



Short population report

Study of Colombia North Wiwa El Encanto Amerindians HLA- genes: Pacific Islanders relatedness

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ABSTRACT

We have studied Wiwa/Sanja Amerindians HLA-A, -B, -C, -DRB1 and DQB1 allele frequencies and extended haplotypes in 52 unrelated individuals from “El Encanto” town at Guanachaca riverside. High frequency alleles were in general present in other Amerindian populations. Also, three extended haplotypes and eight ones were respectively both “new found” and already described in Amerindians from North, Central and South America, including Lakota-Sioux, Mayas, Teeneks, Quechua and Aymaras. Analyses of HLA-A*24:02 and -C*01:02 Wiwa high frequency alleles suggested a specific relatedness with another Amerindian and Pacific Islander ethnic groups (these two particular alleles bearing in high frequencies); they include New Zealand Maoris, Taiwanese, Japanese, Papua New Guinea, and Samoans among others. This may indicate that selective forces are maintaining these two alleles high frequency within this wide American/Pacific area.

Peopling of Americas pathways are nowadays recognized to have been complex [1–3], and not only through Bering Strait from Siberia [1,4–7]. Even concept of “American Peopling” now assimilated to “New World Peopling” is misleading since it implies that America was previously not populated by man comparatively to Eurasia [2,7]; this is nowadays not supported by evidences.

Indeed, we have already concluded from our previous studies on HLA genes that: 1 – First America Natives, have had genetic flow with Pacific Islanders: the latter share high frequency autosomal HLA alleles and haplotypes with them. This fact may have been bidirectional [7]. 2

– More important, Easter Islanders show a probable cultural and genetic exchange with Titikaka Lake Aymaras; this civilization also shares specific traits with European-Iberian megalithic builders [6]. 3 – And, also, a two-way Trans-Atlantic traffic may have occurred before Columbus discovered America; archaeologists in New Mexico and other North America places have recently found tools used 20,000 years ago in Spanish Solutrean culture [1,5,8].

In the present study we have undertaken to find out HLA genes in Wiwa (Arsario) Amerindians that live in North Colombia Caribbean Coast, close to Santa Marta Snowed Sierra (Fig. 1 from Supplementary Material).

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The ethnic group Wiwa is named with different names according to their present day placement. Originally, their original living place was Marokaso, El Rosario and Guamaka; they were displaced by European colonizers to other settlements at Departments of Magdalena and Cesar. In fact, some of them came back in the late XXth century to their original territory at Magdalena Dept. Nowadays; they receive different names according to their placement: Sanja, as other generic name, Guamakas (from Guamaka), Marokaseros (from Marokaso), Arsarios (from “El Rosario”) and Malayos (from the usual “malo” regional patronymic). Our sample was taken from Gotsezhi (“El Encanto”) at Magdalena Dept (<https://es.wikipedia.org/wiki/wiwa>). They speak “Damana language”, which belongs to Chibchan linguistic family; this language is spoken by all Wiwa/Sanja groups of Cesar and Magdalena Departments (https://es.wikipedia.org/wiki/idioma_damana#Escritura_y_literatura). All individuals (n = 52) were unrelated and signed a written consent to participate in this study; they had been born in the area and their four grandparents also been born there. High resolution HLA class I (-A, -B and -C) and class II (-DRB1 and -DQB1) typing was performed by using PCR-SSOP Luminex technique and ambiguities were resolved by direct DNA sequencing, as referenced in [9]. Statistical analysis was performed with Arlequin v3.0 [10].

The expected and observed gene frequency values for HLA-A, -B, -C, -DRB1, and -DQB1 loci do not differ significantly and the population is found in Hardy-Weinberg equilibrium (data not shown). Twenty-three different HLA-A, twenty-eight different HLA-B, and seventeen different HLA-C alleles were found in Wiwa sample. However, only five HLA-A alleles, three HLA-B alleles, and six HLA-C alleles had frequencies higher than 4%. (A*02:01, A*24:02, A*29:02, A*31:01, A*68:01, B*15:01, B*35:43, B*40:02, C*01:02, C*03:04, C*04:01, C*07:02, C*08:02, and C*16:01) (Table 1 from Supplementary Material). With regard to the HLA class II alleles, nineteen different HLA-DRB1 and thirteen different HLA-DQB1 alleles were found. Only four HLA-DRB1 and four HLA-DQB1 alleles had frequencies higher than 4% (DRB1*04:07, DRB1*07:01, DRB1*08:02, DRB1*14:02, DQB1*02:02, DQB1*03:02, DQB1*04:02, and DQB1*06:02) (Table 1 from Supplementary Material) [12]. Most alleles had already been found in Amerindians.

The most common 12 extended HLA-A-B-C-DRB1 and DQB1 haplotypes in Wiwa population are shown in Table 2 from Supplementary Material and also in Table 4 from [11].

Most extended HLA haplotypes in our populations sample are either from Amerindian origin or newly found and bearing typical HLA Amerindian alleles. Genetic HLA distances between Wiwa and other populations show that Wiwa are both close to Meso and South Americans. Indeed, Mayans (Guatemala, Mayan linguistic family), Seri (Mexico, according to some authors belonging to Hokan linguistic family, according to others it is a language isolate) [11], Kogi (Colombia, Chibchan linguistic family), Arhuaco (Colombia, Chibchan linguistic family) and Mayos (Mexico, Uto-Aztecan linguistic family) show the closest genetic distances to Wiwa [11].

Again, these results show that genes and languages do not seem to correlate at the microgeographical level [12–14]. Pacific genetic relatedness with Wiwa population was found with HLA-A*24:02 and

HLA-C*01:02 common and specific high frequencies [11]. Wiwa and Mesoamerindians show the highest frequencies of these alleles together with populations from Pacific Area [11].

All genotype data included in this paper is held in www.allelefreqencies.net under the population name North Colombia Wiwa -Arsario Amerindians and identifier number 3433 [15].

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <https://doi.org/10.1016/j.humimm.2018.04.016>.

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