleles (pink) also appear in Clades 2, 3, and 6. Even macaque alleles (blue) are distributed among several of the same clades: 2, 3, and 4. Hence, alleles are often most closely related to alleles from other species, suggesting extensive TSP and sharing of ancient lineages at least as far back as the ape–old-world monkey split.

The HLA-DQB1 tree suggests even more extensive TSP: human and other great ape alleles are found in Clades 3, 4, 6, and 9; old-world monkeys are found in Clades 2, 3, 4, 5, 6, 7, and 8; new-world monkeys are in Clades 1 and 6. The inset figure highlights an example of TSP between human and new-world monkey alleles. This particular example has strong statistical support. Thus, remarkably, data from HLA-DQB1 indicate the persistence of distinct ancestral lineages for at least 45 million years.

However, while the summary trees in Figure 2 are suggestive of deep TSP, they do not directly quantify the statistical confidence in the TSP model. Moreover, standard approaches to quantifying uncertainty in trees, such as bootstrap support or posterior probabilities for specific clades, do not relate directly to hypothesis testing for TSP. We therefore implemented an alternative approach using *BEAST2* output, as follows (see the Methods for details).

We performed formal model testing for TSP within quartets of alleles, where two alleles are taken from a species (or taxon) A, and two alleles are taken from a different species (or taxon) B. If the alleles from A (and respectively from B) are closest in the unrooted tree, this quartet supports monophyly of A (and of B). But if alleles from A and B are closest in the unrooted tree, then this comparison supports TSP. Since *BEAST2* samples from the posterior distribution of trees, we counted the number of trees that support TSP versus the number that support monophyly as an estimate of the posterior support for each model. We then summarized the relative support for each model by converting these to Bayes factors. The precise interpretation of Bayes factors depends on one's prior expectation; however, following standard guidelines[58] we suggest that Bayes factors > 100 should be considered as strong support in favor of TSP. Bayes factors <1 are evidence against TSP. For each comparison of two taxa, we report the maximum Bayes factor across the possible quartets, as we are interested in whether *any* quartet shows compelling evidence for TSP.

Bayes factors are shown in Figure 3. For each genic region (x-axis), we tested for TSP among humans, non-human apes, OWM, and NWM, with each of the comparisons listed on the y-axis. Each table entry is colored and labeled with the maximum Bayes factor among all tested quartets of alleles belonging to that category. Red indicates support for TSP among the species in that category, while blue indicates evidence against TSP.

At the Class I genes, HLA-A, -B, and -C, we find strong support for TSP within the great apes: between human, chimpanzee, and gorilla for HLA-A and -C, and also with orangutan at -B. We do not find evidence for deeper TSP within Class I (but note that we do not have gibbon alleles apart from HLA-A). Meanwhile, the results for HLA-DRB1 and -DQB1 confirm the presence of ancient TSP. Bayes factors for exon 2 of HLA-DRB1 indicate TSP between humans, chimpanzees, gorillas, and even OWM. (The Bayes factors between human and orangutan are 0, but there are only two orangutan alleles in this dataset.) Even more striking, the Bayes factors indicate TSP in exon 2 of HLA-DQB1 at least as far back as our ancestors with NWM.

There is also extensive support for TSP within the OWM for all genes (except HLA-C, which is only present in the great apes), and within NWM for HLA-B and -DPB1. HLA-DQB1 and -DPB1 also show TSP between OWM and NWM. There is no support for TSP between humans and any of the outgroup species. Supplementary Figures S9-S15 show Bayes factors for all analyses. Thus, in summary, the phylogenetic analyses strongly support the presence of ancient TSP in these genes.

However, the tree-based model has certain limitations: it may not fully account for convergent evolution at functional sites (even though we allow for rate variation among sites) and it ignores recombination. Therefore, we next used a complementary, nonparametric approach based on synonymous nucleotide distances (dS) between pairs of alleles to verify the plausibility of our tree-based results. Pairwise synonymous dis-

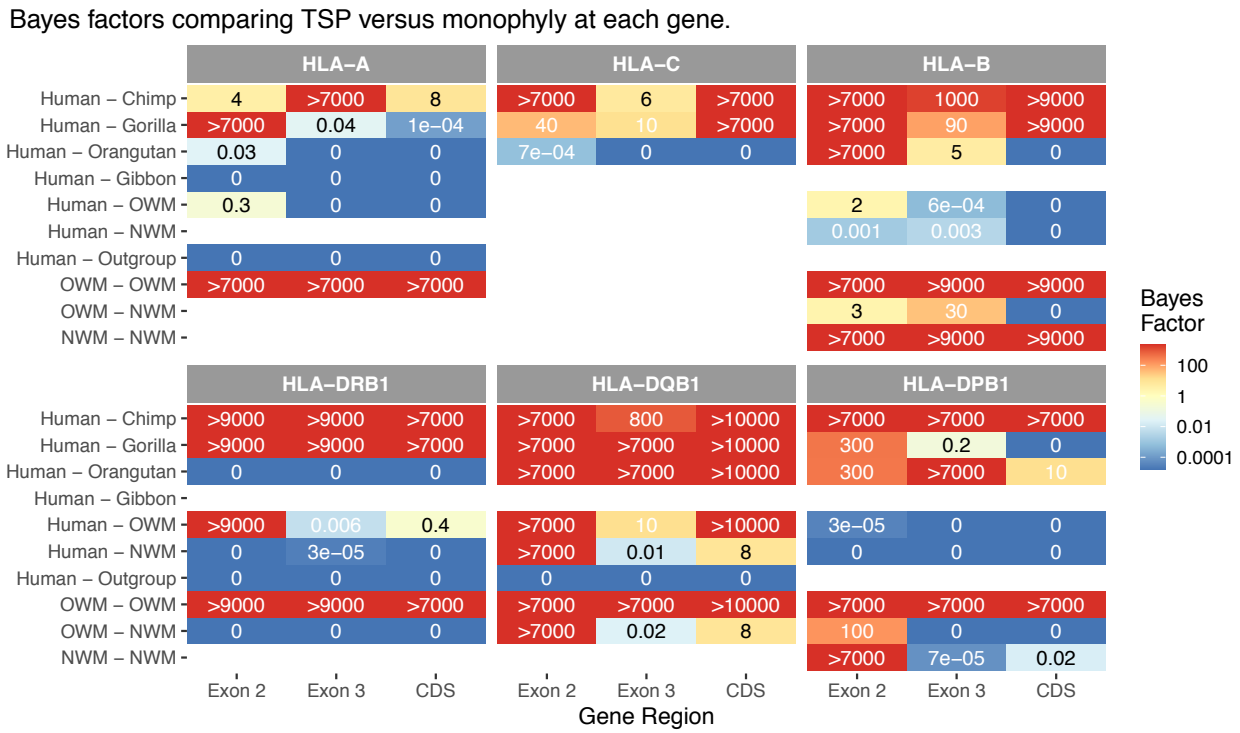

Figure 3: **Strong support for TSP at all six genes.** Bayes factors computed over the set of BEAST trees indicate deep TSP. Different species comparisons are listed on the y-axis, and different gene regions are listed on the x-axis. High Bayes factors (red) indicate support for TSP among the given species for that gene region, while low Bayes factors (blue) indicate that alleles assort according to the species tree, as expected. Bayes factors above 100 are considered decisive. Yellow values show poor support for either hypothesis, while white boxes indicate that there are not enough alleles in that category with which to calculate Bayes factors.

tances make less-efficient use of the data compared to the phylogenetic analysis, but should be robust to both convergent nonsynonymous evolution at functional sites and recombination. In the presence of recombination, dS would simply reflect the mean coalescence time along the sequence, averaged over recombined blocks. We estimated dS between pairs of alleles using *codeml*[59,60].

The dS results are shown in Figure 4. Each data point shows the estimated dS for a pair of alleles within or between the indicated species. We reasoned that the observed dS values reflect a distribution of underlying coalescence times between pairs of alleles. Due to the random sampling error in dS, the true distribution of expected values would usually be narrower than the observed distribution. Therefore, for each comparison we estimated the underlying distribution of expected dS values under a simple model (see Supplement for details); these are indicated by the gray boxed region on each plot.

First, we noticed that even within humans, the dS divergence values can be extraordinarily high. Noting that a conservative upper bound on the mutation rate in primates is $\sim 1 \times 10^{-9}$ per year[61], a value of dS > 0.1, as seen in exon 2 for several genes, suggests a remarkably ancient split time of > 50 MY between pairs of human alleles. Second, we reasoned that in the presence of TSP, the distributions of dS values should overlap within and between the relevant species. For example, in the phylogenetic analysis, HLA-A shows evidence for TSP among human, chimpanzee, and gorilla, but not with other species. Consistent with this, we see overlap of the dS distributions for these three species. However, in most cases we actually see *more* evidence for TSP than in the phylogenetic analysis (Figure 4A). For example, HLA-DRB1 shows overlap between the dS distributions of human-human and human-OWM pairs (though they do not quite overlap for chimpanzee, gorilla, and orangutan), while HLA-DQB1 shows broad overlap of the distributions—including the outgroup species.

In Figure 4B, we see overlap of the human-human and human-NWM distributions in exon 2 of HLA-B, indicating deeper TSP than we see in the phylogeny. We do not observe any overlap for the whole CDS, confirming that the greater recombination across larger regions averages dS across blocks and attenuates signal for TSP. Thus, the dS estimates support ancient allelic structure within these genes, consistent with—if not even more ancient than—the results from phylogenetic analysis.

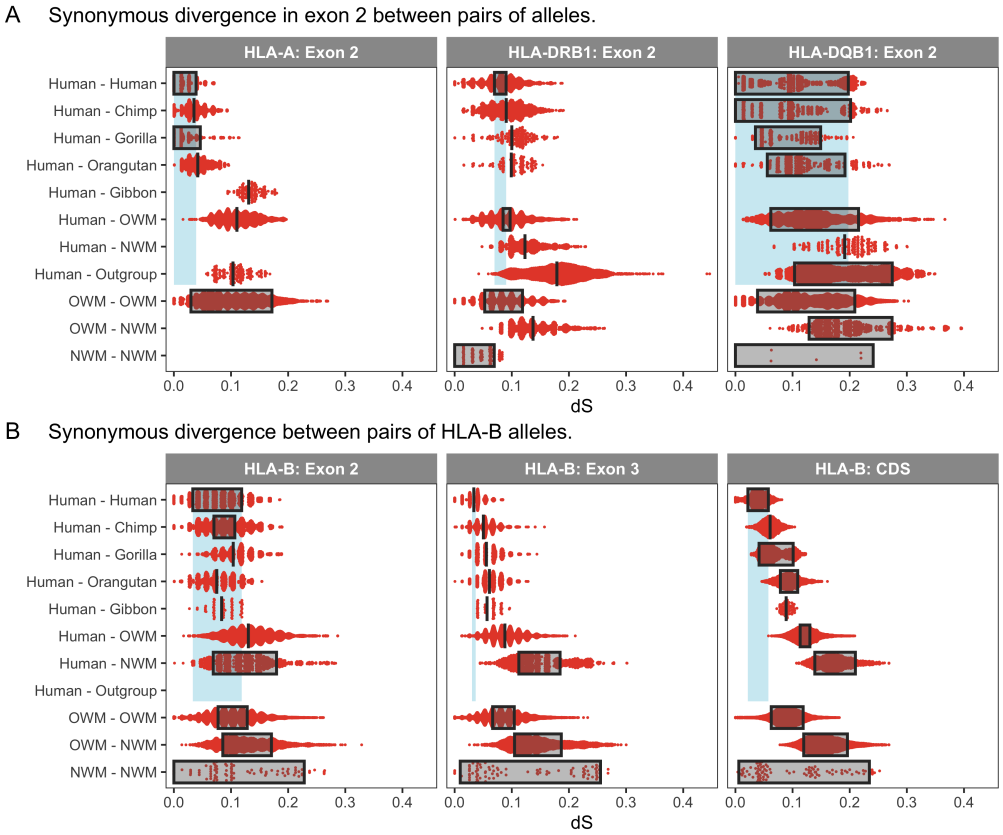

Figure 4: **Synonymous divergence between allele pairs is consistent with ancient TSP.** Each red point represents estimated dS for a pair of alleles (x-axis), sorted by species comparison (y-axis). The gray boxes show estimated ranges of true dS values (details in Supplement) for each comparison. The blue regions extend the gray box for human-human pairs downward across each plot to facilitate visual comparison between species pairs. **A)** In many cases, allele comparisons within humans (Human - Human) show overlapping synonymous divergence values to allele comparisons between humans and other species—for example, between human and OWM alleles in HLA-DRB1. **B)** In HLA-B, the human-human dS distribution overlaps the human-NWM distribution in exon 2, but not in exon 3 or the whole CDS. See Supplementary Figures S16-S20 for dS results for the other genes and regions.

In summary, our data support deep TSP at all six classical MHC genes considered here. The HLA-A, -C, -B, and -DPB1 trees show TSP between human, chimpanzee, and gorilla, while HLA-B and -DPB1 additionally show TSP between human and orangutan. HLA-DRB1 reveals even more extensive TSP, back to our ancestor with OWM. The deepest strongly-supported TSP is at HLA-DQB1, with TSP between humans and NWMs indicating the persistence of ancient lineages for at least 45 million years. The HLA-A, -B, -DRB1, -DQB1, and -DPB1 trees also indicate extensive TSP among OWM. Our dS results corroborate deep TSP at all loci.

From Evolution to Function. Alongside the evidence for ancient TSP, the MHC region is also notable for its high rate of missense substitutions (dN/dS)[9,10] and its large number of GWAS hits for autoimmune and infectious diseases[8,62]. We next aimed to understand how these observations relate to signals of TSP and known features of the MHC proteins.

To explore these questions, we first estimated the per-site evolutionary rates within each gene. As in our TSP analysis, we used the *BEAST2* package *SubstBMA*, which estimates evolutionary rates at every site. We averaged these rates over all states in the chain to get per-site evolutionary rates for each site, then calculated their fold-change relative to the average rate among 4-fold degenerate sites. The results were insensitive to whether the analysis included the entire CDS or smaller subsets (Supplementary Figure S21).

Figure 5A shows the substitution rate fold-change for each nucleotide along the concatenated coding sequence of HLA-A and -DRB1. Exon boundaries are indicated by red dashed lines. We found that nearly all the rapidly-evolving sites lie within the exons that encode the peptide-binding domains of each protein: for example, 80% of sites evolving at more than 4 times the rate of the 4-fold degenerate sites were located in exons 2 and 3 for the Class I gene HLA-A, and 86% of such sites were located in exon 2 for the Class II gene HLA-DRB1. This pattern holds true for the other Class I and Class II genes as well (Supplementary Figure S22).

We then examined where the rapidly-evolving sites lie within the physical protein structures. To do this, we averaged the per-site rates within each codon to get per-amino-acid rates, and mapped these onto the known protein structures. As shown in Figure 5B, rapidly-evolving amino acids (red) tend to be located within the peptide-binding groove. To quantify this, we measured the minimum distance between each amino acid and the bound peptide. Amino acids closer to the peptide have significantly higher evolutionary rates than amino acids further from the peptide, as shown in Figure 5C (see also Supplementary Figures S23-S24). These results are consistent with the expectation that rapid evolution and diversity at the MHC would be mediated by selective pressures for changes in peptide binding.

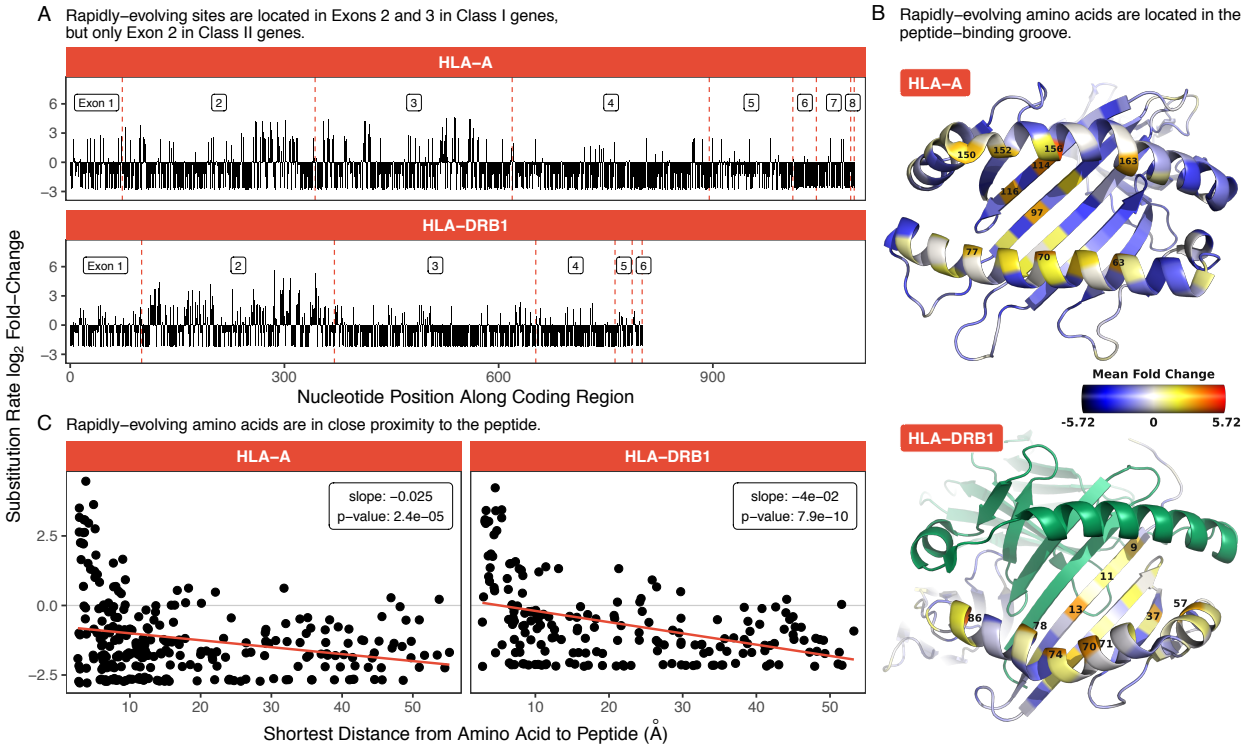

Figure 5: **Rapidly-evolving sites from BEAST2. A)** Rapidly-evolving sites are primarily located in exons 2 and 3. Here, the exons are concatenated such that the cumulative position along the coding region is on the x-axis. The y-axis shows the substitution rate at each site, expressed as a fold-change (the base-2 logarithm of each site's evolutionary rate divided by the average rate among 4-fold degenerate sites within the gene). **B)** Rapidly-evolving sites are located in each protein's peptide-binding pocket. Structures are Protein Data Bank[63] 6D2T[64] for HLA-B and 2IAM[65] for HLA-DRB1, with images created in *PyMOL*[66]. Substitution rates for each amino acid are computed as the mean substitution rate of the three sites composing the codon. Red indicates rapidly-evolving amino acids, while blue indicates conserved amino acids. The top ten fastest-evolving amino acids of each protein are labeled on the structures. **C)** Rapidly-evolving amino acids are significantly closer to the peptide than conserved amino acids. The y-axis shows the *BEAST2* substitution rate, and the x axis shows the minimum distance to the bound peptide, measured in *PyMOL*[66]. Each point is an amino acid. The red line is a regression of substitution rate on minimum distance, with slope and p-value annotated on each panel.

Lastly, since the rapidly-evolving sites are likely involved in peptide binding, they also influence the response to pathogens and self-antigens, presumably affecting risk for infectious and autoimmune diseases. To bridge the gap between evolution and complex traits, we therefore tested whether these sites had known associations with peptide binding, TCR usage, and human disease.

We collected HLA fine-mapping studies for infectious, autoimmune, and other diseases (Supplementary Table S2). These studies report associations between a disease or trait and classical HLA alleles, SNPs, and amino acid variants, often with multiple independent hits per gene, as indicated by the colored blocks in Figure 6A. As expected, we found that all six genes harbor many associations with diverse traits and diseases.

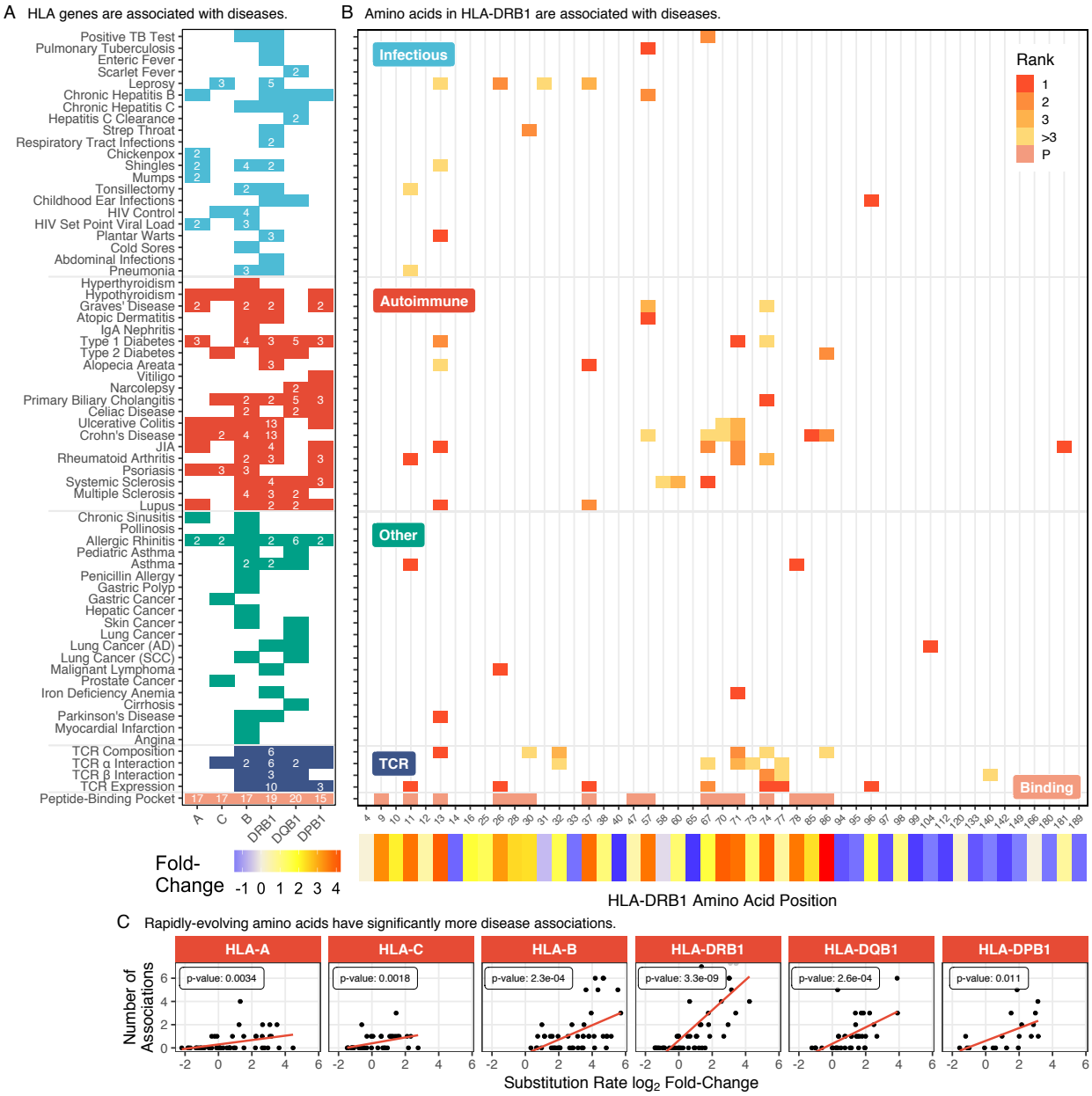

Figure 6: **Disease associations in HLA-DRB1. A)** The six classical HLA genes studied here (x-axis) are associated with many disease and immune-related phenotypes (y-axis). Colored blocks indicate an association between the indicated disease or trait at either SNPs, amino acids, or classical alleles within the corresponding gene. The number of independent associations is indicated when > 1. For the peptide-binding pocket in the bottom row, the printed number indicates the number of critical residues. **B)** Associations between amino acids in HLA-DRB1 and human diseases from HLA fine-mapping studies. The polymorphic amino acid positions ($>$ 1% MAF) within HLA-DRB1 are on the x-axis, and the diseases and traits are on the y-axis. Associations are colored according to whether they were the top hit, second independent hit, and so on. For peptide binding, a pink box indicates that the amino acid is present (P) among the critical residues. The x-axis is annotated with colored boxes representing *BEAST2* evolutionary rates at codon-level. Red indicates rapidly-evolving positions and blue indicates conserved positions. **C)** The *BEAST2* evolutionary rate is significantly associated with the total number of associations for all six genes.

Moreover, the sites that are rapidly-evolving in the primate analysis show specific enrichment for phenotypic associations in HLA fine-mapping studies. This is illustrated in Figure 6B; the x-axis indicates polymorphic amino acid positions, each annotated with the evolutionary rate from *BEAST2*. The amino acid positions most frequently associated with disease are largely concordant with the rapidly-evolving positions, particularly positions 11, 13, 57, 70, and 71. Supplementary Figures S25-S29 show the associations for the other genes.

Indeed, Figure 5D shows that *BEAST2* evolutionary rate is significantly associated with the number of disease and immune-phenotype associations for all six genes. Together, these results suggest that highly functional sites within the peptide-binding domain are both rapidly-evolving and highly enriched for associations. We wondered whether high variability might be a confounding factor – i.e., that highly polymorphic sites are more likely to harbor significant associations. Indeed, while the number of amino acid alleles at each position is significantly associated with the number of associations, the evolutionary rate remains significant for 5 of the 6 genes in a multiple regression controlling for number of alleles, even though this analysis is highly conservative (Supplementary Table S5). Thus, in summary, we find that rapid evolution has primarily targeted amino acids within the peptide-binding region of each gene, and that these specific positions are primary drivers of phenotypic associations at the MHC locus.

Discussion

The MHC region contains the clearest signals of balancing and directional selection in mammalian genomes, including extreme diversity, ancient trans-species polymorphism, and high rates of nonsynonymous evolution between allelic lineages. In humans, MHC/HLA variation is associated with risk for infectious and autoimmune diseases and many other traits, and HLA matching is critical for successful tissue transplantation.

Despite the evolutionary and clinical importance, the extreme diversity of the MHC makes it challenging to study, and basic questions about its evolutionary history remain unresolved. Although past work has hinted at ultra-deep TSP at this locus, in this study we re-examined the region with modern, comprehensive data and a unified analysis framework. Using Bayesian evolutionary analysis, we report conclusive evidence for long-term TSP in all six studied genes, including between humans and OWM at HLA-DRB1, and even between humans and NWM at HLA-DQB1. Thus, remarkably, lineages at HLA-DQB1 have been maintained for at least 45 million years. The evidence for deep TSP is mainly concentrated within the exons that encode the peptide-binding region for each gene (exons 2 and 3 for Class I, and exon 2 for Class II). Comparisons of synonymous divergence within and between species provide further support for extremely ancient lineages, while obviating concerns about model misspecification in the phylogenetic analysis.

Our evidence for TSP at HLA-DQB1 spanning at least 45 million years places this among the most ancient examples of balancing selection known in any species, and almost certainly the oldest in primates. Aside from MHC, the deepest example within primates is at the ABO locus controlling blood type; it exhibits trans-species polymorphism between humans and gibbons, an age of 20 million years[28]. In various chimpanzee species, *OAS1*, which helps inhibit viral replication, contains alleles up to 13my old[67]. TSP between chimpanzee and human includes *LAD1*, a protein that maintains cell cohesion (6my)[68], retroviral transcription factor *TRIM5α* (4-7my in apes and $>$ 8my in OWM)[69,70], and *ZC3HAV1*, an antiviral protein leading to viral RNA degredation (6my)[71], among others[26].

Looking more broadly across the tree of life, ancient trans-species polymorphism occurs widely, albeit rarely. Several of the best examples are found in the MHC locus: MHC polymorphisms have been maintained for 35my in cetaceans[72], 40my in herons[73], 48my in mole rats[74], 70my in tree frogs[75], and over 105my in salmonid fishes[76,77]. There are examples in non-MHC loci as well; in cyanobacteria, polymorphism at the HEP island controlling heterocyst function has been maintained for 74 million years[78], in

plants, S-genes determining self-incompatibility exhibit TSP spanning 36 million years[79,80], and in *Formica* ants, alleles at a supergene underlying colony queen number have been maintained for over 30 million years[81] (See the Supplement for more examples).

Paradoxically, given the extremely long-lived balancing selection acting in these lineages, many authors have also reported strong directional selection[82–84]. Indeed, within the phylogeny we find that the most rapidly-evolving codons are substituted at around 5–7-fold the neutral rate. For all six genes, these rapidly-evolving sites lie within the peptide binding regions of the corresponding proteins, usually very close to the peptide-contact surfaces. Moreover, the primary role of MHC proteins is to present peptides for T cell recognition; we found that the same rapidly-evolving amino acids are consistently associated with shaping T cell receptor (TCR) repertoires.

We further connected our evolutionary results to their functional consequences by examining published associations between HLA variants and immune-related phenotypes. The peptide-presentation and recognition process is integral to the immune response and affects our ability to fight infections and recognize self-antigens. After collating HLA fine-mapping studies of human disease, including infectious, autoimmune, and other diseases, we found that the same rapidly-evolving amino acids are also key sites of disease association.

Taken together, we begin to see a comprehensive picture of the nature of primate MHC evolution. In response to rapidly-changing pathogen pressures, the PBRs of classical MHC proteins evolve to bind changing pathogen antigens and present them to TCRs. Broad lineages of MHC alleles are maintained over tens of millions of years by strong balancing selection, providing defense against a wide variety of different pathogens. Yet within these lineages, alleles turn over quickly in response to new specific threats. This reconciles evidence for TSP, the presence of thousands of alleles, and the existence of rapidly-evolving sites. Because it is challenging to detect pathogens with both specificity and sensitivity, many MHC alleles also happen to bind self-peptides. This results in rapidly-evolving amino acids being associated with both infections and autoimmune conditions, as well as TCR phenotypes and peptide-binding residues.

Although the primate MHC has been of interest to evolutionary biologists for more than 30 years, there is still much to be done to more fully document the evolution of the MHC genes within and between species. Moreover, we still have limited understanding of how sequence changes map to functional differences among alleles, and how these relate to allele-specific profiles of pathogen protection (and autoimmunity risk). However, functional and computational advances will provide key opportunities for progress on these problems[1,85].

Materials and Methods

Data. MHC allele sequences for HLA-A, -B, -C, -DPB1, -DQB1, and -DRB1 were downloaded from the IPD Database[6,7]. The database contains tens of thousands of alleles, but we selected only the alleles for which the entire coding sequence (all exons) was available. In humans, this consisted of 2,819 HLA-A alleles, 3,338 HLA-B alleles, 3,055 HLA-C alleles, 522 HLA-DPB1 alleles, 297 HLA-DQB1 alleles, and 200 HLA-DRB1 alleles. Excluding humans, there were 14 species and 240 alleles for HLA-A, 24 species and 1,334 alleles for HLA-B, 6 species and 61 alleles for HLA-C, 13 species and 185 alleles for HLA-DPB1, 16 species and 288 alleles for HLA-DQB1, and 15 species and 231 alleles for HLA-DRB1. Note that we use the familiar human-centric names (with prefix "HLA-") to refer to these genes in all species, although the gene names with prefix "MHC-" are more accurate in an evolutionary context.

BEAST2 is computationally limited by the number of sequences. Thus, when hundreds or thousands of alleles were available for a single species, we reduced each set to a representative set spanning the species' allelic diversity, according to the alleles' two-digit designations. The final set consisted of 149 alleles for HLA-A, 197 for HLA-B, 61 for HLA-C, 100 for HLA-DPB1, 122 for HLA-DQB1, and 122 for HLA-DRB1 (lists of alleles provided as Supplementary Files).

Alleles for each gene were aligned using *MUSCLE*[86] in *MEGA X*[87] with default settings.

Modern human data was obtained for 2504 unrelated individuals from Phase 3 of the 1000 Genomes Project, from the re-sequencing done at the New York Genome Center and mapped to GRCh38[88,89].

Nucleotide Diversity. The classical MHC region is defined as chr6:28,510,120-33,480,577 (GRCh38)[2]. Nucleotide diversity (π) was calculated on the modern human data using *VCFtools (0.1.15)*[90]. For the entire MHC region (Figure 1A), π was calculated in 5000bp sliding windows with a step size of 1000bp. For each gene separately (Figure 1B-C and Supplementary Figure S1), π was calculated in 50bp sliding windows with a step size of 10bp.

Bayesian Phylogenetic Analysis. We constructed phylogenetic trees using *BEAST2*[53,54] with package *SubstBMA*[55]. *SubstBMA* implements a spike-and-slab mixture model that simultaneously estimates the phylogenetic tree, the number of site partitions, the assignment of sites to partitions, the nucleotide substitution model, and a rate multiplier for each partition. Since we were chiefly interested in the partitions and their rate multipliers, we used the RDPM model as described by Wu et al.[55]. In the RDPM model, the number of nucleotide substitution model categories is fixed to 1, so that all sites, regardless of rate partition, share the same estimated nucleotide substitution model. This reduces the number of parameters to be estimated and ensures that only evolutionary rates vary across site partitions, reducing overall model complexity. Even though the substitution rate is known to be different over the evolutionary time we consider, Wu et al.[55] demonstrated virtually no difference in likelihoods or site partitions when using a strict vs. relaxed molecular clock. Thus, we used a strict clock to further simplify our analyses.

Priors. For the Dirichlet process priors, we used the informative priors constructed by Wu et al.[55] for their mammal dataset. This is appropriate because they include several of the same species and their mammals span approximately the same evolutionary time that we consider in our study. We also use their same priors on tree height, base rate distribution, and a Yule process coalescent prior. We did not specify a calibration point—a time-based prior on a node—because we did not expect our sequences to group according to the species tree.

Running *BEAST2*. We ran *BEAST2* on allele sequences from the IPD Database[5–7], considering subsets of the coding sequence: 1) the entire coding sequence, 2) exon 2 only, 3) exon 3 only,

4) exons 2 and 3 together (the peptide-binding region), and 5) all other exons (excluding exons 2 and 3). Because *BEAST2* runtime scales with the number of samples, we restricted the number of alleles used for each gene. We only considered alleles that 1) have the entire coding sequence available in the database (because many submitted alleles are the result of sequencing exon 2 and 3 alone), 2) do not have a nonsense mutation, and 3) adequately represent the diversity of the species. For example, we restricted human alleles to include at least one allele representing every major type (2-field name). For macaques, which have even more MHC diversity than humans, we limited alleles to 5 randomly-chosen alleles per species that also span several types.

The xml files we used to run *BEAST2* were based closely on those used for the mammal dataset with RDPM model and strict clock in Wu et al.[55](`https://github.com/jessiewu/substBMA/blob/master/examples/mammal/mammal_rdpm_sc.xml`). However, due to the complexity of the MHC, we ran each for 40,000,000 states (instead of 25,000,000), using the first 10% as burn-in and sampling every 10,000 states. The xml files required to run all our analyses are provided as Supplementary Files. Additionally, we ran 4-12 replicates (4 at a time) for each of the 6 genes and each of the 5 subsets of the coding sequence, until we obtained at least 4 replicates whose likelihood and posterior parameter distributions all agreed, as recommended by *BEAST2* and explored in *Tracer* version 1.7.1[91]. This ensures that all of the replicates were exploring the same parameter space and were converging upon the same global optimum, allowing the $\geq$ 4 independent runs to be justifiably combined. We combined the matching replicates using *LogCombiner* version 2.6.3[92], which aggregates the results across all states. We then used the combined results to perform our analyses.

HLA-B. Running *BEAST2* on HLA-B proved difficult due to the number of sequences included as well as the considerable diversity among them. To improve convergence, we employed coupled MCMC in *BEAST2* for the entire coding sequence (subset 1) and exons 2 and 3 combined (subset 4). Coupled MCMC is essentially the same as the regular MCMC used in *BEAST2*, except that it uses additional "heated" chains with increased acceptance probabilities that can traverse unfavorable intermediate states and allow the main chain to move away from an inferior local optimum[93]. Using coupled MCMC sped up these more-difficult *BEAST2* runs and allowed us to obtain 4 valid replicates that could be used for the analysis. Xml files for these runs are also provided as Supplementary Files.

Phylogenetic Trees. Since we sampled every 10,000 states for each *BEAST2* replicate, discarded the first 10% as burn-in, and obtained 4-7 acceptable replicates per gene/sequence subset, we obtained 14,101 - 25,207 phylogenies per gene/sequence subset. We used *TreeAnnotator* version 2.6.3[92] to summarize each set of possible trees as a maximum clade credibility tree, which is the tree that maximizes the product of posterior clade probabilities. Since *BEAST2* samples trees from the posterior, one could in principle perform model testing directly from the posterior samples; the complete set of trees can typically be reduced to a smaller 95% credible set of trees representing the "true" tree[56]. However, given the high complexity of the model space, all our posterior trees were unique, meaning this was not possible in practice. (Since the prior over tree topologies is unstructured, this effectively puts minuscule prior weight on trees with monophyly. Thus, sampling directly from the posterior provides an unacceptably high-variance estimator.)

Bayes Factors. Because we could not perform model testing directly on the full phylogenies, we used an alternative approach—computing Bayes factors for TSP within manageable subsets of the data, i.e., quartets of alleles. Let D be a sample of phylogenies from *BEAST2*, sampled from the posterior with uniform prior. For a chosen species, we have a null hypothesis H, that human alleles form a monophyletic group, and an alternative hypothesis, H^c, that is also the complement of H—that the human alleles do not form

a monophyletic group. The Bayes factor, K, is a ratio quantifying support for the alternative hypothesis:

$$K = \frac{\Pr(D|H^c)}{\Pr(D|H)} = \frac{\Pr(H^c|D)}{\Pr(H|D)} \cdot \frac{\Pr(H)}{\Pr(H^c)}$$

where the first term on the right hand side is the posterior odds in favor of the alternative hypothesis and the second term is the prior odds in favor of the null hypothesis. Bayes factors above 100 are considered decisive support for the alternative hypothesis[58].

Because it is difficult to evaluate monophyly using a large number of alleles, we evaluate Bayes factors considering 4 alleles at a time: 2 alleles of a single species and 2 alleles of different species. For example, to assess support for TSP between humans and chimpanzees, we could use 2 human alleles and 2 bonobo alleles. Or, to assess support for TSP between humans and OWM, we could use 2 human alleles, one baboon, and one macaque allele. Because there are many possible sets of 4 alleles for each comparison, we tested a large number of comparisons, including sets chosen at random and sets that appear to support TSP in the *BEAST2* summary trees. We reported the *maximum* Bayes factor among all tested allele sets to represent evidence for TSP for that species comparison, because our aim was to find *any* evidence of TSP among *any* set of 4 alleles.

Next, we calculated the prior odds of the null hypothesis (that the chosen species, i.e. humans, form a monophyletic group). The prior odds $\frac{\Pr(H)}{\Pr(H^c)} = \frac{1}{2}$, because if the trees were assembled at random, there is 1 possible unrooted tree where the 2 human alleles would form a monophyletic group and 2 possible unrooted trees where the 2 human alleles would not form a monophyletic group, as shown in Figure 7.

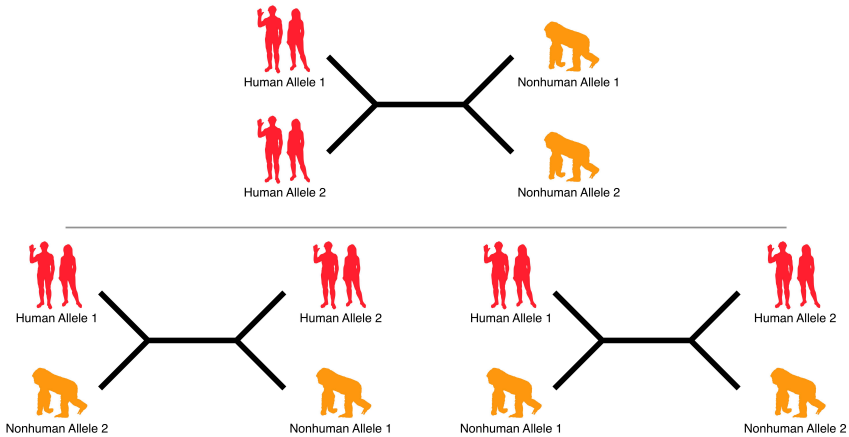

Figure 7: **Possible unrooted trees of 4 alleles.** There is one tree where the human alleles are monophyletic, and two trees where they are non-monophyletic.

The data, D, is the set of *BEAST2* trees, so the posterior odds $\frac{\Pr(H^c|D)}{\Pr(H|D)}$ is the fraction of *BEAST2* trees where the 2 human alleles **do not** form a monophyletic group divided by the fraction of *BEAST2* trees where the 2 human alleles **do** form a monophyletic group. If either fraction is 0, we set its probability to $p = \frac{1}{n+1}$, where n is the number of *BEAST2* trees for that gene/sequence subset, and set the complement's probability to $1 - p$. This is the reason that some labels in Figure 3 contain a $>$ sign (e.g. if no trees in a set of $14,000$ were monophyletic, then the Bayes factor must be at minimum $7,000$).

Bayes factors K were then computed as follows and interpreted according to the scale given by Jeffreys[58].

$$K = \frac{\Pr(H^c|D)}{\Pr(H|D)} \cdot \frac{1}{2}$$

For each gene and genic region, we tested for TSP between human and chimpanzee, gorilla, orangutan, gibbon, OWM, and NWM. We also computed TSP for groups not involving humans, including among OWM themselves, between OWM and NWM, and among NWM themselves. Lastly, we tested for TSP between humans and the outgroups, for which we did not expect to see any evidence of TSP.

Rapidly-Evolving Sites. *BEAST2* places sites into partitions and estimates evolutionary rates for each partition. We averaged these rates over all sampled states, resulting in an overall evolutionary rate for each nucleotide position. To normalize the rates, we divided them by the average evolutionary rate among 4-fold degenerate sites. 4-fold degenerate sites for each gene were identified from our *codeml* analysis using the entire coding sequence.

We expressed the normalized per-site rates as fold-changes by taking the base-2 logarithm. We calculated per-amino-acid rates by averaging the per-site rates among the three sites composing each codon.

Protein Structures. We used *PyMOL* version 2.4.2[66] to visualize the per-codon evolutionary rates on each gene's protein structure. We used model 4F7P[94] from Protein Data Bank[63] (`https://www.rcsb.org/`) for HLA-A, 6D2T[64] for HLA-B, 4NT6[95] for HLA-C, 4P4K[96] for HLA-DPB1, 1UVQ[97] for HLA-DQB1, and 2IAM[65] for HLA-DRB1.

We calculated the distances between all amino acids of the HLA molecule and all amino acids of the peptide in *PyMOL*, then took the minimum distance to represent that amino acid's overall distance to the peptide. We averaged the minimum distances over three alternative structures for each gene, to prevent relying too heavily on a particular structure. We used models 4F7P[94], 6J1V[98], and 3MGO[99] from Protein Data Bank[63] for HLA-A; 6D2T[64], 3BVN[100], and 6PYJ[101] for HLA-B; 4NT6[95], 5W67[102], and 5VGE[103] for HLA-C; 4P4K[96], 3LQZ[104], and 3WEX[105] for HLA-DPB1; 1UVQ[97], 2NNA[106], and 4D8P[107] for HLA-DQB1; and 2IAM[65], 6ATF[108], and 5LAX[109] for HLA-DRB1.

Synonymous Diversity. Synonymous diversity of the IPD alleles was calculated pairwise using *codeml*[59,60] on subsets of the coding sequence. We used a larger set of alleles than we used in *BEAST2*, because codeml is not as computationally limited by the number of samples. We used all alleles that both 1) have the entire coding sequence available in the database (because many submitted alleles are the result of sequencing exons 2 and 3 alone) and 2) do not have a nonsense mutation. This set consisted of 289 alleles for HLA-A, 423 for HLA-B, 138 for HLA-C, 255 for HLA-DPB1, 352 for HLA-DQB1, and 287 for HLA-DRB1 (lists of alleles provided as Supplementary Files). This larger set is a superset of the alleles used for the *BEAST2* analysis. We ran *codeml* using runmode=−2 for pairwise calculation (to avoid relying on a species tree), seqtype=1 for codon-based, CodonFreq=1 to estimate the equilibrium codon frequencies from the average nucleotide frequencies, model=0 and NSsites=0 to specify the basic codon substitution model, fix_kappa=0 to estimate the κ parameter with initial kappa=3 for all genes except HLA-C, where initial kappa=2, and fix_omega=0 to estimate the ω parameter with initial omega=0.5. *codeml* also outputted 4-fold degenerate sites, which we used for normalization of the *BEAST2* rates, as described above.

Disease Literature. We conducted a literature search for papers that used HLA fine-mapping to discover disease associations, limiting our selection to those including at least 1000 cases and which identified putatively independent signals via conditional analysis. We included all independent signals identified as significant by the original authors, regardless of whether they were entire alleles, amino acids, or SNPs. If there was more than one study for the same disease, but in different populations, we included all unique independent hits. References for studies are listed in Supplementary Table S2. We also collected associations between amino acids and TCR phenotypes, with references listed in Supplementary Table S3. References for the anchor residues that make up the peptide-binding pocket are listed in Supplementary Table S4.

Polymorphic Amino Acid Positions. Amino acid allele frequencies were obtained from Luo et al.[110], who imputed HLA variation in 1000G using *SNP2HLA* (`https://github.com/immunogenomics/HLA-TAPAS/blob/master/resources/1000G.bglv4.FRQ.frq`). Amino acid positions with MAF> 1% were considered polymorphic for the purposes of plotting.

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