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Analysis of the most efficient autosomal strs and genetic data for the locus se33 in ecuadorian population

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ABSTRACT

Twenty three autosomal STR markers were analyzed to define which are the most informative in forensic genetic cases in Ecuadorian population. In this study, we report genetic data from 1434 and 1800 unrelated individuals for SE33 and other 22 STRs, respectively. The parameters analyzed were: polymorphism information content (PIC), heterozygosity, power of discrimination and power of exclusion. SE33 was the best marker for forensic identification purposes because it showed the highest polymorphism information content (PIC) of 0.9334; heterozygosity of 0.9191; power of discrimination of 0.9969 and power of exclusion of 0.8345. Hence, we recommend its use in routine and complex paternity cases. After SE33, the subsequent most informative STR markers for Ecuadorian population were PENTA E, FGA, D1S1656 and D19S433, and the less informative markers were VWA, D22S1045, D2S441, TPOX and D3S1358.

1. Introduction

SE33 has been incorporated into several STR kits due to it's high polymorphism, it's power of discrimination and the fact that more than 140 alleles have been reported to date [2,7]. The aim of this study was to compare the forensic efficiency parameters of 23 different STR to assess their forensic application in Ecuadorian Population and also report the genetic data for locus SE33. [1].

2. Materials and methods

The samples analyzed in this study for 22 STR autosomal markers (D3S1358, D1S1656, D2S441, D10S1248, D13S317, PENTA E, D16S539, D18S51, D2S1338, CSF1PO, PENTA D, TH01, VWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, FGA and D22S1045) were 1800 unrelated Ecuadorian individuals, which information were previously reported in Gaviria et al. [3]. For SE33 analysis, DNA samples from 1434 unrelated Ecuadorian individuals were extracted from whole blood following FTA method (Whatman). PCR amplification was performed using AmpFLSTR NGM SElect PCR Amplification kit, according to manufacturer's instructions (Applied Biosystems).

The ABI PRISM 3130 Genetic Analyzer and Genemapper v 3.2 software (Applied Biosystems) were used to analyze PCR products and population genetic analyses were calculated using Arlequin Software v. 3.5.1.3 [4]. Moreover, forensic and population parameters were estimated by Powerstats software [5] (Promega Corporation).

3. Results and discussion

Some forensic efficiency parameters of the 23 autosomal markers investigated in Ecuadorian population are shown and detailed in Fig 1. SE33 marker showed twice the number of alelles: 47 (Table S1), compared to the next most variable STR locus D18S51 with 24.

The range of heterozygosity varied between 0.9191 (SE33) and 0.5251 (VWA), the markers with higher values of Heterozygosity and PIC are SE33, PENTA E, FGA and D1S1656 and the less informative markers were VWA, D22S1045, D2S441 and TPOX. The power of exclusion ranged from 0.8345 (SE33) to 0.2104 (VWA) (Table 1).

The highest degree of heterozygosity, PIC, power of discrimination and power of exclusion in SE33 Locus were reported in other population analyses as U.S, Poland, Germany and Portugal [1,6,8,9]. Following SE33 (0.9969) as the best power of discrimination

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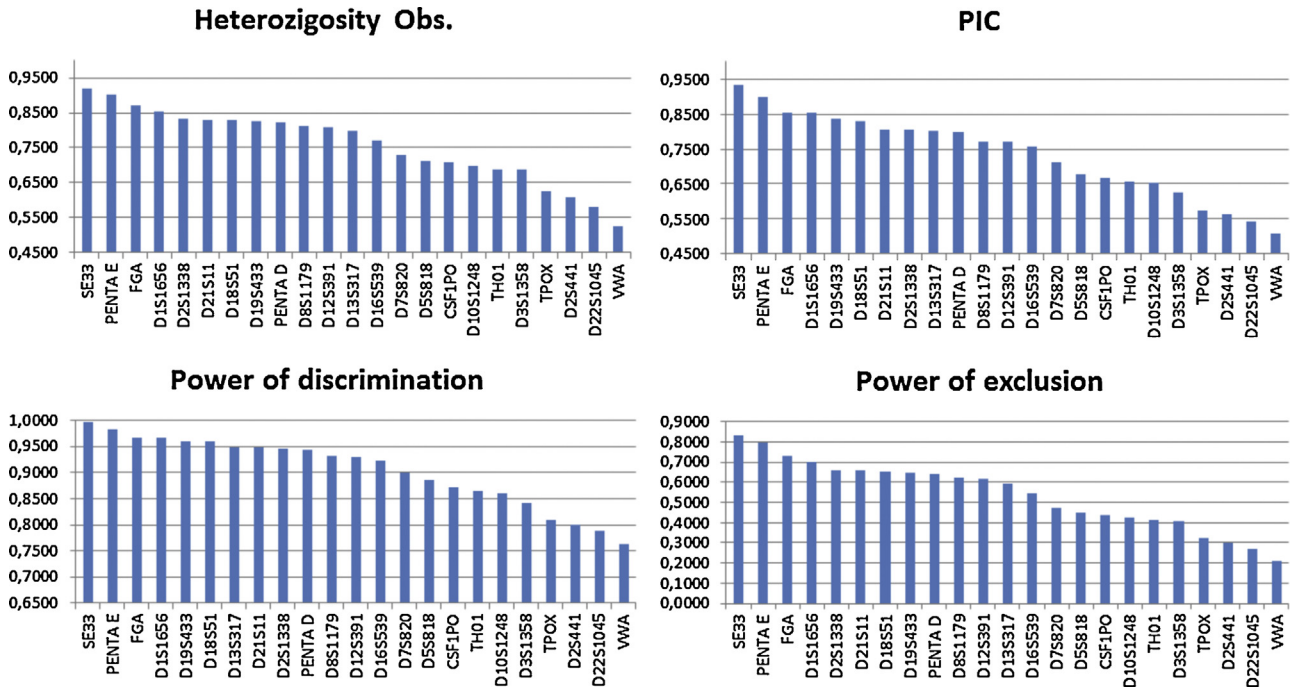

Fig. 1. Heterozygosity, polymorphism information content, power of discrimination and power of exclusion of 23 autosomal markers in Ecuadorian population.

Table 1
Heterozygosity, polymorphism information content, power of discrimination and power of exclusion of 23 autosomal markers in Ecuadorian population.

STR	Number of alleles	Heterozigosity Obs.	Power of coincidence	Power of discrimination	PIC	Power of exclusion	Typical paternity index	Minimal allele frequency
SE33	47	0.9191	0.0031	0.9969	0.9333	0.8345	6.1789	0.0025
D3S1358	10	0.6878	0.1579	0.8421	0.6272	0.4096	1.6013	0.0029
D1S1656	19	0.8533	0.0321	0.9679	0.8540	0.7013	3.4075	0.0033
D2S441	14	0.6074	0.1993	0.8007	0.5650	0.2999	1.2737	0.0027
D10S1248	10	0.6988	0.1407	0.8593	0.6534	0.4264	1.6600	0.0029
D13S317	9	0.7980	0.0505	0.9495	0.8021	0.5953	2.4751	0.0031
PENTA E	20	0.9016	0.0171	0.9829	0.8985	0.7987	5.0816	0.0034
D16S539	9	0.7711	0.0764	0.9236	0.7576	0.5465	2.1842	0.0030
D18S51	24	0.8280	0.0404	0.9596	0.8311	0.6519	2.9064	0.0032
D2S1338	14	0.8323	0.0544	0.9456	0.8039	0.6604	2.9820	0.0032
CSF1PO	12	0.7065	0.1292	0.8708	0.6656	0.4384	1.7038	0.0029
PENTA D	16	0.8233	0.0557	0.9443	0.7986	0.6430	2.8295	0.0032
TH01	8	0.6888	0.1345	0.8655	0.6552	0.4111	0.8655	0.0026
VWA	11	0.5251	0.2361	0.7639	0.5096	0.2104	1.0529	0.0026
D21S11	21	0.8303	0.0522	0.9478	0.8064	0.6565	2.9467	0.0032
D7S820	12	0.7279	0.1004	0.8996	0.7114	0.4727	1.8376	0.0029
D5S818	11	0.7123	0.1133	0.8867	0.6787	0.4475	1.7378	0.0029
TPOX	8	0.6245	0.1913	0.8087	0.5749	0.3213	1.3316	0.0027
D8S1179	11	0.8133	0.0684	0.9316	0.7713	0.6239	2.6774	0.0031
D12S391	21	0.8092	0.0702	0.9298	0.7693	0.6163	2.6211	0.0031
D19S433	20	0.8263	0.0389	0.9611	0.8349	0.6487	2.8786	0.0032
FGA	20	0.8695	0.0320	0.9680	0.8546	0.7336	3.8308	0.0033
D221045	10	0.5803	0.2121	0.7879	0.5411	0.2679	1.1914	0.0027

marker for Ecuadorian population are with 0.9829 (Penta E), 0.9680 (FGA) and 0.9679 (D1S1656).

4. Conclusion

In this study we demonstrate that SE33 is the best STR for forensic identification purposes because it showed the highest: polymorphism information content (PIC) of 0.9334; heterozygosity of 0.9191; power of discrimination of 0.9969 and power of exclusion of 0.8345. Hence, we recommend its use in routine and complex paternity cases. After SE33, the subsequent most informative STR markers for Ecuadorian population were PENTA E, FGA, D1S1656 and D19S433, and the less informative markers were VWA, D22S1045, D2S441, TPOX and D3S1358.

Conflict of interest

None.

Ethical standards

Experiments comply with the current Ecuadorian Laws.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.fsigss.2015.09.038.

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