

ARTICLE

Interleukin-37 gene variants segregated anciently coexist during hominid evolution

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IL37 is a member of IL-1 cytokine family but conveys anti-inflammatory functions. The biological characteristic and genetic heterogeneity of IL37 are not fully understood yet. Here using the whole-genome sequencing data from 1000 Genomes Project, we performed population and evolutionary genetic analysis of human *IL37* gene. First, 2184 *IL37* gene sequences from different human populations were retrieved. The IL37 protein sequences were inferred from the coding DNA sequences and multiple species alignment was made. Then, the phylogenetic tree of IL37 was built and dN/dS ratios were calculated for each evolutionary branch, the classic McDonald and Kreitman test was also performed. Next, we conducted intraspecific evolutionary genetic analysis and built the genealogy network of 116 unique *IL37* haplotypes through median-joining network analysis. Finally, we compared *IL37* sequences between the modern and archaic humans. Our results for the first time provide solid evidence that common IL37 variants other than NCBI reference sequence are present worldwide. Our data also supports that IL37 variants are shaped and maintained by selection instead of neutral evolution. We further identified that human *IL37* variants consist of two major haplogroups and their presence in archaic humans corroborates its ancient origin in hominid evolution. In conclusion, these data indicate that common *IL37* variants are maintained among human populations by selective force, suggesting their potential involvements in immune regulation and human diseases. In addition, the ancient history of *IL37* variants reveals interesting insight into the complicated human evolutionary history.

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INTRODUCTION

IL37, a novel member of the IL-1 family also known as IL-1F7, was discovered by several independent groups in 2000.¹ Its function is not completely understood yet. Interestingly, distinct from most IL-1 family members, which have been characterized as proinflammatory, IL37 has emerged as a fundamental immune inhibitor.² A total of five spliced variants (IL37a–e) exist as IL37 transcripts. Among them, IL37b is the largest member with 218 amino acids and encoded by five exons spanning the *IL37* gene, of which exons 1 and 2 encode the prodomain and exons 3–5 encode the 12 putative β -strands forming β -trefoil structure, which is characteristic of the IL-1 family molecules.^{1,3} The IL37b is a precursor, which is thought to be processed by caspase-1 into the mature form and translocates actively into the cell nucleus.⁴ IL37b mRNA has been found in multiple human tissues, including the lymph node, thymus, bone marrow, placenta, lung and testis.⁵ IL37 protein level in PBMCs and dendritic cells is upregulated when stimulated by TLR ligands or proinflammatory cytokines.¹ *In vitro* overexpression of IL37 in macrophages or epithelial cells could greatly dampen production of major proinflammatory cytokines, including IL-1 α , IL-1 β , TNF- α , IL-6 and MIP-2.^{1,2,6} *In vivo*, IL37 transgene protects mice from LPS-induced shock, chemical-induced colitis.^{7,8} However, the role of IL37 in physiological conditions and its involvement in human diseases remained largely unknown.

With the development of DNA sequencing and genotyping technology, genetic methods become more powerful at unveiling the function of human genes. Among these methods, evolutionary

genetics deals with variations within human populations. The basis for this approach is that evolution will clear the deleterious mutations and select the beneficial ones among human populations, so it leaves behind signal that could be detected using population genetic variation data and statistic tools.⁹ As a complement to clinical and epidemiological genetic approaches, the evolutionary genetic approach has increased our understanding of the evolutionary forces that shape the human genome and provided important insights into the function of selected genes.¹⁰ Human immune system as an interface between the body and external world is especially prone to be affected by selective pressure, for example, various pathogens and other immune disorders. Indeed, genome-wide scanning of selection signals has often found immune genes as preferred candidates.¹¹ Identifying the extents and types of natural selection acting upon genes involved in immunity-related processes has already revealed insights of host defense mediated by them, as well as delineated those genes being essential in host defenses. So far, human pattern recognition receptors and interferons have been analyzed using this approach, attesting its effectiveness in revealing functional aspects of immune genes.^{12–14} However, the extent to which human IL37 have been subject to natural selection remains largely unknown. In addition, we are interested by the fact that *IL37* gene has been lost in human's closest relative chimpanzee during the evolutionary process.¹⁵ Here utilizing data from 1000 Genomes Project,¹⁶ we report that IL37 variant proteins other than reference sequence are common in human populations. Evolutionary genetic investigation of *IL37* variations reveals its significant deviation from neutrality. We present that modern human *IL37* variants consist

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of two major haplogroups and have an early origin during hominid evolution.

MATERIALS AND METHODS

Variant data set and sequences

The 1000 Genomes project phase1 data were downloaded from the data repository (ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/phase1/analysis_results/integrated_call_sets/). This data set contains the phased high-quality variant calls of both single-nucleotide polymorphisms (SNPs) and short insertions and deletions for 1092 individuals from four major populations, including 379 Europeans (EUR), 286 East Asians (ASN), 246 Africans (AFR) and 181 admixed Americans (AMR). The high-quality whole-genome sequence data of archaic human (including Neanderthal and Denisova) were downloaded from <http://cdna.eva.mpg.de/>. Ancestral sequences of human and gorilla were downloaded from Ensembl (<http://www.ensembl.org>). In addition, the low-coverage Neanderthal sequences representing 72% of *IL37* gene locus were retrieved from EBI ftp site (<ftp://ftp.ebi.ac.uk/pub/databases/ensembl/neandertal>).

Among the five *IL37* transcripts, transcript isoform 1 (*IL37b*) is the largest and best characterized one, which was chosen for the current study with no further indication. *IL37* NCBI RefSeq protein (NP_055254.2) and cDNA (NM_014439.3) orthologous sequences for 10 non-human primates and Canis were downloaded from Ensembl website.

Human *IL37* gene sequence reconstruction and linkage disequilibrium block inference

The variant information in human genome region chr2.hg19:g.113670547_113676458 corresponding to transcribed region of *IL37b* were extracted from the downloaded data. The exons were numbered like in NG_029219.1. *IL37* genomic sequences for 1092 individuals were inferred by replacing bases of reference sequence with corresponding variant bases borrowing the same logic as FastaAlternateReferenceMaker tool of GATK software package (https://www.broadinstitute.org/gatk/gatkdocs/org_broadinstitute_gatk_tools_walkers_fasta_FastaAlternateReferenceMaker.php). Haploview 4.2 program was used to infer linkage disequilibrium (LD) patterns and values of the target region as indicated in the figure using polymorphisms with minor allele frequencies >1%.

DNA polymorphism analysis and variant annotation

The DNA polymorphic parameters including the number of segregation site, number of haplotypes, haplotype diversity and nucleotide diversity for human *IL37* gene were analyzed by DnaSP5.10.01 (Barcelona, Spain). The variants in target region were annotated by ANNOVAR.¹⁷ For variant effect prediction, the SIFT (Genomic Institute of Singapore) and Polyphen (Boston, MA, USA) scores were acquired from Ensembl website.

Sequence alignment and phylogenetic analysis

Multiple species alignments of *IL37* protein sequences were performed using Clustal-omega-1.2.0 (Dublin, Ireland) followed by manual curation. The curated protein alignments were then converted to corresponding codon alignments by PAL2NAL online web server.¹⁸ Phylogenetic tree was constructed by SeaView 4.5.0 (Villeurbanne, France) using the method of neighbor joining based on *IL37* cDNA sequence alignments. dN, dS calculation and phylogenetic tree manipulations were performed using python package ETE2.2,¹⁹ which calls codeml of PAML4 package²⁰ with branch model for dN and dS calculation at the backend.

Haplotype network analysis

Haplotype network was constructed using NETWORK 4.6.1.2 (Fluxus)²¹ with method of median joining (MJ). To root the haplotype network, gorilla *IL37* sequence and human-gorilla ancestral sequence were added to 1000 Genomes data set. As the large divergence between Gorilla and human sequences poses challenge for inferring the correct genealogy network, the most recent common ancestor (MRCA) of all human haplotypes were added to facilitate MJ network construction. This MRCA sequence was deduced by a parsimonious way in that all shared derived alleles in 1000 Genomes samples were assigned derived alleles, whereas all other sites should be ancestral alleles. The segregation time of

two major human *IL37* haplogroups from MRCA were estimated based on the lineage specific molecular clock calibrated by the divergence time 10 million years ago (Mya) and 110 divergent sites between gorilla and human in 5.9-kb genomic sequence of *IL37* genes, which is exactly located in the LD block.

McDonald and Kreitman test

McDonald and Kreitman (MK) test was performed by online server tool MKT at <http://mkt.uab.es> with non-synonymous and synonymous changes selected as the types of analysis.

Intraspecific evolutionary genetic analysis

The statistics of Tajima's D, Fu's Fs, Fu and Li's F* and D* for the studied genes were calculated using population variation data by DnaSP5.10.01. Fst values among different populations were calculated using VCFtools (<http://vcftools.sourceforge.net/>).

The statistical significance of each test score was evaluated among an empirical distribution of the corresponding test scores of 1114 known RefSeq immune genes, which are listed in Supplementary Table S5. More detailed information about the methods can be found on the Supplementary Materials.

RESULTS

General population genetic statistics

The *IL37* gene and its 15 kb flanking sequences were retrieved from 1000 Genomes Project data as described in the methods. As many analyses can be performed only effectively on regions that have experienced little or no recombination, we therefore investigated the LD structure of the region and identified a 17 kb LD block that contained the entire transcribed region of *IL37* gene (Supplementary Figure S1). All subsequent genetic analyses were then confined to the transcribed region located in this LD block. In our samples of 2184 chromosomes, we detected in total 114 SNPs and analyzed the summary population statistics (Table 1). We found that both nucleotide and haplotype diversity were much higher in AFR compared with EUR and ASN, consistent with the recent African origin hypothesis of modern human. Our data also showed 14 non-synonymous and 1 nonsense substitutions in *IL37* genes (Supplementary Table S1). Supplementary Table S2 shows the numbers and distributions of missense and nonsense substitutions in *IL37* among different populations.

IL37 variant proteins and their distributions among human populations

The fact that many non-synonymous mutations are common polymorphisms (>5%) indicates that *IL37* variant proteins are common among different human populations. Therefore, we decided to find how many variant proteins there are and how they distributed geographically. Through deducing the protein sequences from the coding DNA sequences, we found in total 14 protein variants among human populations including one truncated protein caused by an early stop codon (Figure 1). Three major variants together account for >97% of all the sequences. Interestingly, the NCBI reference (NP_055254.2) is only dominant in AFR and a variant (*IL37*-Var1) with c.92G>T (p.(Gly31Val)) and c.124A>G (p.(Thr42Ala)) substitutions dominates in non-AFR. The third major variant (*IL37*-Var2), which is roughly 16% in AFR and 7% globally, differs at five sites with other major variants, including c.149C>G (p.(Pro50Arg)), c.161A>G (p.(Asn54Ser)), c.324G>A (p.(Pro108Leu)), c.490T>C (p.(Trp164Arg)) and c.652G>A (p.(Asp218Asn)). Notably, all these five non-synonymous SNPs are in a perfect LD with $r^2 = 1$ in all of our samples (Supplementary Figure S1E). To further reveal their functional consequences, we used scores from both Polyphen and SIFT programs to predict the effects of non-synonymous changes on *IL37* protein (Supplementary Table S1). According to Polyphen scores, five

Table 1 Population genetic parameters of human *IL37* gene

Population	n	S	Hap	Hd	π
AFR	492	84	65	0.904	0.00249
AMR	362	65	29	0.748	0.001385
ASN	572	61	24	0.773	0.000775
EUR	758	64	37	0.737	0.001545
Global	2184	115	115	0.826	0.001729

Abbreviations: AFR, Africans; AMR, Admixed Americans; ASN, Asians; EUR, Europeans; Hap, number of haplotypes; Hd, haplotype diversity; n, number of chromosomes; π , nucleotide diversity; S, number of segregation sites.
5.9-kb-transcribed region of human *IL37* genes were analyzed.

non-synonymous sites were predicted to be possibly damaging (0.453–0.956) and two sites were probably damaging (≥ 0.957). According to SIFT prediction, two and three sites predicted by Polyphen to be probably and possibly damaging respectively were also predicted to be deleterious (≤ 0.05).

Multiple species alignment of IL37 proteins

To assess the evolutionary processes, we downloaded 11 mammalian IL37 protein orthologues from Ensemble database and aligned them with three major human variants (Figure 2). We found that IL37 is conserved from macaque, apes to humans. For example, human

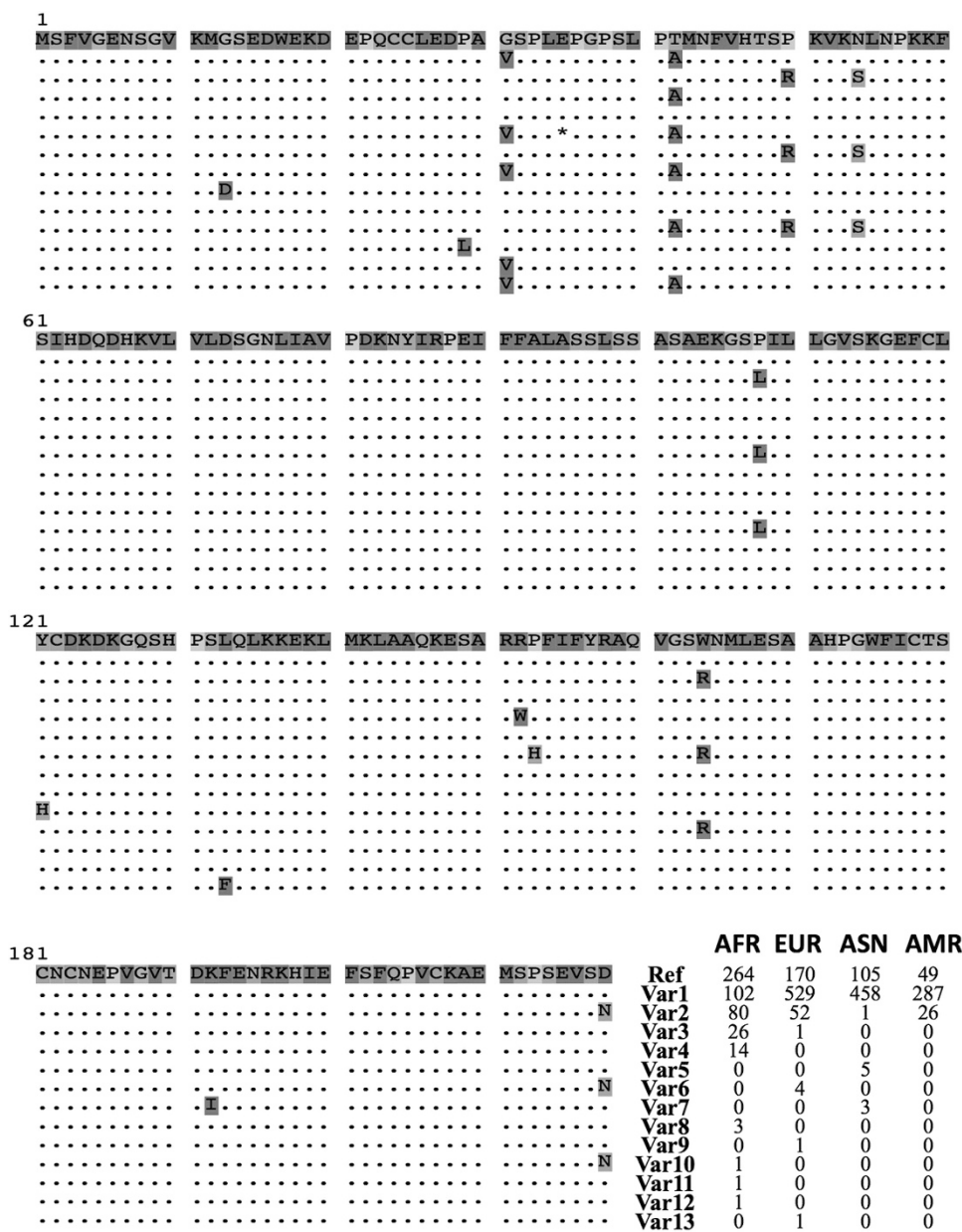


Figure 1 IL37 variant proteins and their distributions among human populations. Fourteen unique protein sequences including the reference IL37 protein sequence (NP_055254.2) from NCBI were identified in 1000 Genomes samples. These protein sequences were aligned by Clustal-omega followed by manual curation. Frequencies of protein variants among different populations are shown to the right of the sequences.

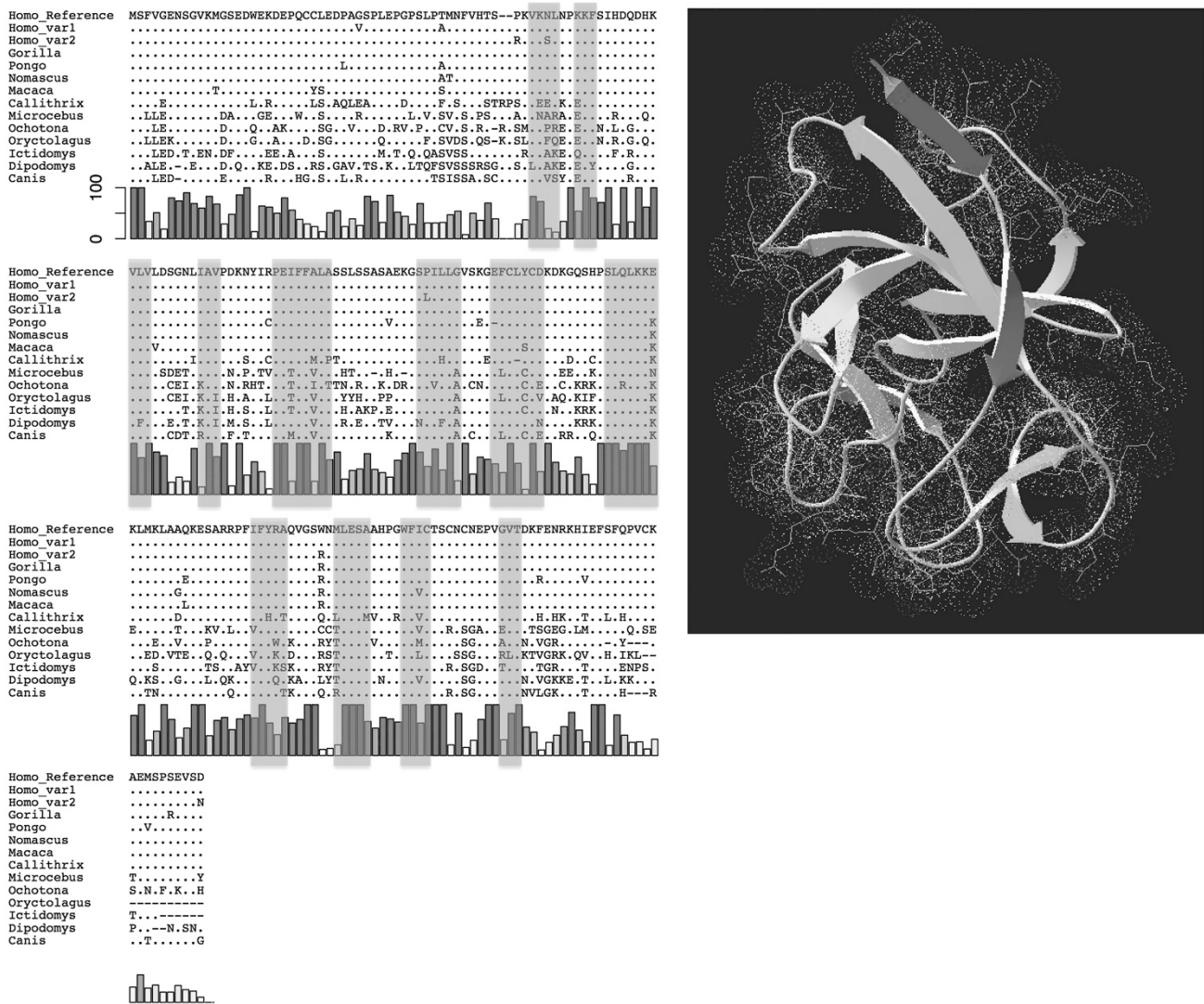


Figure 2 Sequence alignment of IL37 proteins from multiple species. Three major IL37 variant sequences identified in 1000 Genomes samples and 11 non-human mammalian orthologous sequences (10 primates and Canis) were aligned by Clustal-omega. Nucleotide positions identical to human reference IL37 sequence are indicated as dots. Grey bars under the sequence alignment depict the conservation profile of the corresponding amino-acid residues, with 100 indicates complete conservation. Shaded regions correspond to predicted secondary structure of β -sheet in 3D protein structure (right panel), which constitute the basic structural framework of IL-1 family members. The cartoon view in the right panel with predicted 3D protein structure of IL37 was created by SWISS-MODEL (<http://swissmodel.expasy.org>).

reference sequence only differs at two and nine sites with gorilla and macaque sequences, respectively. However, human Var1 and Var2, the two major human variants, differ at seven positions with each other. Clearly, this is a much large divergence than expected.

Evolutionary genetics analysis of human *IL37* genes

One of the key aims of evolutionary genetic study is to find whether the observed genetic variations are shaped by neutrality or selection. For this purpose, we first constructed the phylogenetic tree based on IL37 cDNA sequences using neighbor-joining method. Next, we computed the synonymous (dS) and non-synonymous (dN) substitution rate along each branch of the tree (Figure 3). Our data showed that most dN/dS ratios of the primate lineages, except macaque are less than one indicating a prevalent purifying selection. Interestingly, this purifying selection mode is, however, reversed (indicated by dN/dS > 1 in Figure 3) in most recent lineages leading to modern humans with accumulation of many non-synonymous substitutions and few synonymous ones.

We then used another classical method, the MK test, to confirm the evolutionary forces shaping IL37 diversity after the divergence of the human and gorilla. Under the MK test, the ratio of non-synonymous: synonymous polymorphisms within humans was compared with ratio of fixed non-synonymous: synonymous divergences between human and gorilla, using Fisher's exact test. The ratios of polymorphism and divergence are expected to be equal under neutrality. Our analysis of interspecific divergence between gorilla and humans found 5.12 and 1.00 (Jukes and Cantor corrected) fixed differences at synonymous and non-synonymous sites, respectively. Table 2 contrasts the interspecific divergence with the degree of intraspecific polymorphism found in our samples using the MK test. The significant result ($P=0.01467$) confirmed that human *IL37* genetic varieties deviated from neutrality.

To further reveal the signals of recent selection and local adaptation of *IL37* gene, we used classic tests such as Tajima's D, Fu's Fs, Fu and Li's F* and D* and Fst based on analyzing intraspecific polymorphisms

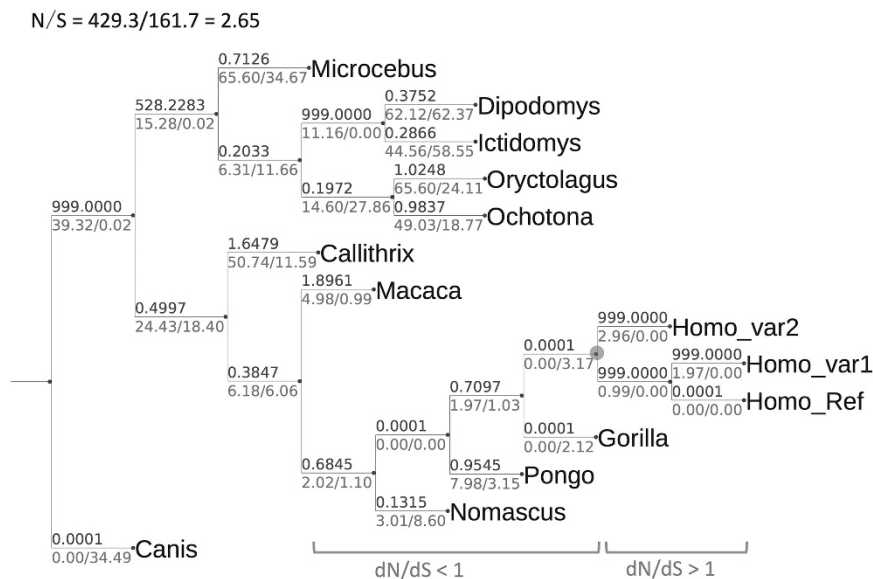


Figure 3 The dN/dS ratios of different evolutionary lineages in primates. Phylogenetic tree was constructed using neighbor-joining method using IL37 orthologous sequences from multiple species. dN and dS for each evolutionary branch was calculated by codeml of PAML4 with branch model. The values above represent dN/dS ratios and the values below correspond to dN and dS, respectively. The enlarged internal node indicates the MRCA of modern humans. Distinct primate evolutionary phases, labeled as $dN/dS < 1$ and $dN/dS > 1$, are indicated before and after this node.

Table 2 Contingency table of MK test for *IL37* gene

	Polymorphism	Divergence ^a	Total
Synonymous	4	5.12	9.12
Non-synonymous	14 ^b	1.00	15
Total	18	6.12	24.12

Abbreviation: MK, McDonald and Kreitman.

^aCorrected by Jukes and Cantor method.

^bExclude the nonsense mutation. P -value=0.01467 (Fisher's exact test).

among different human populations. We calculated the statistic values of 1114 RefSeq immune genes and used the empirical approach to evaluate the significance of corresponding statistics for *IL37* gene (Supplementary Table S3 and Supplementary Figure S2). Our data showed that Tajima's D for AFR were within the 4% of the positive side of the empirical distribution, whereas F_u and L_i 's D^* and F^* for ASN were significantly negative ($P=0.01$) according to both coalescent simulation (data not shown) and empirical distribution (Supplementary Table S3), indicating excess of rare alleles in ASN. Pairwise population genetic differentiation (measured by F_{st} tests) showed that many variant sites of *IL37* gene displayed large genetic differences in AFR vs ASN comparison, including the five non-synonymous sites defining the two major haplogroups of human *IL37* gene (described in the following part of this study), which showed large F_{st} values (Supplementary Figure S2).

MJ network analysis of human *IL37* haplotypes

In our data, 114 haplotypes of human *IL37* were identified (Supplementary Figure S3 and Supplementary Table S4). A MJ network was then constructed to show the genealogical relationships between the inferred haplotypes of the LD block (Figure 4). The topology of this network undoubtedly shows that two major clades (haplogroups 1 and 2) are separated by long branch length, each

containing one haplogroup. Within haplogroup 1, there are two subgroups. Subgroup 1 is substantially of AFR origin, whereas subgroup 2 is dominant in Eurasians. Interestingly, we also noticed two distinct evolutionary phases after the split between human and gorilla (Figure 4). The first phase includes just synonymous mutations and the second phase includes many non-synonymous mutations, suggesting that the human *IL37* variants were shaped by selection during the second phase of human evolution. We next estimated the time to MRCA of the haplogroups using phylogeny-based methods measuring ρ , the average distance of descendant haplotypes from a specified root. On the basis of 110 divergences between human and Gorilla *IL37* sequences where the split time is assumed to be 10 Mya, we estimated the haplogroups 1 and 2 began to diverge around 3.6 Mya.

Two major *IL37* haplogroups in modern humans segregated earlier during hominid evolution

To further confirm the early divergent time between human *IL37* variants, we took advantage of the newly published archaic human sequences, both the Neanderthals and Denisova. In agreement with the early origin of two *IL37* haplogroups, we found that the two archaic human *IL37* sequences exactly belong to haplogroup 1 and 2, respectively (Supplementary Figure S3 and Figure 4). These data strongly suggest that the human *IL37* variants originated from a common ancestor very earlier during hominid evolution and passed down to all the different human lineages ever since.

DISCUSSION

Human *IL37*, a unique member of IL-1 family cytokines, exerts anti-inflammatory rather than proinflammatory functions. This characteristic endows *IL37* as one of the few known inhibitory cytokines that balance immune reactions.² Although its biological function is not elucidated completely, many studies indicate a protective role of *IL37* on immunopathogenesis through reducing anti-inflammatory cytokines from innate immune cells.²² Here to better understand this

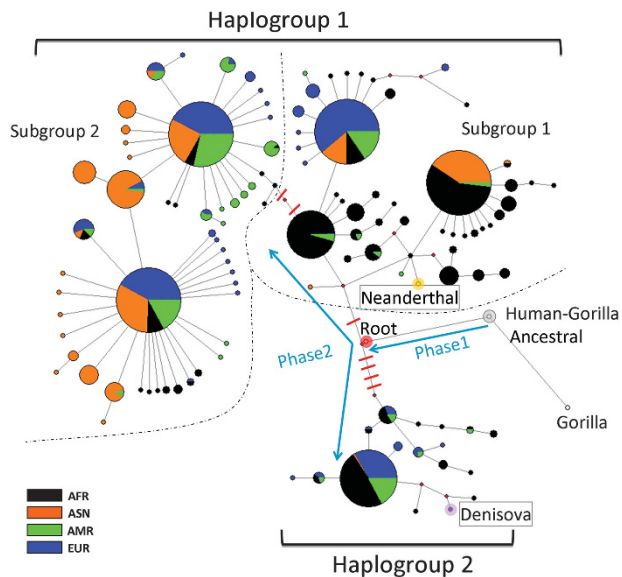


Figure 4 Haplotype network of archaic and modern human *IL37* haplotypes. A total of 119 haplotypes, including 114 modern human, 1 common ancestor of modern human, 2 archaic human, 1 gorilla and 1 human-gorilla ancestor haplotypes, were included for network construction. The sequence of common ancestor of modern human was deduced as described in method section and included to facilitate median-joining network construction. Gorilla and human-gorilla ancestral haplotypes were used to calibrate the molecular clock for evolution time estimation. Node labeled as ROOT (expanded red colored) corresponds to the reconstructed human common ancestor. The human haplotypes are divided into haplogroups 1 and 2 by a long branch with five non-synonymous substitutions. Dashed lines delineate two subgroups of haplogroup 1, which is separated by two non-synonymous substitutions. Phase 1 and phase 2 indicate two phases of hominid evolution after human-gorilla split. Non-synonymous substitutions only occurred at phase 2. Other nodes are labeled as indicated.

novel cytokine, we investigated its variation patterns among different populations using evolutionary approaches and made a few novel findings: (1) *IL37* variant proteins different from reference sequence are common among various human populations; (2) evolutionary genetic analysis suggests that human *IL37* variants have evolved by selection and deviate from neutrality and (3) human *IL37* variants consist of two major haplogroups which segregated anciently and were maintained in ancient hominid lineages leading to *Homo sapiens*. The identification of common *IL37* variant proteins has two important implications for future research. First, a major *IL37* variant (Var2) differs from reference sequence at five non-synonymous sites all located in the core region forming the characteristic IL-1 β -Trefoil structure, likely leading to a different function. Therefore, we propose that the biological functions of *IL37* variants need to be verified and compared with earlier experimental results using NCBI reference protein.^{4,8,22} Second, our data provides valuable guidance on picking SNPs for disease association studies. Previous reports suggested that *IL37* was involved in the development of various inflammatory conditions, including ankylosing spondylitis and rheumatoid arthritis.^{23–25} However, all these studies were based on genotyping rs3811047:A>G, which result in c.124A>G (p.(Thr42Ala)) substitution and does not differentiate between major *IL37* variants identified in this study. On the basis of our data, we recommend genotyping any one of the five non-synonymous SNPs, rs2708943:C>G, rs2723183:A>G, rs2723187:C>T, rs2708947:C>T or rs2723192:A>G, to

differentiate between *IL37* haplogroups 1 and 2, which differ at least at five non-synonymous sites and probably result in different susceptibility to human diseases.

Interestingly, *IL37* gene was lost owing to deletion in Chimpanzee during evolution while conserved in other great apes and modern humans.¹⁵ The complete loss of *IL37* in Chimps without pathological consequences indicates a nonessential role of *IL37* in overall fitness of Chimpanzee. However, its function in other species or diseased settings should not be excluded concomitantly. As recent data suggested, there are human disease causing loci but rather fixed in gorillas with normal phenotype.²⁶ Indeed, our data supports that *IL37* has an important role in immune regulation in humans and other primates. First, the dN/dS ratios in gibbon, orangutan and gorilla all indicate a purifying selection suggesting a longstanding critical role of *IL37* along with primate evolution. Second, the dN/dS ratios of human *IL37* variants and MK test all show that human *IL37* variations deviate from neutrality. Third, we noticed that the five non-synonymous sites defining the *IL37*-Var2 all congregate in the predicted functional region of the protein, consistent with that human *IL37* variation is shaped by selection and not neutral changes. During modern human evolution, pathogens constantly represent as an important selective force and therefore the adaptation of the immune system has been influenced by these pressures. Many studies have revealed that immune genes were indeed enriched for adaptive selection.^{9,10} On the basis of the fact that human *IL37* genes consist of two clearly separated haplogroups, we postulated that this could be formed by balancing selection when earlier hominid faced new challenges, such as novel infectious agents or inflammatory diseases. Although it is still hard to predict the true selective forces and the relation between genotype and phenotype, we are attempted to think a counterbalance between the beneficial and deleterious effects of different variants leading to *IL37* selection, as this mechanism has been recently suggested to be involved in shaping the diversity of many other innate immune genes.^{27–29}

We believed that our genealogical analysis of *IL37* variants revealed interesting fact about the genome and human evolution. We calculated the time to MRCA (tMRCA) of human *IL37* and certainly it is an outlier in the human genome with 3.6 million years compared with the reported average 800 000 years.³⁰ This unusually long tMRCA supports the proposed balancing selection of human *IL37* gene. However, this could also be regarded as a relic of an ancient admixture event in Africa, which resulted in a deep divergence of the two *IL37* haplogroups, in agreement with the genetic communications among African archaic humans that gains more support recently.^{31,32} From the MJ network analysis, we immediately noticed the two phases of *IL37* evolution divided by a branching point. The first phase is characterized with no amino-acid changing substitutions after the split of gorilla and human ancestor, indicating a purifying selection phase and probably reflecting a stable environment during this stage of hominid evolution. The second phase is characterized by the accelerated non-synonymous changes with two haplogroups segregated eventually. The two-phase scenario is similar to the evolutionary selection patterns revealed by dN/dS ratios that support accelerated accumulation of non-synonymous substitutions during late phase of human evolution. We affirmed that these two haplogroups were maintained in human ancestors over million years as extinct Neanderthals and Denisova also harbored the corresponding *IL37* variants inherited from ancient ancestors. We speculate that coexistence of both the *IL37* haplogroups could benefit the survival of our African ancestors and it will be interesting to test whether there is a

heterozygous advantage when our ancestors facing new environment challenges.

Finally, we found that *IL37* haplogroup 2 had almost been completely lost in East ASN and the subgroup 2 in haplogroup 1 was now the dominant version in Eurasians. Recent positive selection and local adaptation to specific environment can result in such changes. In agreement with this speculation, we have detected signals of decreased genetic diversity in ASN and relatively high *Fst* scores of many *IL37* SNPs between ASN and AFR, including the five non-synonymous sites defining the two haplogroups, supporting the potential local adaptation in ASN. However, the complex demographic history in ASN, such as numerous migrations, bottleneck events and subsequent enhanced genetic drifts can easily result in loss of the minor haplogroup. This complexity prevented us to make a definite conclusion about the recent selection and local adaptation of *IL37* at this point.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

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