False Positive DNA Matches

Iain Kennedy

November 2019

The arrival of a detailed Y chromosome SNP tree starting around 2012-3 enabled us to measure the accuracy of the earlier legacy STR tests. Take this set of results as an example. I've sorted it by SNP result even though its an STR test.

Genetic STR distance	SNP group	True or False
4	A5387	False
4	A725	False
4	S659	False
4	S659	False
4	FGC5856	True
4	S7814	False

SNP discovery prefixes:

FGC = Dr. Greg Magoon (Full Genomes, Inc)

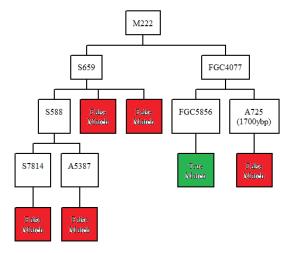
S = Dr. Jim Wilson (ScotlandsDNA)

A = Iain Kennedy and Dr. Thomas Krahn (YSEQ)

Left off the chart are a further 5 'matches' who are only tested down to the M222 level at an STR distance of 3 or 4. This SNP result is insufficient to determine if the match is tue or not.

Consulting a reduced SNP tree with just these markers on it:

True and False Positive Matches



'Matches' as reported by legacy STR testing. Tester is FGC5856+ hence 5/6 or 85% are false.

and we can see that A725 is the closest of the false match branches and is dated to around 1700 years ago. Hence all the other false match branches must be at least that far back or further – you can check the dates on the Yfull tree but it isn't strictly necessary.

Since only one of the six SNP-tested STR matches is correct we can calculate the true positive rate as 1/6. Put another way the False Positive Rate of this person is 5/6 or 85%. In plain English the test is almost completely wrong.

My project no longer uses STR testing.

The false positive rate of the Kennedy SNP testing project is ZERO.