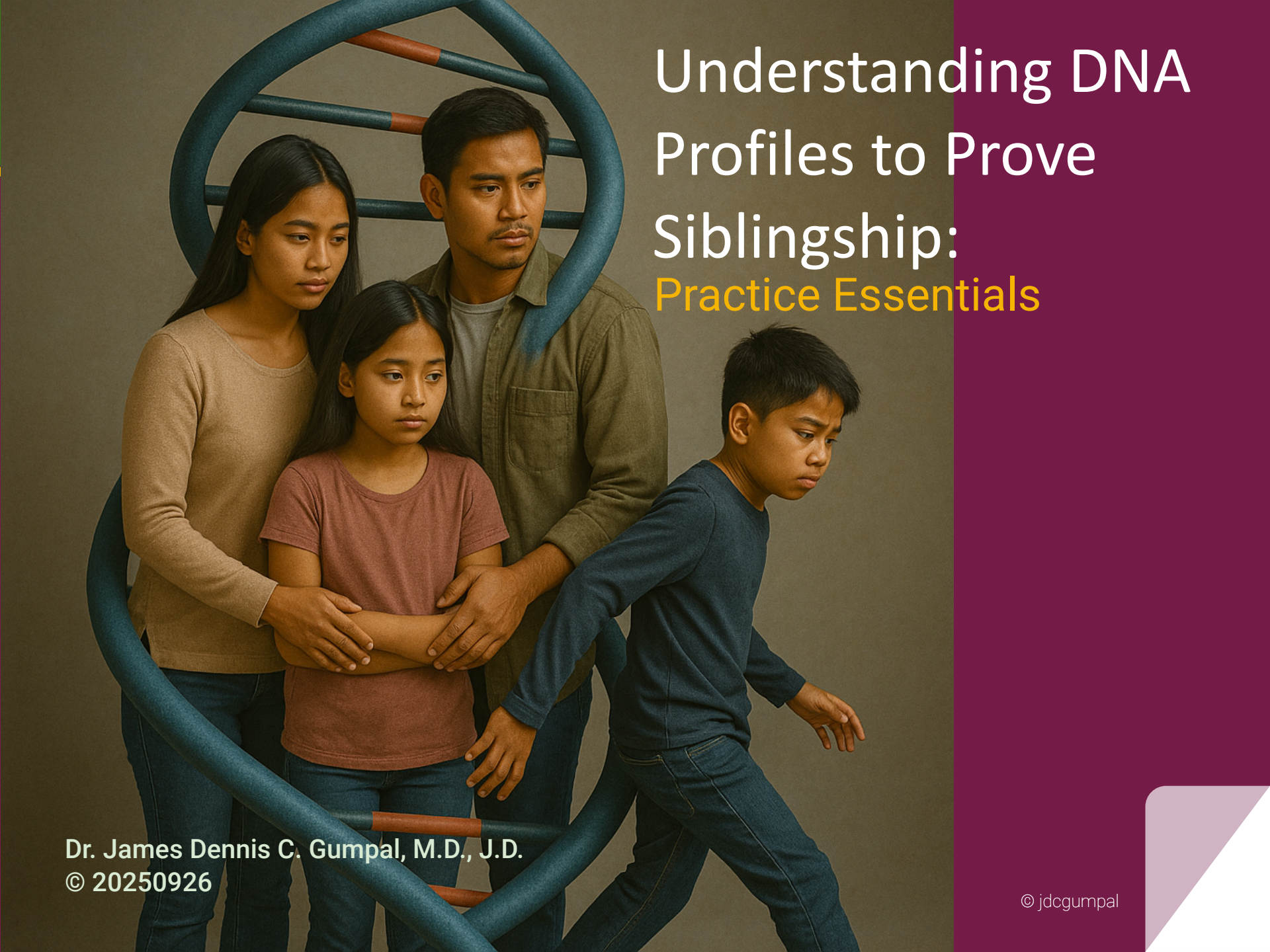


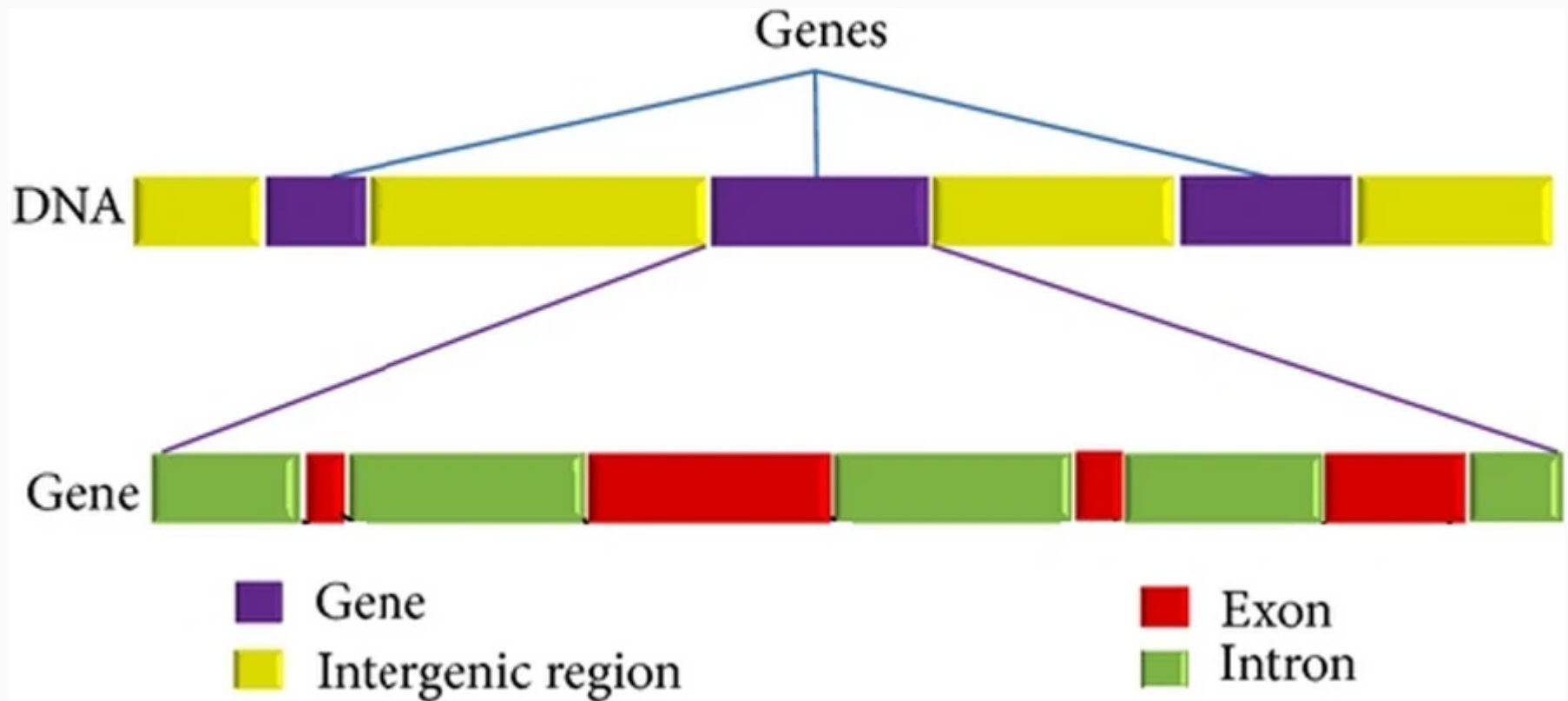


Understanding DNA Profiles to Prove Siblingship: Practice Essentials

Dr. James Dennis C. Gumpal, M.D., J.D.
© 20250926

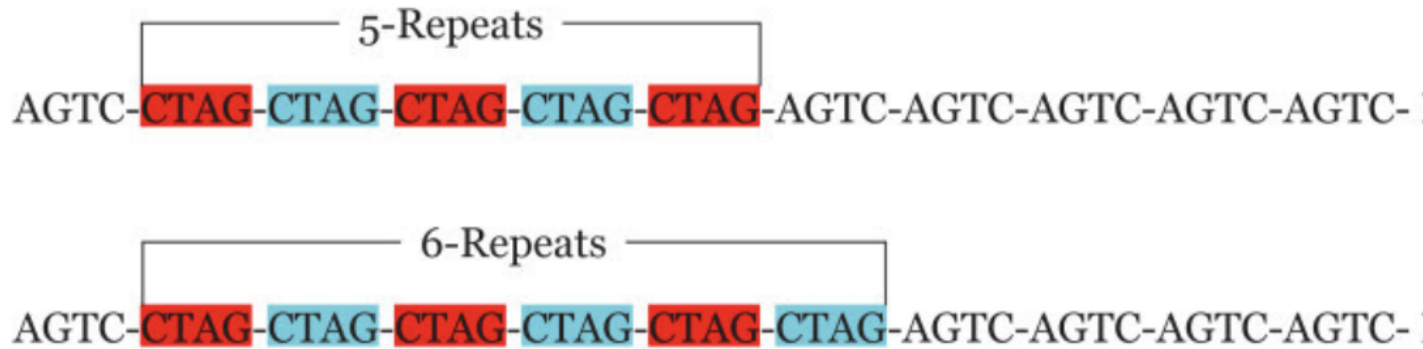
© jdcgumpal

Introns - location of most STRs



Intron - STR locus: **D7S820** (5,6)

SOURCE



Mother

Father

[/journals.library.columbia.edu/](http://journals.library.columbia.edu/)

Siblingship DNA Tests



Differences between a Full Sibling and a Half-Sibling DNA Test

Aspect	Full-Sibling Test	Half-Sibling Test
Shared parents	Both mother and father	One parent only
Expected allele sharing	~50%	~25%
Allele-sharing patterns used	IBS2, IBS1, IBS0	IBS1, IBS0 mostly
Index name	Full Siblingship Index (FSI)	Half Siblingship Index (HSI)
Interpretation strength	Higher typical SI and PoK	Lower typical SI and PoK
Common use	To confirm both parents are shared	To test same mother or same father when one parent is missing

IBS in Siblingship Tests

IBS Type	Meaning	Shared Alleles	Example	Typical in
IBS2	Both alleles are identical in both individuals	2 shared alleles	Sibling 1: 14,16 Sibling 2: 14,16	Full siblings
IBS1	One allele is shared between the individuals	1 shared allele	Sibling 1: 14,16 Sibling 2: 14,18	Full or half-siblings
IBS0	No alleles are shared	0 shared alleles	Sibling 1: 14,16 Sibling 2: 17,18	Unrelated individuals

In DNA testing for siblingship, IBS means “Identical by State.” It describes how many alleles (DNA versions) two people share at a genetic marker, regardless of where they came from.

IBS2 – both alleles are the same in both siblings (they share both copies).

IBS1 – they share only one allele at that marker.

IBS0 – they share no alleles at all.

- In full siblings, you often see many loci with IBS2 and IBS1 because they share both parents.
- In half-siblings, most shared loci are IBS1, since they share only one biological parent. These IBS patterns are used to calculate the Siblingship Index to estimate how likely the relationship is.

Full Sibling Test



Full Sibling DNA Test

STR Locus	Mother's Alleles	Putative Child #1 Alleles	Putative Child #2 Alleles	Putative Child #3 Alleles	Sibling shared allele	Allele Frequencies (p)	Full Sibling Index (FSI) = 1/p
D3S1358	15, 16	15, 18	15, 16	12, 13	15	15: 0.22; 16: 0.25; 18: 0.10; 12: 0.11; 13: 0.14	1/0.22 = 2.833
vWA	16, 17	16, 18	17, 18	14, 15	18	16: 0.18; 17: 0.22; 18: 0.12; 14: 0.14; 15: 0.09	1/0.09 = 1.5
FGA	21, 22	22, 25	21, 22	19, 24	22	21: 0.11; 22: 0.16; 25: 0.07; 19: 0.14; 24: 0.10	1/0.16 = 2
D7S820	8, 9	8, 10	9, 10	11, 12	10	8: 0.19; 9: 0.15; 10: 0.12; 11: 0.08; 12: 0.13	1/0.12 = 1.217
D8S1179	13, 14	14, 15	13, 14	10, 11	14	13: 0.14; 14: 0.11; 15: 0.09; 10: 0.10; 11: 0.08	1.700

Combined Full Siblingship Index (CFSI)

$$\begin{aligned}\text{CFSI} &= 2.833 \times 1.5 \times 2 \times 1.217 \times 1.7 \\ &= 17.5835811 \\ &\approx 17.6\end{aligned}$$

This means that the DNA profiles of Sibling #1 and Sibling #2 are about 17.6 times more likely to be observed if they are full siblings (sharing both biological parents) than if they are unrelated individuals.

CFSI Value (Likelihood Ratio)	Strength of Genetic Evidence	Interpretation / Meaning
< 1	Evidence against full siblingship	More likely to be unrelated
1 – 10	Weak or inconclusive support	Cannot distinguish between unrelated and full siblings
10 – 100	Moderate support	DNA results are moderately more likely if they are full siblings
100 – 1,000	Strong support	DNA results are strongly more likely if they are full siblings
> 1,000	Very strong support	DNA results practically prove full siblingship

In other words, the Combined Full Siblingship Index (CFSI) of 17.6 provides moderate support for full siblingship – not conclusive, but it indicates a higher likelihood of biological relationship compared to unrelated persons.

Probability of Full Siblingship (PoFS)

Probability of Full Siblingship (PoFS):

$$\begin{aligned}\text{PoFS} &= \text{CSFI}/\text{CSFI} + 1 = 17.6/17.6 + 1 = 17.6/18.6 \\ &= 0.9462365591 = 94.6\%\end{aligned}$$

A PoFS of 94.6% means there is strong support that Putative Child #1 and Putative Child #2 are full siblings.

PoFS Value	Interpretation	Meaning
> 99%	Practically proven full siblingship	Very strong genetic evidence of same parents
90–99%	Strong support	Highly likely to be full siblings
50–89%	Moderate support	Some shared genetic traits but not conclusive
≈ 50%	Inconclusive	Equally likely related or unrelated
< 50%	Evidence against siblingship	Profiles more consistent with unrelatedness



Half Sibling Test

Half-Sibling DNA Test

STR Locus	Mother's Alleles	Putative Sibling #1	Putative Sibling #2	Putative Sibling #3	Sibling-shared allele	Allele frequencies used (p)	HSI = (1+p)/4p
D3S1358	15,16	15,18	16,14	12,13	0	12:0.11; 14:0.15; 15:0.22; 16:0.25; 18:0.10	HSI(BS0) =0.50
vWA	16,17	16,18	17,14	14,15	0	14:0.14; 16:0.18; 17:0.22; 18:0.12; 15:0.09	HSI(BS0) =0.50
FGA	21,22	22,25	21,24	19, 24	24	21:0.11; 22:0.16; 25:0.07; 24:0.10 ; 19:0.14	$1+0.10/4 \times 0.10 = 2.75$
D7S820	8,9	8,10	9, 11	11 ,12	11	8:0.19; 9:0.15; 10:0.12; 11:0.08 ; 12:0.13	$1+0.08/4 \times 0.08 = 3.375$
D8S1179	13,14	14,15	13, 10	10 ,11	10	13:0.14; 14:0.11; 15:0.09; 10:0.10 ; 11:0.08	$1+0.10/4 \times 0.10 = 2.75$

$HSI (AB/AC) = (1 + p) / (4p)$, where p is the frequency of the shared allele.

If there are no shared allele, HSI (BS0) = 0.50

Combined Half-Siblingship Index (CHSI)

Combined Half-Siblingship Index (CHSI)

$$\begin{aligned}\text{CHSI} &= 0.50 \times 0.50 \times 2.75 \times 3.375 \times 2.75 \\ &= 6.380859375 = 6.38\end{aligned}$$

- This means that Putative Sibling #1 and #2 are 6.38 times more likely to be half-siblings or have only 1 common parent than when they are unrelated.
- A CHSI greater than 1 supports half-siblingship, while a CHSI less than 1 suggests the individuals are more likely unrelated.

CHSI Value (Likelihood Ratio)	Strength of Genetic Evidence	Interpretation / Meaning
< 1	Evidence against half-siblingship	DNA results support that they are unrelated
1 – 5	Weak support	Inconclusive — could be half-siblings or unrelated
5 – 10	Limited support	Slightly more likely to be half-siblings
10 – 100	Moderate support	Moderately more likely to be half-siblings
100 – 1,000	Strong support	Strong genetic evidence for half-siblingship
> 1,000	Very strong support	Practically proven half-siblingship

Probability of HS (PoHS)

Probability of Half-Siblingship (PoHS)

$$\begin{aligned}\text{PoHS} &= \text{CHSI} / (\text{CHSI} + 1) = 6.38 / (6.38 + 1) = 6.38 / 7.38 \\ &= 0.864498645 \\ &= 86.45\%\end{aligned}$$

PoFS Value	Interpretation	Meaning
> 99%	Practically proven full siblingship	Very strong genetic evidence of same parents
90–99%	Strong support	Highly likely to be half-siblings
50–89%	Moderate support	Some shared genetic traits but not conclusive
≈ 50%	Inconclusive	Equally likely related or unrelated
< 50%	Evidence against siblingship	Profiles more consistent with unrelatedness

This means that putative siblings #1 and #2 shared some genetics traits but not conclusive of half-siblingship.

If we increase the sample 5 STRs to 20 STRs, it may be possible to yield a different result

References

- Ge, J., Sun, Q., Chen, X., ... & (other authors). (2020). How many familial relationship testing results could be wrong? *Forensic Science International: Genetics*, 48, 102335. <https://doi.org/10.1016/j.fsigen.2020.102335> PMC
- Linacre, A. (2014). Forensic DNA profiling: State of the art. *Research and Reports in Forensic Medical Science*, 4, 1–14. <https://doi.org/10.2147/RRFMS.S60955> Taylor & Francis Online
- Neuhuber, F., (et al.). (2012). An unusual case of identification by DNA analysis of siblings. *Forensic Science International: Genetics Supplement Series*, (Supplement 1), S1-S? ScienceDirect
- Sosiawan, A., Yudianto, A., Furqoni, A. H., Nzilibili, S. M., & Nuraini, I. (2019). Full-sibling allelic frequency and sharing among Madurese: STR technique by 12 locus and the sex-typing amelogenin gene. *Egyptian Journal of Forensic Sciences*. <https://ejfs.springeropen.com/track/pdf/10.1186/s41935-019-0143-5> Universitas Airlangga Official Website
- Yudianto, A., Setiawan, F., & Sumino, R. (2025). Paternity test through kinship analysis as forensic identification technique. (Unpublished manuscript or conference paper) ResearchGate
- Yudianto, A., (et al.). (2022). Sibling pair analysis in the identification of siblings using 13 STR CODIS loci. *Human Genetics / Forensic Genetics Journal*. PMC