

Probabilities in Paternity and Kinship Scenarios

DNA test results for paternity and kinship studies are typically expressed by three sets of numbers. Paternity results use the paternity index (PI), the combined paternity index (CPI) and the probability of paternity (W). Kinship results are expressed similarly; however the term likelihood ratio, or LR, is utilized in lieu of paternity index.



Paternity Index (PI) or Likelihood Ratio (LR)

Paternity index or **likelihood ratio** is the statistic that summarizes all of the information provided by the genetic testing and is defined as the probability that some event will occur under a particular set of assumptions divided by the probability that the same event will occur under a different set of mutually exclusive assumptions. For example, in the case of paternity, the primary assumption is that the results for an individual genetic marker support the assumption that the tested man is the true biological father rather than an untested randomly selected unrelated man.



Combined Paternity Index (CPI) or Cumulative Likelihood Ratio (CLR)

The **combined paternity index** or **cumulative likelihood ratio** is determined by multiplying the paternity or likelihood ratio index values for each genetic marker tested. The value can range from 0 to infinity. Values less than 1 are indicative of non-paternity or non-kinship and if less than 0.001, exclusion of paternity or kinship. A value of one is neutral and does not provide evidence either way. Values greater than 1 suggests the tested man is the father or is evidence for kinship. The greater the CPI value, the stronger the genetic evidence. Most states accept a CPI of 100 or greater as the standard to establish paternity.



Probability of Paternity (W)

The **probability of paternity** is an expression of the strength of one's belief in the hypothesis that the tested man is the father, based on all evidence in the case, including nongenetic evidence.



Kinship Simulation

Kinship simulation is a computer generated set of statistics for a hypothetical pedigree. The program utilizes a Monte Carlo genotype generator that assigns genotypes in a random, consistent and unbiased fashion. Through the use of multiple simulations, a range of expected likelihood ratios can be generated.

Setting the Standard for Quality DNA Identification



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Simulation Results

The following table shows the results for the simulation of some popular scenarios calculated with the Caucasian database. Approximately 100 simulations were performed for each scenario. The ultimate probability and likelihood ratio of any genetic test is going to lie in the race, the frequency of the measured alleles in that population and the measured values themselves. While general in nature, the simulation results are useful as a guide for test selection.

Simulation Studies for Select Scenarios Using Identifiler Genetic Profile (16 Markers)

Test	Tested Individuals	Average Probability	Typical CLR or CPI	Range of Estimate*
Full Sibling or unrelated	Child A, Child B	97.10%	24,000	14,000-38,000
Full or Half Sibling	Child A, Child B, Mother	90.20%	450	280-700
Paternity	Child, Father	99.98%	89,000	67,000-120,000
Paternity	Child, Mother, Uncle	91.50%	140	100-200
Paternity	Child, Mother, Father	99.9999%	24,000,000	18,000,000-32,000,000,000
Paternity	Child, Uncle	79%	11	8.7-14
Paternity	Child, Mother, 1 Grandparent	88%	22	13-36
Paternity	Child, Mother 2 Grandparents	99.95%	38,000	29,000-48,000
Paternity	Child, 1 Grandparent	82%	13	11-17
Paternity	Child, 2 Grandparents	97.10%	420	320-550

*One standard deviation

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