DNA fingerprinting using STR CODIS Typing

CODIS (Combined DNA Index System) Typing

CODIS technology is a human identity testing system primarily used in forensic science. The system employs the identification of STR (Short Tandem Repeat) polymorphisms at 9 or more different loci and the Amelogenin present on the sex chromosomes. The markings are used to determine sex and distinguish between individuals. The combination of these polymorphisms across all loci in one person is known as their "DNA fingerprint." See **Table 1** for an example of some CODIS typings.

The Research Cell Bank (RCB) uses DNA typing as a Quality Control method. After typing, the fingerprint of each DNA sample is used to confirm the identity of samples in an inventory. Before typing, stock DNA samples are diluted to a concentration of 0.1 ng/uL. The samples are prepared for amplification using the *AmpFLSTR Profiler Plus* kit from Applied Biosystems.Inc. The kit contains primers for 9 well documented STR locations as well as the Amelogenin loci. The prepared samples are then incubated in the PCR machine and diluted again prior delivery to the Biotech Center located within FHCRC. Capillary Electrophoresis (3730xl DNA analyzer) reads the fluorescently labeled DNA to generate a peak pattern representative of the individuals DNA fingerprint. The peak data from the Biotech Center is analyzed back in the lab using GeneScan software.

CODIS offers the highest sample identity confidence level at 99.99% (see **Table 2**), however it is also the most expensive QC method that the RCB offers. The confidence level indicates that if two samples have the same CODIS type, it is 99.99% probable that they are from the same individual.

Table 1. UCI genotypes of selected B-LCL

	Genomic Locus									
Cell	**D3S1358**	**vWA**	**FGA**	**Amelo.**	**D8S1179**	**D21S11**	**D18S51**	**D5S818**	**D13S317**	**D7S820**
9014	**16, 18**	**16, 19**	**22, 26**	**X, X**	**12, 14**	**30, 31**	**15, 15**	**11, 11**	**9, 12**	**10, 11**
9016	**16, 16**	**16, 17**	**19, 24**	**X, X**	**10, 13**	**30, 31.2**	**13, 18**	**11, 11**	**9, 14**	**9, 12**
9021	**16, 17**	**15, 18**	**19, 22**	**X, Y**	**13, 15**	**27, 28**	**15, 19**	**12, 12**	**11, 11**	**8, 10**
9024	**14, 15**	**17, 18**	**21, 22**	**X, X**	**14, 15**	**30, 30**	**16, 19**	**10, 11**	**9, 11**	**8, 12**
9030	**15, 18**	**15, 17**	**22, 23**	**X, Y**	**13, 13**	**30, 31**	**15, 16**	**11, 11**	**8, 9**	**9, 12**

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Table 2. Statistical values of interest for the Hardy–Weinberg equilibrium

	D13S358	VWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820
Observed homozygosity	18.1%	17.5%	9.9%	19.3%	15.2%	11.7%	30.4%	20.5%	25.7%
Expected Homozygosity	20.4%	18.1%	12.9%	17.1%	16.1%	12.7%	27.6%	19.7%	19.9%
Homozygosity test (*P*)	0.463	0.848	0.245	0.435	0.745	0.705	0.417	0.797	0.054
Likelihood Ratio test (*P*)	0.955	0.110	0.052	0.278	0.531	0.505	0.268	0.247	0.006[a]
Exact test (Guo–Thompson) (*P*)	0.955	0.133	0.071	0.130	0.487	0.425	0.331	0.151	0.003[a]
Probability of Discrimination (PD)	0.923	0.937	0.960	0.942	0.949	0.964	0.875	0.923	0.924
Probability of Exclusion (PE)	0.593	0.635	0.733	0.658	0.679	0.739	0.480	0.611	0.606

[a] =significant, probability of discrimination (PD) and probability of exclusion (PE); for all the nine loci together, PD= 0.999997 and PE= 0.99991.

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