

The Philippine genetic database of Short Tandem Repeats (STR) in DNA-based paternity testing

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Philippine Journal of Science. 2002, 131(1):1-8. The utility of the Philippine genetic database for paternity testing was investigated. The seven Short Tandem Repeat markers used were HUMvWA, HUMTH01, HUMCSF1PO, HUMDHFRP2, HUMFES/FPS, HUMF13A01 and D8S306 with a combined Power of Paternity Exclusion of 99.17%. The Probability of Paternity (W) of 50 volunteer mother-child-father (family trios) calculated using the DNAView™ software ranges from 96.49% to 99.99%. The range of the Probability of Paternity ($W_{-mother}$) of the same 50 volunteer families, albeit excluding the mother's DNA was 79.76% - 99.99%, which were lower than the range of W values.

A mismatch possibly due to an insertion or deletion of a tetra-nucleotide repeat was detected at the HUMD8S306 locus in one family. This result highlights the need for at least two DNA mismatches prior to positively excluding a man from being the father of a child.

DNA testing of the 50 family trios and simulated motherless cases (man-child) was compared using 11 non-Philippine population databases. Variations in W reflected the variation of the allelic distributions of the STR markers included in these databases which, in some instances, could lead to false presumptions of paternity. The results of the present study underscore the need to implement scientific and legal guidelines for DNA-based paternity testing in the Philippines.

KEYWORDS

Philippine genetic database, short tandem repeats, family trios, paternity exclusion