

Analysis of NGM STR loci in South Portuguese Population

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INTRODUCTION

The Amp/STRs NGM Kit has five loci - D10S1248, D22S1045, D2S441 (mini-STRs) and D1S1656, D12S391 (midi-STRs) validated (1,2) - not present in any other kit used in our laboratory (Powerplex 16 System and Identifiler Plus). These five loci included in the European Standard Set were recommended by the European Network of Forensic Science Institutes (ENFSI) and European DNA Profiling Group (EDNAP). Due to National DNA Databases growing there is a need to use new markers to increase discriminative power of current identification kits (3).

MATERIAL AND METHODS

Blood stain samples were obtained from 452 unrelated individuals from South of Portugal involved in paternity testing casework. DNA was extracted using the Chelex® Resin. STR amplification was performed according to reaction conditions described in Amp/STRs® NGM™ Kit literature for GeneAmp 9700 PCR system. Amplified products were separated and detected by capillary electrophoresis using an Applied Biosystems® 3130 xl Genetic Analyzer and GeneMapper® v 3.2.1 software for allele determination.

Allele frequencies and Hardy-Weinberg equilibrium determination were carried out using Arlequin V3.5 software. Forensic parameters were calculated with Powerstats v1.2 (4)

DISCUSSION AND CONCLUSION

No evidence of Hardy-Weinberg equilibrium deviation was found (P value>0.05). Observed heterozygosity (Ho) values varies between 0.773 for D2S441 and 0.914 for D1S1656. Power of discrimination (PD) was smaller for D22S1045 and higher for D1S1656 and D12S391. Power of exclusion (PE) ranges from 0.533 for D16S539 and D2S441 to 0.824 for D1S1656.

❖ Being all loci highly polymorphic, typing of the 5 STR loci additionally to the previously established 17 autosomal STRs provides a good tool for forensic purposes.

❖ In our laboratory, this new kit is used as a complement tool in forensic investigation and complex paternity testing.

RESULTS

Allele frequencies and population parameters for the 15 NGM STR loci are shown in Figure 1 and Table 1.

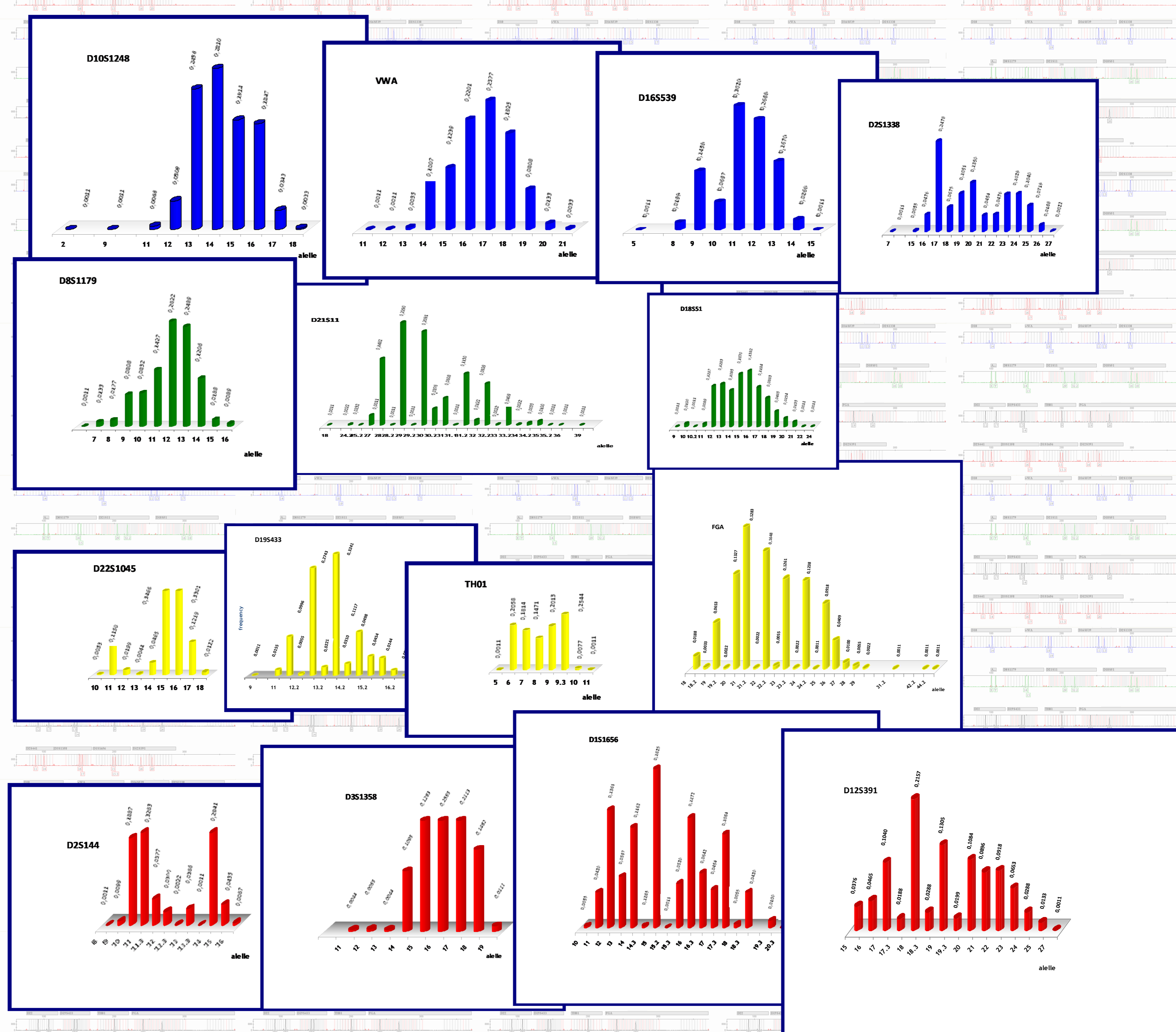


Figure 1 - Allele frequencies for 15 AmpliFSTR® NGM™ STR loci.

Table 1 – Forensic parameters for AmpliFSTR® NGM™ in a South Portuguese population.

	D10S1238	VWA	D16S539	D2S1338	D8S1179	D21S11	D18S51	D22S1045	D19S433	TH	FGA	D2S441	D3S1358	D1S1656	D12S391
Ho	0.7788	0.832	0.763	0.863	0.836	0.845	0.858	0.765	0.808	0.783	0.865	0.773	0.774	0.914	0.896
He	0.7870	0.8167	0.7828	0.8722	0.8206	0.8533	0.8801	0.7407	0.7971	0.7986	0.8708	0.7635	0.7942	0.8916	0.8879
HWE	0.1457	0.1729	0.9642	0.1003	0.6791	0.5073	0.3177	0.4926	0.4145	0.7228	0.1836	0.6231	0.255	0.6851	0.6693
Mp	-0.082	0.064	-0.079	0.032	0.057	0.039	0.028	-0.117	0.078	-0.072	0.033	0.093	0.075	0.024	-0.024
PD	0.918	0.936	0.921	0.968	0.943	0.961	0.972	0.883	0.922	0.928	0.967	0.907	0.925	0.976	0.976
PIC	0.75	0.790	0.749	0.859	0.797	0.84	0.870	0.7	0.766	0.770	0.860	0.729	0.76	0.881	0.878
PE	0.56	0.659	0.533	0.720	0.668	0.681	0.712	0.541	0.613	0.568	0.720	0.533	0.552	0.824	0.796
TPI	2.26	2.974	2.112	3.645	3.054	3.18	3.530	2.15	2.598	2.310	3.650	2.112	2.22	5.795	5.022

Ho-heterozygosity observed;He-heterozygosity expected; Hardy-Weinberg equilibrium based on exact test ; Mp-Matching Probability; PD - Power of Discrimination; PIC-polymorphism information content; PE- Power of Exclusion; TPI- Typical Paternity Index

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