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Abstract

The classical HLA class I genes (HLA Ia) were extensively studied because of their implication in clinical fields and anthropology. Less is known about worldwide genetic diversity and linkage disequilibrium for non-classical HLA class I genes (HLA Ib) and HLA pseudogenes. Notably, *HLA-H,* which is deleted in a fraction of the population, remains scarcely explored. The aims of this study were 1/ to get further insight into *HLA-H* genetic diversity and into how this variability potentially affects its expression and 2/ to define HLA Ib worldwide allelic diversity and linkage.

Exome sequence data from the 1,000 Genomes Project were used to define second field HLA-A, -E, -F, -G and -H typing using PolyPheMe software. Allelic and two-loci haplotype frequencies were estimated using Gene[Rate] software both at worldwide and continental levels.

Eleven novel *HLA-H* alleles identified in exome data were validated by NGS performed on 25 genomic DNA samples from the same cohort. Phylogenetic analysis and frequency distribution of *HLA-H* alleles revealed three clades, each predominantly represented in Admixed American, European and East Asian populations, African populations and South Asian populations. Among these eleven novel alleles, two potentially encode complete transmembrane HLA proteins.

We confirm the high LD between *HLA-H* and *-A,* and between *HLA-H* and *-G*, and show the three genes have distinct worldwide allelic distribution. Conversely, *HLA-E* and *HLA-F* both showed little LD, displayed restricted allelic diversity and practically no difference in their distribution across the planet.

Our work thus reveals an unexpectedly high *HLA-H* genetic diversity, with alleles highly represented in Asia possibly encoding a functional HLA protein. Functional implication of these results remains to be explored, both in physiological and pathological contexts.

Keywords: genetic diversity; allele; haplotype; HLA Ib; Next Generation Sequencing

Abbreviations: Linkage Disequilibrium: LD; Natural Killer: NK

1. Introduction

The Major Histocompatibility Complex (MHC) region is the most studied genetic region of the human genome, in large part thanks to the presence of classical HLA class I *(HLA-A, -B* and *-C*) and HLA class II (*HLA-DR* and *-DQ*) genes. Its huge genetic diversity is challenging because of functional implication in many clinical fields such as transplant and graft outcome, or viral escape. However, this diversity also deeply contributed to anthropological science by helping to define *Homo sapiens* evolution and the earliest worldwide migration routes [1]. Conversely, less is known about worldwide genetic diversity and Linkage Disequilibrium (LD) of non-classical HLA class I genes (*HLA-E, -F* and *-G*) and of HLA class I pseudogenes. Among these, *HLA-E* and *-G* are the most studied, both at genetic diversity and at functional levels [2, 3]. The 1,000 Genomes Project [4] gives the outstanding opportunity to contribute to studying these loci [5-7].

Non classical HLA-E, -F and -G (HLA Ib) display specific features compared to classical HLA class I (HLA Ia) such as very low genetic polymorphism and restricted pattern of antigens presentation. Their role is not to elicit an immune response but rather to inhibit its activation.

HLA-E regulates natural killer cells (NK) and cytotoxic T-lymphocyte cells via its inhibitory receptor CD94/NKG2 [8-10]. HLA-E mRNA is expressed in most tissues [11] and HLA-E is mobilized at the cell surface by leader peptides of HLA Ia and HLA-G molecules. HLA-E also binds peptide ligands from stress proteins and viruses [12, 13]. The two main *HLA-E* alleles*, E*01:01* and *E*01:03*, display similar frequencies worldwide, suggesting an advantage for heterozygous carriers; *E*01:03* is associated with higher expression [5, 6, 14-19].

HLA-G modulates NK and cytotoxic T-lymphocyte mediated activity as well as B-lymphocyte proliferation and is involved in epithelial cell differentiation [9, 20, 21]. Many diseases involving immune tolerance were studied in regards to HLA-G expression variation, especially in pregnancy [22, 23]. Several studies associated genetic polymorphisms both at coding level and in regulatory regions with inter-individual expression variation [23]. *HLA-G* displays five main alleles with unequal worldwide distribution [7, 14, 18, 24-28].

HLA-F mRNA is expressed in most cell types and the protein is intracellular, and is mobilized at the cell surface of activated monocytes, NK, B-lymphocyte and T-lymphocyte [29, 30]. HLA-F, expressed in an open conformer form and whose function seems independent of peptide loading [31, 32] is implicated in immune system regulation in pregnancy, infection, autoimmunity and cancer, especially via its interaction with the inhibitory receptor KIR3DS1 [33, 34]. *HLA-F* displays four alleles defined at second field resolution, with *F*01:01* representing 90% of allelic diversity [14, 26, 35, 36].

We formerly reported in a French cohort that *HLA-A* and *-G* were both in highly significant pairwise Global Linkage Disequilibrium (GLD) with the HLA-H locus ($p<0.001$), but displayed no exclusive association with either *HLA-E* or *HLA-F* [26].

HLA-H (formerly named *HLA-12.4* or *HLA-AR*), located at 55 Kbp away from the telomeric side of *HLA-A,* is more related to HLA-A than to *HLA-B* or *–C* [37, 38] and together with *HLA-J* and *-G* forms a group defined as *HLA-A* related genes [39].

HLA-H has orthologs in chimpanzees, bonobos and gorillas, hence the separation between *HLA-H* and other *HLA-A*-related genes predates the divergence of these species [40-42]. A proposed model of evolution suggests the duplication of an ancestral MHC-A/H block 30 million years ago evolving respectively into two genomic blocks containing MHC-A and MHC-H/AL loci [43]. A second duplication of the MHC-H/AL-containing block generated the MHC-H and MHC-AL blocks seven million years later. The latter was subsequently lost in humans but is retained in ~50% of chimpanzees by a balancing selection process [41, 43, 44].

Similarly to *HLA-E, -F* and *-G,* limited *HLA-H* polymorphism is documented in the IPD-IMGT/HLA Database 3.33. Indeed, the 12 *HLA-H* allelic variants display less than one hundred SNPs and deletions [45]. Sequence preservation can be interpreted by strong selection of primordial biological functions, or as inactivation by deleterious mutation of genes [38].

Although no transcription signals could be detected upstream from the signal coding sequence in the earliest study describing one *HLA-H* allele, the authors added in their note-added proof that in vitro transcription experiments showed a major transcript initiated upstream of the signal sequence [37]. In a recent study based on GeneChip Whole Transcript from Affymetrix, HLA-H transcriptional activity was shown [46]; these authors analyzed transcript profile modulation on breast cancer cells siRNA and drugs assays and showed a 2.3 to 2.5 fold upregulation of HLA-H, -F, -G, -E and -A.

One of the first *HLA-H* sequence descriptions showed that all exon/intron junctions were provided with the requisite splicing signal [37]. This allele (corresponding to *HLA-H*02:06* in the IPD and IMGT/HLA database) was described to encode 362 amino-acids in the Uniprot database (UniProtKB: P01893), whereas the *HLA-H*01:01:01:01* allele encodes 295 amino-acids. Although the peptide signal and non-cytoplasmic topological domain are encoded by most *HLA-H* alleles described in the IPD and IMGT/HLA database, none but *HLA-H*02:06* displays a full length transmembrane domain. Furthermore all HLA-H alleles lack the cysteine at codon 164 (amino-acid 188 including peptide signal length) critical for the disulfide bond of the α2 domain, impairing the antigen presenting function [38]. They do, however, present three of the four critical cysteines (position 101, 203, 259) (amino-acid 125, 227 and 283 including peptide signal length) and the invariant glycosylation site at position 86 (amino-acid 110 including peptide signal length) [37].

HLA-H was thus defined as a non-functional gene, or pseudogene, reinforced by its genetic deletion in a significant fraction of the population. This deletion of more than 50 kb between *HLA-G* and *HLA-A* loci, spanning *HLA-H*, is in LD with *HLA-A*23/24* and *HLA-G*01:04* alleles [15, 26, 47-49] Therefore, genetic and/or functional studies on HLA Ib have paid little, if any, attention to *HLA-H* genetic diversity.

The aims of this study were 1/ to get further insight into *HLA-H* genetic diversity and its possible implication in expression and 2/ to better define HLA Ib worldwide allelic diversity and haplotypic structure data.

2. Material and methods

1.1 Material

Analyses were performed both on exome sequence data from 2,693 individuals forming the 1,000 Genomes Project [4] and on 25 genomic DNA samples from the same cohort (Coriell Institute, Camden, New Jersey, USA).

1.2 *HLA* allelic typing from the 1,000 Genomes Project

HLA-A second field allelic typing was from [50]. *HLA-E, -F, -G* and *-H* allelic assignment at the second field was performed with the PolyPheMe software v1.2 (Xegen, Gemenos, France) [50] using the IPD-IMGT/HLA Database 3.33 as reference [45] .Briefly, HLA typing first involved isolation of all the reads related to *HLA* loci using Bowtie 2 [51]. The reads thus isolated were assigned to each locus targeted (*HLA-E, -F, -G* and *-H*) using an "end to end" mapping step with Bowtie 2 [51]. The positive reference datasets included all the *HLA* alleles of each locus investigated. The negative reference dataset included all the alleles from related loci (*HLA* gene and pseudogene sequences except *HLA-E, -F, -G* and *-H*). FASTQ files containing exclusively the specific sequence reads for each locus were generated. For each locus, first field-level types were determined and resolution was then incremented to second field. In this analysis, all loci with at least 300 specific reads identified were analyzed and typed using all the variable positions described in the IPD-IMGT/HLA Database 3.33 [45].

1.3 *HLA-H* new allele identification and confirmation, phylogenetic analysis and putative protein prediction

HLA-H typing was not possible for many samples' exome sequence data, *i.e.* no allele from the IPD-IMGT/HLA Database 3.33 corresponded to the observed SNP combination. Whole sequence analysis revealed unreported SNP combinations and/or sequence variations in the IPD-IMGT/HLA Database 3.33 [45]. These new alleles were thus explored in samples which were hemizygous for *HLA-H*, *i.e.* displaying one allele *HLA-A*23/24* [15, 26, 47-49].
These new *HLA-H* alleles identified in exome sequence data were confirmed using targeted Next Generation Sequencing (NGS) of 25 genomic DNA samples hemizygous for *HLA-H* from the 1,000 Genomes Project (Coriell Institute, Camden, New Jersey, USA). *HLA-H* was amplified by long-range PCR (primer sequences CAAACTCCGTGGGTGASTTT and TGGCTGCTACTCTGGGTTCT, from position -483 to 4418 according to the IPD-IMGT/HLA Database [45]), generating an amplicon of approximately 4,900 bp depending on alleles. PCR fragments were sequenced as previously described [52] using a MiSeq NGS platform (Illumina, Eindhoven, The Netherlands). NGS data were analyzed using PolyPheMe software v1.2.

HLA-H cDNA sequences were aligned using the multiple sequence alignment tool MUSCLE in the Molecular Evolutionary Genetics Analysis (MEGA) software version X [53]. Evolutionary relationships among *HLA-H* cDNA sequences were inferred using the Neighbor-Joining method with 1,000 bootstrap replicates. Evolutionary distances were computed using the p-distance method and units were the number of base differences per site.

Putative protein prediction from *HLA-H* alleles was performed based on *HLA-H* cDNA sequences using Expasy [54]. *HLA-A*02:01:01:01, G*01:01:01:01, H*01:01:01:01* and *H*02:06* alleles were added for reference *HLA-A*02:01:01:01, HLA-G*01:01:01:01, HLA-H*01:01:01:01* alleles were selected because of their high frequency in populations of European descent; they are also commonly used as reference sequences, particularly in the IMGT/ HLA database. *HLA-H*02:06* was selected because it encodes the protein with the longest amino-acid sequence with putative functional patterns. Peptide sequence characteristics for specific domains, motifs or sites were analyzed according to Prosite (https://prosite.expasy.org/), Uniprot (https://www.uniprot.org/) and Phobius (http://phobius.sbc.su.se/). Prosite relies on documentation entries describing protein

domains, families and functional sites. Uniprot uses the Basic Local Alignment Search Tool (BLAST) to find regions of local similarity between sequences. Phobius is used for prediction of transmembrane topology and signal peptides [55-57].

1.4 *HLA-A, E, -F, -G* and *-H* allelic and two-loci haplotype analysis

Allelic and two-loci haplotype frequencies were estimated based on typing results of each individual at a worldwide population level and at continental level in African populations, Admixed American populations, European populations, East Asian populations and South Asian populations (see [4] for population description). Missing data at a locus led to the exclusion of the concerned sample from further analyses. No multiple imputations were used.

Frequencies were estimated using an EM algorithm implemented in the Gene[Rate] computer tools [58]. Two-loci Linkage Disequilibrium (LD) was investigated according to locus proximity, *i.e. HLA-E~HLA-A, HLA-A~HLA-H, HLA-H~HLA-G* and *HLA-G~HLA-F*. LD was assessed by a likelihood-ratio test on the frequency estimations [58] and was provided for specific pairs of alleles as a list of standardized residuals for each observed haplotype. Values greater than |2| were considered to be a significant deviation [59].

3. Results

1.1 HLA-H worldwide diversity analysis identifies 11 novel alleles

Eleven *HLA-H* novel alleles identified in exome data were validated by concordance with targeted NGS performed on identical DNA samples (Table 1). *HLA-H* novel alleles, submitted to Genbank and to the IPD-IMGT /HLA Database are described in Appendice Table 1. Official names for the eleven *HLA-H* novel alleles identified in this study submitted to the IPD-IMGT /HLA Database have been officially assigned by the WHO Nomenclature Committee. This followed the agreed policy and was subject to the conditions stated in the most recent Nomenclature Report [60].

1.2 HLA-H phylogenetic analysis defines three distinct groups

All *HLA-H* sequences, i.e. from the IPD-IMGT/HLA Database 3.33 and identified in this study (N=22), were aligned and evolutionary relationships among these cDNA sequences were inferred using the Neighbor-Joining method. The resulting phylogenetic tree (Figure 1A) shows three main clades. The first clade contains all the *HLA-H*01* alleles and the *H*03:01* allele; the second clade includes six *HLA-H*02* sequences (*HLA-H*02:01/02/03/03:02/05/11*); the third clade includes nine *HLA-H*02* sequences, seven of which are novel (*HLA-H*02:04/06/07/08/09/10/12/13/14*). The first and third clades contain sequences that were not observed in the individuals forming the 1,000 Genomes Project (*H*03:01* and *H*02:06* alleles, respectively) and that display divergent sequences (long branches). Thus, a second alignment containing all observed *HLA-H* sequences except the *H*03:01* and *H*02:06* alleles (N=20) was performed and their evolutionary relationships are shown in Figure X (Figure 1B). This phylogenetic tree displays the same groupings as the former one, without the divergent sequences.

1.3 Two novel HLA-H alleles display all patterns of full-length HLA protein

Putative protein prediction from the novel *HLA-H* alleles based on *HLA-H* cDNA sequences using Expasy [54] ranged from 18 amino-acid (AA) to 362 AA (Table 2). Peptide sequence analysis using Prosite, Uniprot and Phobius [55-57] are described in Table 2. Reference protein sequences encoded by *HLA-A*02:01:01:01, G*01:01:01:01* and *H*02:06* displayed all patterns of full-length HLA proteins whereas those encoded by *H*01:01:01:01* and *H*02:04* did not show any of them. Specific patterns of transmembrane HLA protein were found in new alleles *HLA-H*02:07* and *HLA-H*02:14:* a peptide signal, a non-cytoplasmic domain, a transmembrane domain, a cytoplasmic domain, a glycosylation site and a disulfide bond. The other alleles newly reported, as well as all *HLA-H* alleles described so far in the IPD-IMGT /HLA Database [45] lacked all or part of these critical domains and/or sites.

Coriell Samples	*HLA-H* Allele	IMGT Submission Number	Genbank Submission Number
HG03673 and NA20524	H*02:07	HWS10053785	MK387860
HG03419 and HG03679	H*02:08	HWS10053787	MK387861
HG03057 and HG03740	H*02:09	HWS10053789	MK387862
NA19143 and NA20510	H*01:03	HWS10053791	MK387859
HG03078 and NA19119	H*02:10	HWS10053793	MK387863
HG03061 and NA20805	H*01:01:02	HWS10053795	MK387856
HG03457 and NA18487	H*01:04	HWS10053797	MK387857
HG03894 and NA20540	H*02:03:02	HWS10053799	MK387864
NA19118	H*02:11	HWS10053801	MK387865
HG02851	H*02:12	HWS10053803	MK387866
HG03548	H*02:13	HWS10053805	MK387867
HG03838	H*02:14	HWS10053807	MK387868
NA20587	H*01:05	HWS10053809	MK387858
NA20521	H*01:02	NA	NA
HG02870	H*02:02	NA	NA
NA20535	H*02:04	NA	NA
HG03076	H*02:05	NA	NA

Table 1. DNA samples from the 1,000 Genomes Project used as control and validation samples.
DNA samples from the 1,000 Genomes Project (Coriell Institute, Camden, New Jersey, USA) displaying new *HLA-H* alleles identified in exome sequence data or displaying alleles used as controls (in grey) used in Next Generation Sequencing (NGS) analysis. All samples are hemizygote for *HLA-H*. NA: Not-Applicable.

Allele	IMGT Number	Genbank Number	Protein length prediction (Expasy)	Predicted features by Prosite tool (Expasy)	Predicted features by Uniprot (Blast)	Predicted features by Phobius
*A*02:01:01:01*	NA	NA	365	Domain Ig-like: 209-295 Disulfide bound: 227-283	Signal peptide: 1-24 Topological Domain: 25-307 Transmembrane Domain: 308-332 Topological Domain: 333-365	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-307 Transmembrane Domain: 308-332 Cytoplasmic Domain: 333-365
*G*01:01:01:01*	NA	NA	338	Domain Ig-like: 209-287 Disulfide bound: 227-283	Signal peptide: 1-24 Topological Domain: 25-307 Transmembrane Domain: 308-332 Topological Domain: 333-338	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-307 Transmembrane Domain: 308-332 Cytoplasmic Domain: 333-338
*H*01:01:01:01*	NA	NA	295	Domain Ig-like: 209-245 Absent feature: Disulfide bound	No annotation hit	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-295
*H*02:06*	NA	NA	362	Domain Ig-like: 209-297 Disulfide bound: 227-283	Signal peptide: 1-24 Glycosylation: 110 Disulfid bound: 227 283 Topological Domain: 25-307 Transmembrane Domain: 308-332 Topological Domain: 333-362	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-307 Transmembrane Domain: 308-332 Cytoplasmic Domain: 333-362
*H*02:07*	HWS10053785	MK387860	362	Domain Ig-like: 209-297 Disulfide bound: 227-283	Signal peptide: 1-24 Glycosylation: 110 Disulfid bound: 227 283 Topological Domain: 25-307 Transmembrane Domain: 308-332	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-307

					Topological Domain: 333-362	Transmembrane Domain: 308-332 Cytoplasmic Domain: 333-362
*H*02:08*	HWS10053787	MK387861	18	No hit	No BLAST hit	No hit
*H*02:09*	HWS10053789	MK387862	18	No hit	No BLAST hit	No hit
*H*01:03*	HWS10053791	MK387859	295	Domain Ig-like: 209-245 Absent feature: Disulfide bound	No annotation hit	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-295
*H*02:10*	HWS10053793	MK387863	215	No hit	Signal peptide: 1-26 Glycosylation: 112 Topological Domain: 27-215	Signal peptide: 1-26 N-Region: 1-8 H-Region:9-21 C-Region: 22-26 Non-Cytoplasmic Domain: 27-215
*H*01:01:02*	HWS10053795	MK387856	295	Domain Ig-like: 209 245 Absent feature: Disulfide bound	No annotation hit	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-295
*H*01:04*	HWS10053797	MK387857	295	Domain Ig-like: 209-245 Absent feature: Disulfide bound	No annotation hit	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-295
*H*02:03:02*	HWS10053799	MK387864	293	Domain Ig-like: 207-243 Absent feature: Disulfide bound	Signal peptide: 1-22 Glycosylation: 108 Topological Domain: 23-293	Signal peptide: 1-22 N-Region: 1-7 H-Region:8-17 C-Region: 18-222 Non-Cytoplasmic Domain: 23-293

*H*02:11*	HWS10053801	MK387865	295	Domain Ig-like: 207-243 Absent feature: Disulfide bound	Signal peptide: 1-24 Glycosylation: 110 Topological Domain: 25-295	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-295
*H*02:12*	HWS10053803	MK387866	18	No hit	No BLAST hit	No hit
*H*02:13*	HWS10053805	MK387867	221	No hit	Signal peptide: 1-26	Signal peptide: 1-26 N-Region: 1-8 H-Region:9-21 C-Region: 22-26 Non-Cytoplasmic Domain: 27-221
*H*02:14*	HWS10053807	MK387868	362	Domain Ig-like: 209-297 Disulfide bound: 227-283	Signal peptide: 1-24 Glycosylation: 110 Disulfid bound: 227 283 Topological Domain: 25-307 Transmembrane Domain: 308-332 Topological Domain: 333-362	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-307 Transmembrane Domain: 308-332 Cytoplasmic Domain: 333-362
*H*01:05*	HWS10053809	MK387858	254	Domain Ig-like: 209-254 Absent feature: Disulfide bound	Signal peptide: 1-24	Signal peptide: 1-24 N-Region: 1-7 H-Region:8-19 C-Region: 20-24 Non-Cytoplasmic Domain: 25-254

Table 2. Putative protein prediction from new *HLA-H* alleles' analysis
Putative protein prediction from new *HLA-H* alleles based on *HLA-H* cDNA sequences using Expasy [54]. Specific patterns are shown according to analysis using Prosite, Uniprot and Phobius [55-57]. For Uniprot analysis, alignment of the best match is shown. Different *HLA* alleles are shown as examples (in grey: *HLA-A*02:01:01:01, HLA-G*01:01:01:01, HLA-H*01:01:01:01* and *HLA-H*02:06*). NA: Not-Applicable.

1.1 HLA-A, -G and *-H* display distinct worldwide allelic distribution conversely to *HLA-E* and *–F.*

From the exome sequence data for 2,693 individuals forming the 1,000 Genomes Project, 2,160 (80%) were accurately resolved (*i.e.* defined without ambiguity at second field level) for *HLA-A, -E, -H, -F and -G* loci. Typing results for each sample and each locus are given in Appendice Table 2. Their allelic frequencies are given in Tables 3A to 3E. While thirty-seven second field *HLA-A* alleles represent over 95% of all worldwide alleles, the different populations defined at continental level display however a great disparity regarding the most representative *HLA-A* alleles (Table 3A). For instance, *HLA-A*11:01* was barely present in Africa, whereas it was most frequent in East Asian populations and found at intermediate frequencies in European populations.

Five second field *HLA-E* alleles represent more than 97% of frequencies (Table 3B), in concordance with published data showing an equal distribution between *HLA-E*01:01* and *E*01:03* [5, 6, 14-19]; *E*01:06* and *E*01:05* are respectively virtually only observed in Europe and in Africa. *HLA-E*01:09* displays very low frequencies everywhere and was not observed in Asia.

Four second field *HLA-F* alleles represent more than 96% of worldwide alleles (Table 3C), *F*01:01* was the most frequent. *F*01:03* was observed at over 10% in all continents, except in East Asian populations.

Five second field *HLA-G* alleles are observed (Table 3D), in accordance with published data [7, 14, 18, 24-28, 61, 62]. *HLA-G*01:06* is mostly present in South Asia and to a lesser extent in Europe, whereas *HLA-G*01:05N* has a higher frequency in Africa.

Nineteen second field *HLA-H* alleles represent 99% of worldwide frequencies, among which 11 novel alleles (Table 3E), displaying an unreported allelic frequency. *HLA-H*01:01* is the most frequent allele except in Africa, where *HLA-H*02:05* is more common. The deletion encompassing *HLA-H* (named *HLA-H*Del*) is observed at over 10% in all continents and is highly represented in East Asia. The new allele *HLA-H*02:07* has a higher frequency both in East and South Asian populations but is absent in Africa. This is in accordance with this allele, referred to as *H*02:04new* and defined by a silent G>A substitution at position 368 compared to *H*02:04,* being observed at ~9% in a French population [26]. Of note, *H*03:01* and *H*02:06* alleles, reported in early studies on *HLA-H* [37, 38] are not observed in the 1,000 Genomes Project panel.

HLA-A alleles	ALL (N=2157)	AFR (N=592)	EUR (N=416)	AMR (N=294)	EAS (N=446)	SAS (N=409)
*A*02:01*	**0.139**	**0.115**	**0.307**	**0.222**	**0.076**	**0.032**
*A*11:01*	**0.093**	0.001	**0.058**	**0.041**	**0.234**	**0.160**
*A*24:02*	**0.090**	0.007	**0.073**	**0.124**	**0.171**	**0.124**
*A*01:01*	**0.070**	0.028	**0.127**	**0.043**	0.020	**0.155**
*A*03:01*	**0.065**	**0.054**	**0.150**	**0.086**	0.011	**0.051**
*A*33:03*	**0.049**	**0.058**	0.006	0.005	**0.076**	**0.087**
*A*68:01*	**0.035**	**0.030**	0.030	**0.054**	0.007	**0.066**
*A*23:01*	**0.034**	**0.095**	0.024	0.025	0.000	0.005
*A*26:01*	**0.030**	0.019	**0.035**	0.014	**0.030**	**0.056**
*A*30:02*	0.030	**0.078**	0.016	**0.036**	0.000	0.004
*A*30:01*	0.029	**0.078**	0.011	0.012	0.014	0.009
*A*02:07*	0.026				**0.128**	
*A*31:01*	0.025	0.007	0.026	**0.045**	**0.034**	0.024
*A*68:02*	0.023	**0.070**	0.005	0.024		
*A*32:01*	0.022	0.011	**0.044**	0.019	0.006	**0.036**
*A*29:02*	0.022	0.026	**0.038**	**0.054**		
*A*02:11*	0.018	0.001		**0.032**		**0.075**
*A*74:01*	0.016	**0.056**		0.007		
*A*02:06*	0.015		0.001	0.018	**0.043**	0.019
*A*02:03*	0.015				**0.055**	0.020
*A*02:02*	0.013	**0.040**		0.015		
*A*33:01*	0.012	0.029	0.006	0.019		
*A*34:02*	0.011	**0.040**		0.003		
*A*36:01*	0.011	**0.041**				
*A*02:05*	0.009	0.016	0.006	0.012	0.001	0.009
*A*66:01*	0.008	0.023	0.006	0.003		0.001
*A*11:02*	0.007				**0.034**	
*A*29:01*	0.005	0.001		0.009	0.017	0.004
*A*24:07*	0.005				0.006	0.020
*A*23:17*	0.004	0.015		0.002		
*A*01:02*	0.004	0.014	0.001	0.002		
*A*66:02*	0.004	0.014				
*A*25:01*	0.004	0.000	0.016	0.005		
*A*80:01*	0.004	0.010	0.001	0.003		
*A*03:02*	0.002	0.001	0.002	0.003		0.005
*A*66:03*	0.002	0.006				
*A*02:22*	0.002			0.012		
Total	0.951	0.982	0.989	0.949	0.962	0.960

Table 3A.

HLA-E alleles	ALL (N=2157)	AFR (N=592)	EUR (N=416)	AMR (N=294)	EAS (N=446)	SAS (N=409)
*E*01:01*	**0.501**	**0.581**	**0.558**	**0.509**	**0.332**	**0.526**
*E*01:03*	**0.465**	**0.405**	**0.391**	**0.462**	**0.661**	**0.433**
*E*01:05*	0.004	0.013	0.004			
*E*01:06*	0.008		**0.036**	0.005		0.004
*E*01:09*	0.001	0.001	0.002	0.002		
Total	0.979	1.000	0.991	0.978	0.992	0.962

Table 3B.

HLA-F alleles	ALL (N=2157)	AFR (N=592)	EUR (N=416)	AMR (N=294)	EAS (N=446)	SAS (N=409)
*F*01:01*	**0.843**	**0.781**	**0.757**	**0.879**	**0.977**	**0.925**
*F*01:03*	**0.112**	**0.173**	**0.176**	**0.117**	0.011	**0.069**
*F*01:02*	0.005	0.017		0.003		
*F*01:05*	0.002				0.010	
Total	0.963	0.971	0.933	1.000	0.998	0.995

Table 3C.

HLA-G alleles	ALL (N=2157)	AFR (N=592)	EUR (N=416)	AMR (N=294)	EAS (N=446)	SAS (N=409)
*G*01:01*	**0.658**	**0.567**	**0.825**	**0.706**	**0.682**	**0.612**
*G*01:04*	**0.185**	**0.231**	**0.082**	**0.150**	**0.251**	**0.190**
*G*01:03*	**0.052**	**0.110**	0.028	**0.085**	0.006	0.027
*G*01:06*	**0.046**	0.004	**0.054**	0.028	0.015	**0.152**
*G*01:05N*	0.029	**0.078**	0.011	0.012	0.014	0.009
Total	0.970	0.990	0.999	0.981	0.966	0.990

Table 3D.

HLA-H alleles	ALL (N=2157)	AFR (N=592)	EUR (N=416)	AMR (N=294)	EAS (N=446)	SAS (N=409)
*H*01:01*	**0.234**	**0.121**	**0.310**	**0.311**	**0.360**	**0.152**
*H*Del*	**0.170**	**0.120**	**0.108**	**0.160**	**0.218**	**0.172**
*H*02:05*	**0.108**	**0.256**	**0.050**	**0.103**	0.019	**0.075**
*H*02:07*	**0.086**	0.001	**0.058**	**0.042**	**0.196**	**0.158**
*H*02:01*	**0.069**	0.021	**0.129**	**0.044**	0.020	**0.158**
*H*02:04*	**0.064**	**0.048**	**0.143**	**0.089**	0.011	**0.057**
*H*01:02*	**0.061**	**0.059**	**0.060**	0.028	**0.046**	**0.105**
*H*02:08*	**0.039**	**0.056**	0.006	0.005	**0.070**	**0.039**
*H*02:09*	**0.037**	**0.047**	0.027	**0.051**	**0.035**	0.026
*H*02:02*	0.027	0.027	**0.038**	**0.063**	0.016	0.004
*H*01:01:02*	0.023	**0.054**	0.015	**0.033**		0.004
*H*01:03*	0.022	**0.056**	0.006	0.028	0.001	0.010
*H*02:03:02*	0.021	0.013	**0.043**	0.015	0.003	**0.036**
*H*02:10*	0.017	**0.064**		0.002		
*H*01:04*	0.008	0.025	0.001	0.005		
*H*02:12*	0.006	0.009	0.006	0.016		
*H*02:11*	0.005	0.018		0.003		
*H*02:03*	0.002		0.001	0.003	0.005	0.004
*H*02:13*	0.002	0.006				
Total	0.999	1.000	0.999	1.000	1.000	0.999

Table 3E

Tables 3A, 3B, 3C, 3D and 3E. *HLA-A, -E, -F, -G* and *-H* allelic frequencies.
HLA-A, -E, -F, -G and *-H* allelic frequencies, observed in at least 0.2%, in worldwide populations (ALL) and in African populations (AFR), Admixed American populations (AMR), European populations (EUR), East Asian populations (EAS) and South Asian populations (SAS) (see [4] for population description). Number of individuals included in each group is given in brackets. Frequencies above 3% are in bold.

1.1 High two-loci linkage disequilibrium between *HLA-H* and *-A,* and between *HLA-H* and *-G*

Haplotypes estimated between each pair of loci and their combined frequencies are given in Tables 4A to 4D. Strong LD is observed between *HLA-A* and *-H,* and *HLA-H* and *-G* alleles, as all haplotypes with a frequency above 3% were in significant LD with very high standardized residual values.

In contrast, *HLA-E* and *-A,* and *HLA-G* and *-F* alleles display few significant associations with standardized residuals very close to the threshold value for significance; indeed the main *HLA-E* and *-F* alleles (i.e. *E*01:01* and *E*01:03* and *F*01:01* and *F*01:03*) were not observed to be exclusively associated with *HLA-A* and *-G* alleles, with the exception of *E*01:01~A*01:01* in Europe and South Asia.

The tight associations found between *HLA-A* and *-H,* and *HLA-H* and *-G* are concordant with results previously observed at the scale of a French population [26] and further confirm known associations, like the deletion encompassing *HLA-H* with *A*23* and *A*24* alleles, but also reveal unobserved exclusive associations between *HLA-A* and *-H*, such as that between *HLA-A*11:01* and *-H*02:07.*

Populations	ALL (N=2157)		AFR (N=592)		AMR (N=294)		EAS (N=446)		EUR (N=416)		SAS (N=409)	
HLA-E~HLA-A haplotypes	obs	stdres	obs	stdres	obs	stdres	obs	stdres	obs	stdres	obs	stdres
*E*01:03~A*02:01*	**0.074**	**2.4**	**0.097**	**7.8**	**0.072**	**2.2**	**0.042**	1.1	**0.128**	0.6	0.016	0.5
*E*01:01~A*02:01*	**0.065**	1.2	0.016	**6.5**	**0.134**	1.4	0.019	1.1	**0.178**	0.4		
*E*01:01~A*01:01*	**0.063**	**9.6**	0.015	0.4	**0.034**	1.9	0.020	**4.9**	**0.124**	**5.5**	**0.140**	**5.6**
*E*01:03~A*11:01*	**0.055**	**3.7**			0.010	1.5	**0.166**	0.8	0.017	1.2	**0.091**	**2.2**
*E*01:03~A*24:02*	**0.055**	**4.1**	0.004	1.0	**0.079**	**2.1**	**0.111**	0.2	**0.032**	0.6	**0.071**	**2.1**
*E*01:03~A*03:01*	**0.040**	**3.5**	0.027	1.2	**0.067**	**3.2**	0.011	1.3	**0.082**	**2.7**	**0.034**	**2.3**
*E*01:01~A*11:01*	**0.038**	**2.6**			0.026	0.9	**0.067**	1.1	**0.041**	1.4	**0.070**	1.3
*E*01:01~A*33:03*	**0.037**	**5.1**	**0.033**	0.1	0.005	1.2	**0.059**	**6.4**	0.002	0.5	**0.083**	**4.8**
*E*01:01~A*24:02*	**0.035**	**3.0**			**0.045**	1.7	**0.059**	0.3	**0.041**	0.0	**0.052**	1.4
*E*01:01~A*30:01*	0.028	**7.2**	**0.074**	**4.5**	0.012	1.8	0.014	**4.0**	0.011	1.8	0.009	1.7
*E*01:01~A*23:01*	0.027	**4.7**	**0.073**	**2.5**	0.017	1.0			0.015	0.5	0.003	0.3
*E*01:03~A*02:07*	0.024	**7.7**					**0.116**	**3.8**				
*E*01:01~A*30:02*	0.022	**3.8**	**0.065**	**3.1**	0.013	0.9			0.005	1.1	0.004	1.1
*E*01:01~A*68:01*	0.018	0.3	0.008	**2.6**	0.020	1.2	0.005	1.4	0.022	1.2	**0.039**	0.6
*E*01:03~A*68:02*	0.018	**4.6**	**0.055**	**5.3**	0.016	1.2			0.002	0.2		
*E*01:01~A*03:01*	0.018	**5.4**	0.027	0.9	0.015	**3.3**			0.029	**5.2**	0.012	**2.5**
*E*01:03~A*29:02*	0.017	**4.8**	0.017	**2.0**	**0.048**	**3.4**			**0.036**	**4.9**		
*E*01:03~A*68:01*	0.017	0.4	0.022	**2.9**	**0.035**	1.4			0.008	1.0	0.028	0.1
*E*01:01~A*32:01*	0.017	**4.1**	0.010	1.5	0.010	0.1	0.006	**2.6**	**0.034**	1.6	0.026	1.5
*E*01:01~A*26:01*	0.016	0.1	0.012	0.2	0.003	1.4	0.008	0.6	0.015	0.9	**0.037**	1.3
*E*01:01~A*74:01*	0.015	**4.9**	**0.051**	**3.5**	0.007	1.4						
*E*01:03~A*26:01*	0.015	0.3	0.007	0.2	0.010	1.0	0.022	0.4	0.019	1.4	0.020	0.8
*E*01:03~A*02:03*	0.014	**5.2**					**0.048**	1.8			0.020	**3.5**
*E*01:03~A*02:11*	0.014	**4.1**			0.003	**2.3**					**0.072**	**6.1**
*E*01:03~A*33:03*	0.012	**4.8**	0.025	0.3			0.016	**4.5**			0.006	**4.7**
*E*01:03~A*31:01*	0.012	0.3	0.003	0.1	0.014	1.2	0.025	0.5	0.020	**2.6**		
*E*01:03~A*02:02*	0.010	**3.3**	0.030	**3.8**	0.010	0.9						
*E*01:01~A*36:01*	0.010	**3.7**	**0.039**	**3.3**								

*E*01:01~A*33:01*	0.009	**2.5**	0.022	1.4	0.019	**2.3**			0.004	0.3		
*E*01:03~A*02:06*	0.008	1.0			0.010	0.4	0.024	0.8			0.008	0.0
*E*01:01~A*34:02*	0.008	**2.2**	0.029	1.2	0.003	1.0						
*E*01:01~A*31:01*	0.008	**2.8**	0.004	0.0	0.017	0.9	0.008	1.0	0.007	1.9	0.005	1.9
*E*01:03~A*30:02*	0.008	**3.3**	0.013	**3.5**	0.022	1.0			0.010	1.5		
*E*01:06~A*03:01*	0.008	**21.6**			0.005	**5.4**			**0.037**	**12.4**	0.004	**7.3**
*E*01:03~A*11:02*	0.007	**4.2**					**0.033**	**2.1**				
*E*01:03~A*66:01*	0.007	**3.2**	0.017	**2.9**	0.003	1.1			0.006	**2.2**		
*E*01:03~A*01:01*	0.007	**9.3**	0.013	0.4	0.009	1.8						
*E*01:01~A*02:06*	0.007	0.5			0.008	0.3	0.020	1.3			0.008	0.5
*E*01:03~A*23:01*	0.006	**5.3**	0.009	**5.2**	0.007	1.0			0.009	0.2		
*E*01:01~A*68:02*	0.005	**4.0**	0.015	**4.3**	0.008	1.0			0.003	0.0		
*E*01:01~A*02:05*	0.005	0.6	0.008	0.5	0.006	0.1					0.009	1.7
*E*01:01~A*29:01*	0.005	**3.4**			0.009	1.5	0.017	**4.4**			0.004	1.1
*E*01:03~A*32:01*	0.004	**3.7**			0.009	0.0			0.011	1.4	0.010	1.3
*E*01:03~A*02:05*	0.004	0.4	0.008	0.6	0.004	0.6			0.003	0.6		
*E*01:03~A*24:07*	0.004	**2.1**					0.002	1.0			0.016	**2.4**
*E*01:03~A*01:02*	0.004	**2.4**	0.014	**3.7**	0.002	0.8						
*E*01:01~A*25:01*	0.004	**2.8**			0.005	1.2			0.016	**2.1**		
*E*01:01~A*29:02*	0.004	**4.5**	0.007	**2.1**	0.003	**3.5**						
*E*01:01~A*80:01*	0.003	2.0	0.009	1.2	0.003	1.0						
*E*01:03~A*34:02*	0.003	**2.3**	0.011	1.5								
*E*01:01~A*02:11*	0.003	**4.4**			0.025	1.7						
*E*01:03~A*33:01*	0.003	**2.2**	0.007	1.6								
*E*01:01~A*02:02*	0.003	**2.8**	0.010	**3.0**	0.004	1.0						
*E*01:01~A*66:02*	0.003	1.4	0.010	0.9								
*E*01:03~A*23:17*	0.002	0.5	0.003	1.1								
*E*01:01~A*23:17*	0.002	0.7	0.008	0.3	0.002	0.7						
Total	0.930		0.927		0.888		0.918		0.967		0.897	

Table 4A

Populations	ALL (N=2157)		AFR (N=592)		AMR (N=294)		EAS (N=446)		EUR (N=416)		SAS (N=409)	
HLA-A~HLA-H haplotypes	obs	stdres	obs	stdres	obs	stdres	obs	stdres	obs	stdres	obs	stdres
*A*02:01~H*01:01*	**0.139**	**38.1**	**0.115**	**29.3**	**0.223**	**13.7**	**0.076**	**8.7**	**0.305**	**18.7**	**0.032**	**11.1**
*A*24:02~H*Del*	**0.090**	**39.3**	0.007	**7.2**	**0.125**	**17.9**	**0.170**	**20.3**	**0.073**	**21.2**	**0.121**	**19.4**
*A*11:01~H*02:07*	**0.081**	**53.3**			**0.041**	**23.0**	**0.171**	**17.1**	**0.058**	**27.1**	**0.158**	**23.5**
*A*01:01~H*02:01*	**0.064**	**56.0**	0.007	**8.9**	**0.043**	**23.1**	0.020	**29.2**	**0.127**	**24.7**	**0.155**	**23.6**
*A*03:01~H*02:04*	**0.063**	**59.9**	**0.048**	**30.6**	**0.085**	**21.2**	0.011	**29.4**	**0.150**	**25.0**	**0.051**	**25.4**
*A*33:03~H*02:08*	**0.038**	**54.1**	**0.056**	**31.6**	0.005	**23.4**	**0.067**	**25.2**	0.006	**28.7**	**0.039**	**17.4**
*A*68:01~H*02:05*	**0.035**	**33.1**	0.030	**8.4**	**0.055**	**15.9**	0.007	**17.3**	0.030	**21.2**	**0.066**	**24.9**
*A*23:01~H*Del*	**0.034**	**24.4**	**0.095**	**26.8**	0.025	**8.0**			0.024	**12.1**	0.005	**4.0**
*A*26:01~H*01:02*	0.030	**43.4**	0.018	**17.6**	0.014	**16.8**	**0.030**	**23.1**	**0.035**	**20.7**	**0.056**	**18.6**
*A*30:01~H*02:05*	0.029	**30.5**	**0.079**	**14.1**	0.012	**7.4**	0.014	**24.6**	0.011	**12.7**	0.009	**9.0**
*A*31:01~H*02:09*	0.024	**51.3**	0.006	**10.8**	**0.045**	**21.8**	**0.034**	**28.4**	0.026	**28.0**	0.024	**27.0**
*A*02:07~H*01:01*	0.024	**16.1**					**0.119**	**10.7**				
*A*30:02~H*01:01:02*	0.023	**55.8**	**0.054**	**26.3**	**0.032**	**22.1**			0.014	**27.1**	0.004	**28.5**
*A*68:02~H*02:05*	0.023	**27.0**	**0.070**	**13.3**	0.024	**10.4**			0.005	**8.5**		
*A*29:02~H*02:02*	0.022	**57.0**	0.026	**33.1**	**0.054**	**21.1**			**0.038**	**27.8**		
*A*32:01~H*02:03:02*	0.019	**57.8**	0.011	**31.2**	0.015	**21.5**			**0.043**	**27.4**	**0.032**	**24.6**
*A*02:11~H*01:01*	0.018	**14.1**			**0.032**	**5.3**					**0.076**	**17.0**
*A*74:01~H*02:05*	0.016	**22.0**	**0.054**	**11.3**	0.007	**5.6**						
*A*02:06~H*01:01*	0.015	**12.5**			0.016	**3.5**	**0.043**	**6.6**			0.019	**8.5**
*A*02:03~H*01:01*	0.015	**12.7**					**0.055**	**7.4**			0.020	**8.8**
*A*02:02~H*01:03*	0.013	**49.0**	**0.040**	**27.3**	0.015	**17.6**						
*A*11:01~H*01:01*	0.013	**4.0**					**0.063**	**2.1**				
*A*33:03~H*01:02*	0.012	**10.7**	0.003	0.5			0.009	**2.8**			**0.049**	**11.9**
*A*36:01~H*02:10*	0.011	**51.3**	**0.041**	**25.9**								
*A*02:05~H*01:03*	0.009	**40.6**	0.016	**17.4**	0.012	**15.5**			0.006	**28.7**	0.009	**26.5**
*A*66:01~H*01:02*	0.008	**22.6**	0.023	**20.1**	0.003	**8.2**			0.006	**8.6**		
*A*30:02~H*01:04*	0.007	**30.4**	0.024	**17.5**	0.003	**5.8**						
*A*11:02~H*02:07*	0.007	**16.7**					**0.033**	**9.8**				

*A*33:01~H*02:12*	0.006	**45.9**	0.009	**19.0**	0.015	**21.4**			0.006	**28.7**		
*A*33:01~H*02:09*	0.006	**16.4**	0.019	**16.1**	0.003	1.9						
*A*34:02~H*02:09*	0.006	**17.9**	0.022	**15.9**								
*A*01:01~H*02:10*	0.006	**8.7**	0.021	**15.7**								
*A*34:02~H*02:11*	0.005	**44.3**	0.018	**21.6**	0.003	**24.2**						
*A*24:07~H*Del*	0.005	**9.3**					0.006	**3.7**			0.020	**8.0**
*A*29:01~H*02:02*	0.005	**28.6**			0.009	**8.4**	0.017	**30.1**			0.004	**28.5**
*A*25:01~H*01:02*	0.004	**15.2**			0.005	**10.1**			0.016	**13.9**		
*A*01:02~H*02:01*	0.004	**15.1**	0.014	**27.3**								
*A*66:02~H*02:05*	0.004	**10.8**	0.014	**5.9**								
*A*23:17~H*Del*	0.004	**8.6**	0.014	**10.5**								
*A*80:01~H*01:02*	0.003	**13.5**	0.009	**12.3**	0.003	**8.2**						
*A*32:01~H*02:03*	0.002	**20.9**			0.003	**10.2**	0.005	**26.6**			0.004	**8.8**
*A*02:22~H*01:01*	0.002	**4.2**			0.012	**3.3**						
*A*03:02~H*02:04*	0.002	**11.1**			0.003	**4.3**			0.002	**3.2**	0.005	**8.1**
*A*03:01~H*02:13*	0.002	**9.6**	0.006	**10.8**								
Total	0.948		0.966		0.944		0.947		0.982		0.955	

Table 4B

Populations HLA-H~HLA-G haplotypes	ALL (N=2157) obs	 stdres	AFR (N=592) obs	 stdres	AMR (N=294) obs	 stdres	EAS (N=446) obs	 stdres	EUR (N=416) obs	 stdres	SAS (N=409) obs	 stdres
*H*01:01~G*01:01*	**0.235**	**12.5**	**0.121**	**6.6**	**0.306**	**3.9**	**0.364**	**6.2**	**0.310**	**3**	**0.152**	**5.2**
*H*Del~G*01:04*	**0.128**	**35.1**	**0.117**	**18.1**	**0.141**	**18.1**	**0.176**	**15.1**	**0.075**	**20**	**0.143**	**17.2**
*H*02:07~G*01:01*	**0.082**	**6.9**			**0.041**	1.6	**0.176**	**3.2**	**0.058**	1	**0.156**	**5.1**
*H*02:05~G*01:01*	**0.081**	**2.2**	**0.178**	**2.7**	**0.090**	1.5	0.006	1.8	**0.039**	0	**0.066**	**2.6**
*H*02:04~G*01:01*	**0.064**	**6.8**	**0.047**	**4.0**	**0.088**	**2.3**	0.011	1.2	**0.145**	**2**	**0.057**	**3.3**
*H*01:02~G*01:01*	**0.060**	**6.6**	**0.059**	**4.7**	0.029	1.5	**0.045**	**2.2**	**0.059**	1	**0.106**	**4.6**
*H*02:01~G*01:06*	**0.046**	**49.8**	0.004	**15.2**	0.028	**18.5**	0.015	**24.8**	**0.054**	**16**	**0.153**	**23.4**
*H*02:08~G*01:04*	**0.038**	**24.0**	**0.054**	**12.4**	0.005	**3.8**	**0.070**	**11.7**	0.006	**7**	**0.039**	**10.4**
*H*02:05~G*01:05N*	0.029	**30.3**	**0.078**	**14.0**			0.014	**24.6**				
*H*02:02~G*01:01*	0.027	**4.6**	0.027	**3.2**	**0.063**	**2.1**	0.016	1.6	**0.039**	1	0.004	0.9
*H*02:09~G*01:03*	0.025	**33.7**	**0.044**	**18.6**	**0.042**	**13.8**	0.005	**9.2**	0.016	**16**	0.016	**16.4**
*H*01:01:02~G*01:01*	0.023	**4.1**	**0.054**	**4.5**	**0.033**	1.6			0.015	1	0.004	0.9
*H*02:01~G*01:01*	0.022	**7.1**	0.015	1.1	0.017	1.9	0.005	**2.4**	**0.075**	**3**		
*H*01:03~G*01:03*	0.021	**38.4**	**0.052**	**20.2**	0.027	**12.4**	0.001	**13.2**	0.006	**13**	0.010	**16.8**
*H*02:03:02~G*01:01*	0.021	**3.7**	0.012	1.7	0.015	1.0	0.003	0.7	**0.043**	1	**0.036**	**2.6**
*H*02:10~G*01:04*	0.015	**13.7**	**0.057**	**11.8**								
*H*02:09~G*01:01*	0.012	**5.1**	0.003	**5.0**	0.009	**3.4**	0.029	1.0	0.011	**2**	0.010	1.3
*H*Del~G*01:01*	0.010	**18.9**	0.003	**8.4**			0.013	**9.7**	0.024	**6**	0.018	**7.3**
*H*01:04~G*01:01*	0.008	**2.2**	0.025	**3.2**	0.003	0.1			0.001	0		
*H*02:12~G*01:03*	0.006	**20.0**	0.008	**7.9**	0.015	**9.3**			0.006	**13**		
*H*02:11~G*01:01*	0.005	1.9	0.018	**2.5**	0.003	0.2						
*H*02:03~G*01:01*	0.002	1.3			0.003	0.2	0.005	0.8	0.001	0	0.003	0.3
*H*02:07~G*01:04*	0.002	**7.4**			0.002	1.4					0.003	**4.4**
*H*02:13~G*01:01*	0.002	1.1	0.006	1.5								
Total	0.961		0.980		0.960		0.953		0.981		0.975	

Table 4C

Populations	ALL (N=2157)		AFR (N=592)		AMR (N=294)		EAS (N=446)		EUR (N=416)		SAS (N=409)	
HLA-G~HLA-F haplotypes	obs	stdres	obs	stdres	obs	stdres	obs	stdres	obs	stdres	obs	stdres
*G*01:01~F*01:01*	**0.581**	1.5	**0.510**	**2.5**	**0.618**	0.1	**0.665**	0.1	**0.624**	0.1	**0.551**	0.5
*G*01:04~F*01:01*	**0.133**	**3.5**	**0.083**	**7.2**	**0.122**	0.7	**0.252**	0.3	**0.041**	**2.4**	**0.185**	0.5
*G*01:01~F*01:03*	**0.058**	**3.6**	0.020	**8.2**	**0.087**	0.4	0.009	0.6	**0.134**	0.8	**0.061**	**2.4**
*G*01:04~F*01:03*	**0.051**	**13.4**	**0.149**	**18.4**	0.029	**2.0**			**0.041**	**6.4**	0.005	**2.1**
*G*01:03~F*01:01*	**0.050**	1.8	**0.105**	**2.1**	**0.085**	0.9	0.005	0.4	0.028	1.3	0.027	0.3
*G*01:06~F*01:01*	**0.044**	1.8	0.003	0.3	0.027	0.4	0.013	0.4	**0.054**	1.8	**0.153**	0.8
*G*01:05N~F*01:01*	0.029	1.9	**0.077**	0.0	0.011	0.1	0.013	0.2	0.011	0.8		
*G*01:01~F*01:02*	0.004	1.1	0.015	1.9								
Total	0.951		0.961		0.979		0.956		0.932		0.981	

Table 4D

Tables 4A, 4B, 4C and 4D. *HLA-E~HLA-A, HLA-A~HLA-H, HLA-H~HLA-G* and *HLA-G~HLA-F* Linkage Disequilibrium (LD) and frequencies.

HLA-E~HLA-A, HLA-A~HLA-H, HLA-H~HLA-G and *HLA-G~HLA-F* Linkage Disequilibrium (LD) provided for pairs of alleles observed in at least 0.2% in worldwide populations (ALL) and in African populations (AFR), Admixed American populations (AMR), European populations (EUR), East Asian populations (EAS) and South Asian populations (SAS) (see [4] for population description). Number of individuals included in each group is given in brackets. Observed frequencies (obs) above 3% and standardized residuals (stdres) for each observed haplotype with values greater than |2| are in bold.

4. Discussion

The aim of this study was to investigate worldwide HLA Ib genetic diversity. To achieve this goal, we used public data from exome sequencing and confirmed novel sequences experimentally. This approach allowed to 1/ get further insight into *HLA-H* genetic diversity and how this plasticity can potentially lead to functional diversity and 2/ to analyze worldwide *HLA-E, -F* and *-G* allelic distribution and LD. Indeed, exome sequence data from the 1,000 Genomes Project [4] constitute a priceless public resource allowing genetic diversity studies [5-7].

Our main result is the description of 11 novel *HLA-H* alleles, and thanks to the 1,000 Genomes Project associated DNA collection, their confirmation using targeted NGS. We show in particular that the *HLA-H* locus displays an unexpected diversity with 18 second field alleles at worldwide level with frequency above 0.2%, with unequal distribution across the five continents. We further confirm the high LD between *HLA-H* and *-A,* and between *HLA-H* and *-G,* though at a lower extent. However, *HLA-G* has a greater diversity in its regulatory regions (5'URR and 3'UTR), that are structured in conserved haplotypes and in stronger LD with *HLA-H* [26]. We also confirm the observation that *HLA-G* second field allelic distribution, like that of *HLA-H* and *HLA-A,* is different from one part of the globe to another. Conversely, *HLA-E* and *HLA-F* both show little, if any, LD with their loci neighbors, display very restricted allelic diversity and little difference in their worldwide distribution.

Phylogenetic analysis and frequency distribution of *HLA-H* alleles described in the IPD-IMGT /HLA Database and newly identified here, revealed three clades, each predominantly represented in Admixed American, European and East Asian populations (Clade containing *H*01:01*), African populations (Clade containing *H*02:05*) and South Asian populations (Clade containing *H*02:07*), suggesting a strong genetic drift. The genetic deletion encompassing *HLA-H* could not be included in phylogenetic analysis but was present in at least 10% of every population and above 20% in South Asian populations. Due to this deletion of the *HLA-H* locus and to the fact that most *HLA-H* alleles described so far encode truncated proteins, *HLA-H* is considered to be a pseudogene. Some studies however, linked its transcriptional expression with inter-individual variations in immune responsiveness [46, 63, 64], that might imply an activity for this locus. *HLA-H* allelic diversity and worldwide distribution could also be due to hitchhiking with the *HLA-A* locus [65], reflected by their high LD. The observation of the new alleles *H*02:07* and *H*02:14* that possibly encode a protein with all the patterns of a transmembrane HLA protein, opens up new perspectives for this locus. The fact that these 'complete' HLA-H sequences display three out of four cysteines (lacking the one at codon 164) that are important antigen presenting function [38] whereas HLA-E, -F and -G displayed all four of them remains to be investigated, as this cysteine was not implicated in the disulfide bond predicted in all of the HLA protein sequences included in this study.

Our results on HLA Ib allelic frequencies and two-loci haplotypes estimation on worldwide populations further supports the LD between *HLA-A, -H* and *-G.* Although their worldwide distribution displays considerable differences, their strong LD is observed in all populations investigated. Conversely, *HLA-E* and *HLA-F,* whose genetic diversity was lower at second field resolution, displayed no LD. This difference could be an echo of their specific expression and function. Indeed, whereas HLA-G is expressed in a tissue-specific manner with documented inter-individual variations and coding polymorphisms [23, 66, 67], HLA-E and HLA-F appear to be mobilized at the cell surface upon activation [9, 33, 34, 68], and HLA-E has one high and one low expressing allele. The apparent shared function of HLA Ib, *i.e.* inhibition of immune activation, might thus have evolved and be regulated by two independent pathways, one driven by a population genetics drift and adaptation to specific environments, and the other led by cellular compensation mechanisms.

Furthermore, HLA Ib two-loci haplotypes may be helpful in clinical fields as the involvement of HLA-G and HLA-E, both at genetic polymorphism and expression levels, has been well described in solid organ transplant and grafts. Given that HLA-A typing of recipients and donors is systematically and routinely performed in immunogenetics laboratories, our results on LD results could potentially improve transplant matching strategies.

5. Conclusions

In conclusion, our work reveals an unexpected *HLA-H* genetic diversity with alleles highly represented in Asia potentially encoding a functional HLA protein. This study also contributes to better define worldwide *HLA-E, -F* and *-G* genetic diversity, distribution and LD. Functional implication of these results remains to be explored, both in physiological and pathological contexts.

6. Appendices

Appendice Table 1. *HLA-H* novel alleles. Novel HLA-H alleles names, Genbank and IPD-IMGT /HLA Database submissions numbers, nearest allele and description as compared to the nearest allele.

Appendice Table 2. *HLA-A, -E, -H, -F and –G* second field level typing results.
HLA-A, -E, -H, -F and -G second field level typing results for 2,160 samples accurately resolved for all locus (i.e. defined without ambiguity) from exome sequence data for 2,693 individuals forming the 1,000 Genomes Project [4].

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9. Figure

Figures 1A and 1B. Phylogenetic relationship between *HLA-H* alleles defined at second field.
Phylogenetic trees contain either all 22 *HLA-H* allelic sequences from the IPD-IMGT /HLA Database and sequences from new *HLA-H* alleles described in this study (Figure 1A), or 20 *HLA-H* allelic sequences, excluding *H*03:01* and *H*02:06* alleles not observed in this study (Figure 1B). Optimal trees are shown (respectively with the sum of branch length = 0.05748059 (Figure 1A) and 0.04361905 (Figure 1B)). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [69]. Trees are drawn to scale, with branch lengths in the same units (base differences per site) as those of the evolutionary distances used to infer the phylogenetic tree. Evolutionary distances were computed using the Maximum Composite Likelihood method [70] and units are the number of base substitutions per site. There were a total of 1105 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [53].

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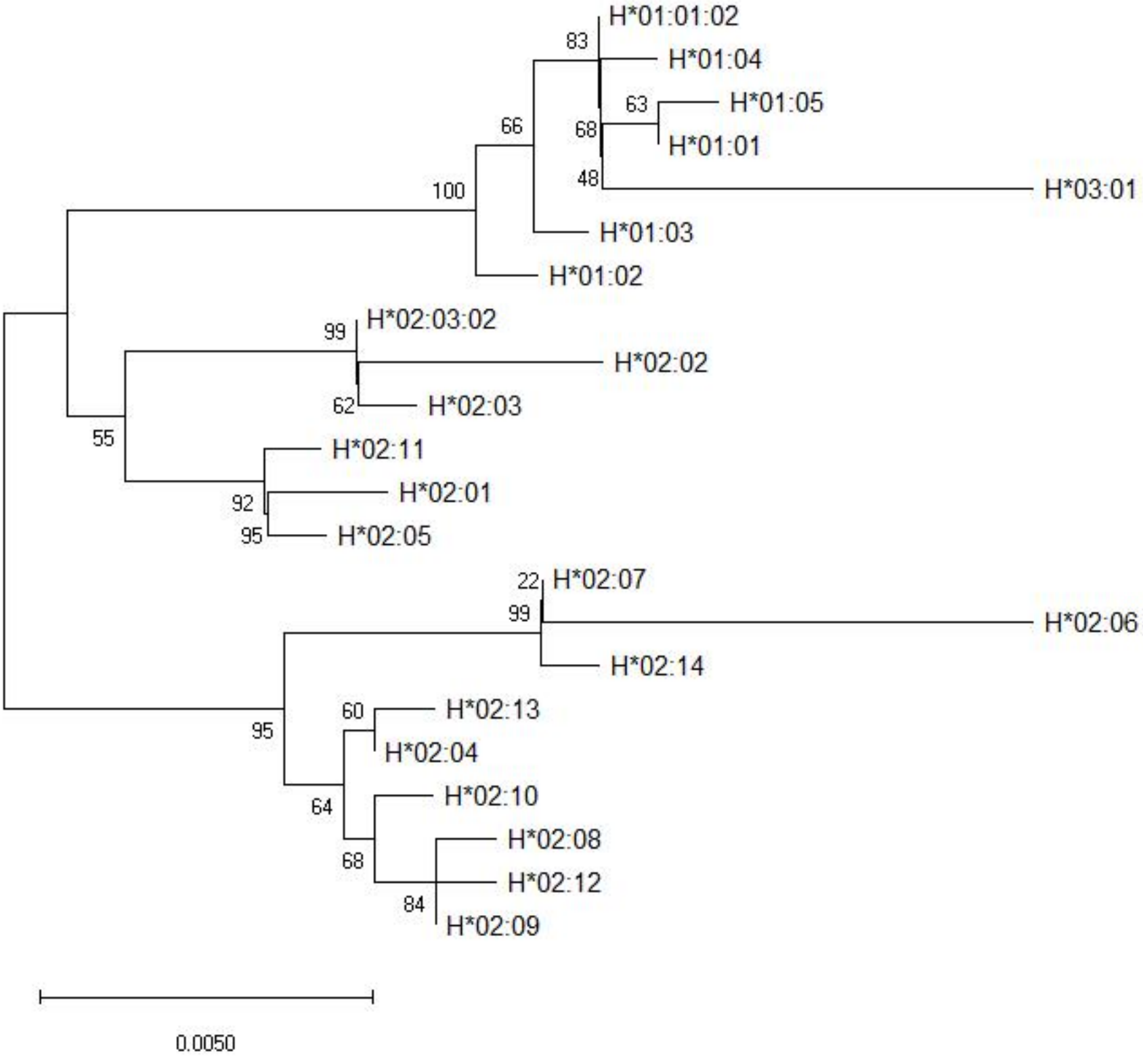
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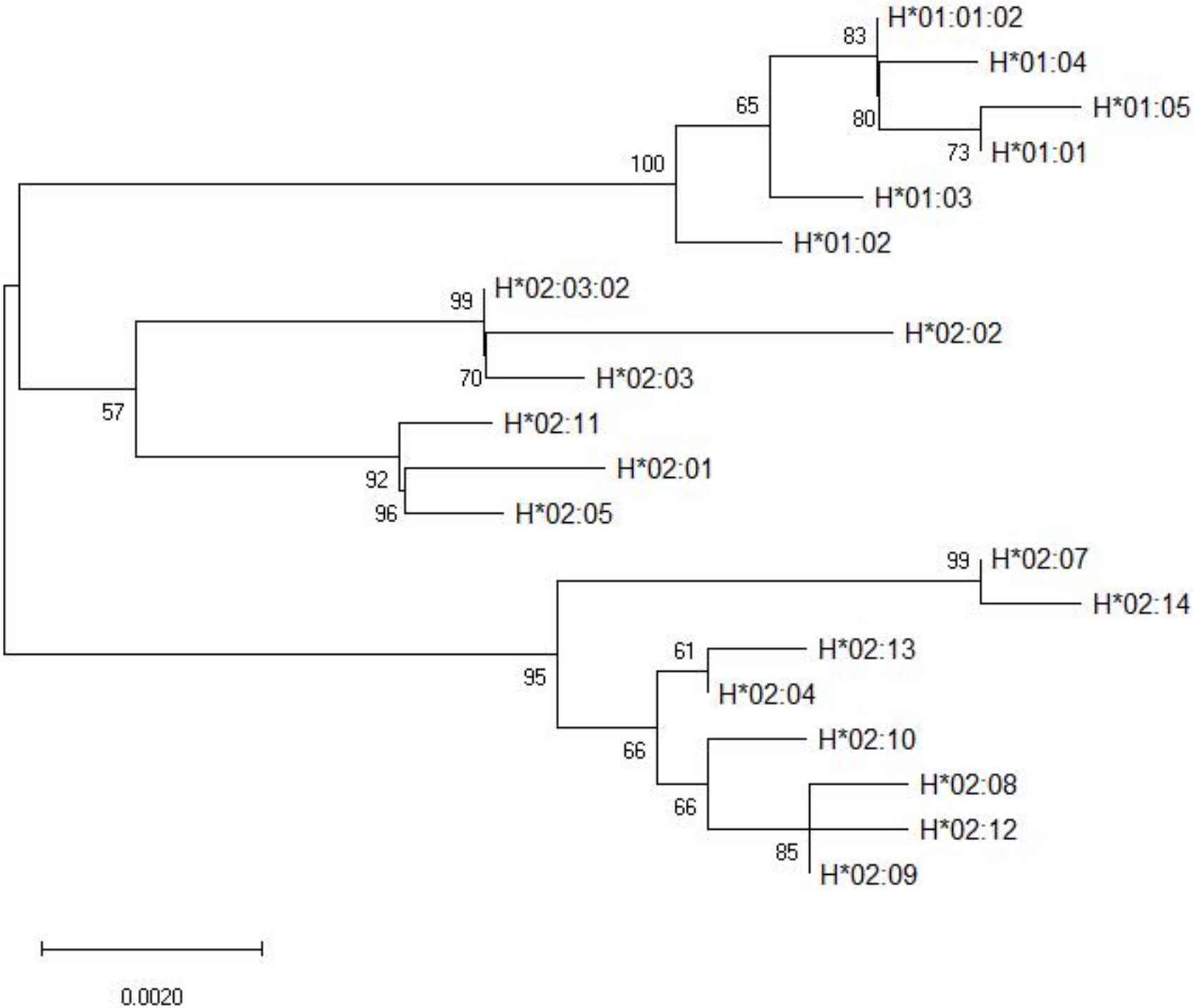
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