RESOLUTION OF 3-PEOPLE STR-DNA MIXTURES USING LEAST-SQUARE DECONVOLUTION—INITIAL RESULTS

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Least Square Deconvolution (LSD) is a mathematical methodology previously developed by the authors to resolve 2-people STR-DNA mixtures. LSD uses the relative peak areas (or heights) of the allele peaks at each STR locus to develop the 'best fitting' genotype combinations and mass coefficients for the two contributors. Each locus is processed independently from all other loci, so that the best mass coefficients for each locus can be developed independent of all other loci, to allow a different best-fit mass ratio to fit at different locus. No reference genotype information is required to run LSD. Results to date have shown that LSD works very well and leads to correct and confident resolution at almost all loci in a 2-people mixture sample.

Due to the success of Least Square Deconvolution in resolving 2-people STR DNA mixtures, a similar approach was attempted for resolution of 3-people mixture samples. Because of the sheer number of genotype combinations possible at each locus with the respective observed mixture allele genotype, simply extending basic LSD methods to 3-people mixtures turned out to be less feasible. However, when a reference genotype profile was brought in to eliminate some of the genotype combination cases at each locus, LSD results showed a much more clear-cut resolution at most 4, 5, and 6-allele loci. For each of the 2 and 3-allele loci, several expert rules have been developed to aid in choosing the more applicable genotype combination. In general, for these loci, the genotype combination case with a best-fit DNA mass ratio that is consistent with those at higher-allele loci is selected to be the candidate resolution. Using the fitting errors and the best-fit mass ratio coefficients, a visual display of the clustering pattern of resolution combination cases was developed to aid in interpretation. As a result, confident resolutions for six to ten loci are often possible for a typical 3-people mixture sample. Extensive sensitivity studies of resolution quality to peak imbalance have also been carried out extensively, as well as evaluation of effectiveness of other modifications to the basic LSD algorithm. Results will be reported during the presentation.

In summary, extension of the LSD methodology to 3-people mixtures with the incorporation of a reference genotype, has shown to be promising in yielding confident resolution at more than half of the loci in a typical 13-loci profile. Future work includes the incorporation of statistics and other modifications to the basic LSD methodology to render a more robust resolution algorithm.

[1] Wang, T. W., N. Xue, and R. Wickenheiser, Least-Square Deconvolution (LSD): A New Way of Resolving STR/DNA Mixture Samples, 13th International Symposium Human Identification, October 7-10, 2002, Phoenix, AZ.