Complex Family Relationship Analysis to Solve a Problem of Supposed Kinship

<u>Anu Aaspõllu</u>, Ingrid Sumeri, <u>Merike Kelve</u> Institute of Chemical Physics and Biophysics, Tallinn EE0026, Estonia

Our laboratory recently worked on a problem of a half-sibling-ship. A DNA analysis was performed on two women and their children on a claim that the children had a common father. The supposed father died in a marine accident; his body was never found. To carry out the task we used Amplitype and STR systems. The probability of common parenthood was estimated in accordance with statistical analysis. The following equations were used to calculate the paternity index:

- if the children have the same paternal allele, the paternity index for the locus is 0.5 +1/(2b), "b" denoting the occurrence frequency of paternal allele;
- for a locus in which they have different paternal alleles the paternity index is 0.5;
- for a locus in which mother and child have the same allele, the paternity index is 0.5 +1/(a+b), "a" and "b" denoting the occurrence frequencies of respective alleles.

We obtained a combined paternity index between 7.23 and 383.81. Such a wide range is due to the impossibility to differentiate between the alleles inherited from the father and those inherited from the mother in some loci. Consequently, in some cases it is impossible to claim that both children have the same paternal allele in the locus. Calculations were made for both possibilities as we cannot say whether or not the children have the same paternity allele in the locus.

The range of the paternity index values could be narrowed. The further analysis of genetic relatives of the putative father (e.g. his genetic parents) would be absolutely necessary.

ഗ്രര