Genetic characterization of the Brazilian immigrant population in Lisboa with InDel genetic markers

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Introduction

Migration is one of the main factors for genetic variability within populations[1]. Currently, the Portuguese population, and particularly the population from Lisboa, welcomes a considerable number of immigrants. Brazilian immigrants are the main foreign community in Portugal, with about 80 000 individuals in 2015[2].

Insertion/deletion polymorphisms - InDels -, are characterized by the presence or absence of small DNA sequences[3]. These variations constitute a group of genetic markers with advantages for forensic identification, especially in highly degraded biological samples, due to the small size of the amplification fragments[4,5]. Furthermore, InDels have lower mutation rates, making them useful for complex cases of biological kinship[6].

Objectives

Presently, there is no available data for InDel markers of the Brazilian immigrant population in Lisboa. Thus, our aim is to characterize this population by typing a group of individuals with a panel of 30 InDel and compare it with other main immigrant populations living in Lisboa (Angola, Cabo Verde, Moçambique, Guiné-Bissau and São Tomé e Príncipe).

Materials and Methods

We studied 207 Brazilian immigrants. Samples were typed with the Investigator DIPplex® Kit. Fragments were detected by capillary electrophoresis using the ABI PRISM 3130 *xl* automated sequencer and results analyzed with GeneMapper v1.2 software. Statistical inference of data was carried out with Arlequin v3.5 software[7], PowerStatsV12 and Mega7[8].

Results

The Brasil population sample frequency distributions (Table 1) showed no deviations from HWE. Forensic parameters, revealed a discrimination power equal or higher than 0.6 in all markers but HLD70 and HLD58, HLD99, HLD48 and HLD122. The achieved genetic data allowed us to evaluate genetic distances between Portuguese Caucasian population and immigrant populations with available genetic data. A microvariant allele was found at locus HLD56 with a frequency of 0,0024.Figure 1 is a schematic representation of the genetic distance amongst studied populations.

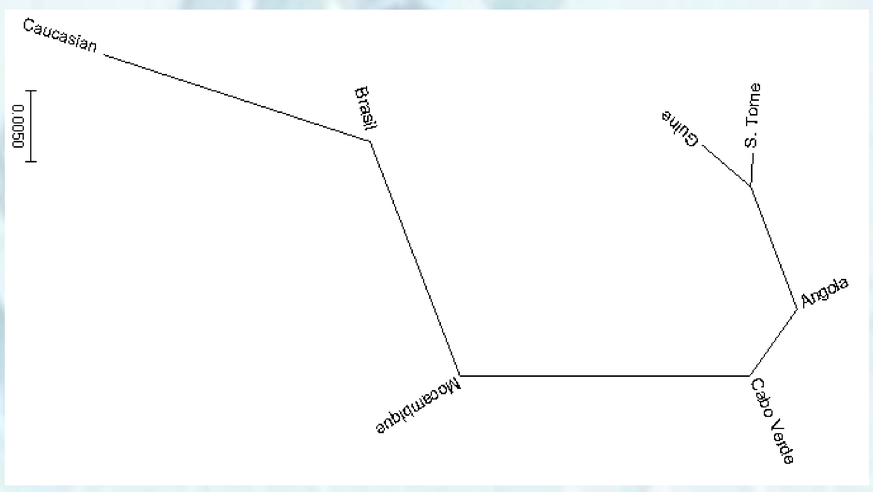

Figura1- Schematic representation of the genetic distance amongst studied populations.

Table 1 – Allelic distributions and some genetic and forensic efficiency parameters of 30 InDel markers in the Brazilian immigrant population (n = 207)

Markers	Del (af)	In (af)	HWE	OH	EH	DP	EP
HLD77	0,5942	0,4058	1,0000	0,4831	0,4834	0,6150	0,1730
HLD45	0,5145	0,4855	0,5790	0,4783	0,5008	0,6350	0,1690
HLD131	0,4275	0,5725	0,0230	0,4106	0,4907	0,6470	0,1210
HLD70	0,2995	0,7005	0,5087	0,4444	0,4206	0,5680	0,1430
HLD6	0,5362	0,4638	0,4834	0,4734	0,4986	0,6350	0,1650
HLD111	0,5169	0,4831	0,2124	0,4541	0,5006	0,6440	0,1500
HLD58	0,6280	0,3720	0,1049	0,5217	0,4684	0,5810	0,2070
HLD56	0,3816	0,6159	0,8590	0,4879	0,4761	0,6050	0,1750
HLD118	0,5990	0,4010	0,4689	0,4541	0,4816	0,6250	0,1500
HLD92	0,5459	0,4541	0,0920	0,4348	0,4970	0,6470	0,1370
HLD93	0,4420	0,5580	0,3261	0,4589	0,4945	0,6360	0,1540
HLD99	0,3961	0,6039	0,0419	0,5507	0,4796	0,5740	0,2360
HLD88	0,4251	0,5749	0,4760	0,4638	0,4900	0,6300	0,1580
HLD101	0,4444	0,5556	0,4802	0,5217	0,4950	0,6070	0,2070
HLD67	0,4082	0,5918	0,3149	0,4493	0,4843	0,6300	0,1470
HLD83	0,4879	0,5121	0,0174	0,4155	0,5009	0,6560	0,1240
HLD114	0,4662	0,5338	0,8889	0,5073	0,4989	0,6190	0,1940
HLD48	0,3527	0,6473	0,2879	0,4928	0,4577	0,5850	0,1810
HLD124	0,4783	0,5217	0,2063	0,4541	0,5003	0,6440	0,1500
HLD122	0,5628	0,4372	0,2574	0,5362	0,4933	0,5970	0,2210
HLD125	0,5821	0,4179	0,6683	0,4686	0,4877	0,6260	0,1610
HLD64	0,3261	0,6739	0,1144	0,3913	0,4406	0,6010	0,1090
HLD81	0,4928	0,5072	0,2680	0,5411	0,5011	0,6020	0,2260
HLD136	0,3527	0,6473	1,0000	0,4541	0,4577	0,6010	0,1500
HLD133	0,4686	0,5314	0,2137	0,4541	0,4992	0,6430	0,1500
HLD97	0,5145	0,4855	0,0124	0,4106	0,5008	0,6570	0,1210
HLD40	0,5411	0,4589	0,6779	0,4831	0,4978	0,6300	0,1730
HLD128	0,5024	0,4976	0,7823	0,5121	0,5012	0,6190	0,1980
HLD39	0,5797	0,4203	0,3981	0,5217	0,4885	0,6010	0,2070
HLD84	0,3865	0,6135	0,5588	0,4541	0,4754	0,6190	0,1500

Del (af) deletion allelic frequency, *In (af)* insertion allelic frequency, *HWE* Hardy-Weinberg Equilibrium, *OH* Observed Heterozygosity, *EH* Expected Heterozygosity, *DP* Discrimination Power, *PE* Exclusion Power

Conclusion

With Investigator Diplex Kit ® complete genetic profiles were obtained for all individuals. Moreover, results showed that this kit could be suitable for kinship analysis, as a complementary method combined with STRs. Our results confirm genetic differences between Portuguese Caucasian population, Brazilian and PALOP´s immigrant populations.

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