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FROM THE X-FILES: ARE X-DNA MATCHES USUALLY MORE DISTANT THAN AUTOSOMAL MATCHES?

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Are X-DNA matches usually more distant than autosomal matches?

By Brit Nicholson

Abstract

Our intuition might lead us to believe that an X-DNA match of a given number of centiMorgans would be from a more distant ancestor than an autosomal match of the same size. After all, the X Chromosome is recombined less and passed fully intact more often than the autosomes. This study shows that it would be reasonable to apply this logic to one particular chromosome, but not when comparing the X Chromosome to all autosomes combined.

Introduction

The X Chromosome has different properties than the autosomal chromosomes, which are named named Chromosomes 1-22. As of September of 2021, averages and ranges of shared X Chromosome DNA (X-DNA) have been available online here: https://dna-sci.com/2021/09/07/shared-x-dna-between-relatives/.

One will notice that, unlike with autosomal DNA (atDNA), average shared X-DNA is different depending on the sexes of intermediate ancestors even for a given relationship type. For example, of the four different types of 1st cousins, there are three different sets of averages and ranges of X-DNA. The reason that X-DNA has different averages within the same relationship type is that it has different rules for recombination than atDNA.

X-DNA, which is not passed from fathers to sons and is passed wholly intact from fathers to daughters, has only half of the opportunities for recombination compared to atDNA. This effect of fewer opportunities for recombination might lead some to believe that X-DNA shared between relatives usually comes from a more distant ancestor than atDNA.

This hypothesis seems to have never been tested. It is important to understand the limits of what that hypothesis proposes. The X Chromosome is much smaller than all atDNA combined. And only Chromosomes 1-6 are larger than the X Chromosome.[1]

If someone asked you whether a cousin with whom you share DNA only on the X Chromosome was from a more distant ancestor than one with whom you share the same amount on Chromosome 7, you would likely say “yes,” and with good reason. Based on parent/child matches compared in the chromosome browser

at 23andMe, Chromosome 7 and the X Chromosome are of similar size[1], but we know that the X Chromosome experiences fewer recombination events than the autosomes.

While this line of reasoning is intuitive, it must have a limit. What if we asked the same question about Chromosome 6? What if we asked it about Chromosome 1? What if we compared the X Chromosome against all atDNA combined? What if the amount of atDNA in the human genome was so large that X-DNA could not possibly "outlast" it over the course of many generations? Previously, there has been no attempt to evaluate those questions.

The X Chromosome has different recombination rules than the autosomes. Females typically have two copies of the X Chromosome while males usually only have one copy. Interesting results of this are that calico cats are always female and that women are less likely to be color blind than men. In genetic genealogy, we must keep in mind that X Chromosomes only recombine when passed from mothers to their children. Fathers transmit no X Chromosome to their sons and, since they only have one X Chromosome, will pass it un-recombined to their daughters.

Since X-DNA cannot be passed from a father to a son, a male will have fewer potential X-DNA ancestors than a female. With further generations back the number of a woman's potential X-DNA ancestors in a given generation approaches the inverse of the golden ratio, or ~0.618. A male has half as many potential X-DNA ancestors in a given generation.

As discussed above, that X Chromosome DNA (X-DNA) has fewer opportunities for recombination than autosomal DNA (atDNA) may lead us to believe that a X-DNA match will typically come from a more distant common ancestor than an atDNA match. But this question is meaningless unless we rephrase it to be more specific. A meaningful question would compare matches of the same centiMorgan (cM) size. I will call this Question 1: *Will a match who shares a given amount of X-DNA usually share a more distant common ancestor than an atDNA match of the same amount?*

We would need a tool that calculates probabilities in order to answer Question 1. But a similar question will give us the same results. Question 2: *Are we likely to share more X-DNA with distant cousins than atDNA? Question 2 is easier to evaluate but harder to understand. How are Question 1 and Question 2 related?*

If we are likely to share more X-DNA with distant cousins than atDNA, then the answer to Question 1 is yes: an X-DNA match would typically be more distant for a given cM amount. If we are likely to share more atDNA with distant cousins

than X-DNA, then the answer to Question 1 is no: an atDNA match would typically be more distant for a given cM amount.

The answers to Questions 1 and 2 must be the same. To help visualize why that is true, consider Table 1 below.

Relationship	Hypothetical Avg. atDNA (cMs)	Hypothetical Avg. X-DNA (cMs)
15C	0	1
14C	1	2
13C	2	4
12C	4	8
11C	8	16

Table 1. Hypothetical average shared X-DNA vs. atDNA for distant cousins. Chr., chromosome; cMs, centiMorgans; 15C, 15th cousin, etc. The only purpose of this table is to show that, if X-DNA typically comes from a more distant shared ancestor for a given cM value, then the amount of X-DNA for a given distant relationship type will also be greater, on average, than the amount of shared atDNA for that relationship type.

The numbers in Table 1 are completely made up. The only purpose of this table is to show that Questions 1 and 2 must have the same answer. In Table 1 we imagine that a 15th cousin will share the same number of cMs of X-DNA, on average, as the number of cMs of atDNA that a 14th cousin will share, on average. We imagine that this trend continues to slightly less distant cousins until we get to 11th cousins sharing atDNA and possibly even more recent.

If the values in Table 1 were true averages, then it would show that X-DNA is typically more distant than atDNA for a given cM amount. So the answer to Question 1 would be yes. It would also show that we are likely to share more X-DNA than atDNA for a given distant relationship. So the answer to Question 2 would also be yes. Table 1 shows the trends that we would see if the answers to both questions were yes. If the column labels in Table 1 were reversed, then the answer to both questions would be no.

Before we get started, we already know the answer to Question 1 in cases of close relatives. An X-DNA match who shares a full copy of the X Chromosome will share about 182 cMs of X-DNA with you. More often than not, relatives who share a full copy of the X Chromosome are very close family members, such as a sibling, parent/child, or grandparent/grandchild. On the other hand, according to Orogen relationship predictions[2] an atDNA match of 182 cMs is more likely to be a 2nd cousin once removed. If X-DNA really is typically more distant than atDNA for a given cM value, that is certainly not the case for close relatives and at some degree of cousinship X-DNA will overtake atDNA as the source of more shared cMs.

This study will use a published simulation tool called Ped-sim[3,4,5] to generate a dataset of distant cousins, who may or may not share atDNA or X-DNA. Because very distant cousins rarely share DNA, the dataset for this study must be very large.
It would not be possible to do this analysis with empirical data. Any empirical dataset would be orders of magnitude smaller than the dataset that will be available from simulations. Additionally, empirical data are very messy in genetic genealogy. The nature of this study requires a clean dataset without endogamy or double relationships. The question of whether or not X-DNA is typically from a more distant common ancestor cannot be answered if there are multiple relationships, especially if some of them are unknown, because we would not know which ancestor(s) the atDNA and X-DNA came from.

Ped-sim runs based on the genetic map of Bhérer et al. (2017)[5]. While this is a refined map comprised of over 800,000 atDNA single nucleotide polymorphisms (SNPs) and over 18,000 X-DNA SNPs, the genetic map is not comprehensive[5]. For example, this map does not include information about the small pseudo-autosomal regions that exist between the X and Y Chromosomes in human DNA. The accuracy of the results from Ped-sim will be limited by the data that are included in the genetic map of Bhérer et al. As the human genome is studied further, we may want to revisit studies such as this one. However, the important factors that will drive these results are the number of recombinations per chromosome and the size of each chromosome. These factors have not changed substantially as our knowledge of the human genetic map has improved.

For the same reason that empirical data would fall far short as the primary dataset for this study, empirical data would also be of no use to supplement or validate this study. A small dataset of empirical data used to conduct such a study would surely show different results than the large dataset of data from Ped-sim, but it would be the empirical data that were incomplete and less

accurate. Because Ped-sim has been validated with empirical data[3], no further validation will need to be done here.

In addition to introducing Ped-sim as a new tool, Caballero et al. (2019)[3] performed an analysis on close relatives, including showing the importance of crossover interference and sex-specific genetic maps. Sex-specific genetic maps are important up to sixth cousins (6C) and less important for more distant cousins[3]. Caballero et al. stressed the importance of close relative research in genetic genealogy. However, the tool is built to simulate any distant relationships, so long as the constraints of the computer are not exceeded.

Being an advanced peer-reviewed model that uses the refined genetic map of Bhérer et al., Ped-sim is the ideal choice for a comparison of atDNA to X-DNA for distant relatives.

Methodology

This study will compare the shared atDNA and X-DNA between distant cousin pairs from 6th cousins (6C) to 15th cousins (15C). For simplicity, only cases in which both DNA testers are female or both are male will be analyzed. Using Ped-sim, I will simulate 500,000 pairs for each degree of cousin. Half cousins and cousins from different generations than each other (removed) will not be considered in this analysis.

Ped-sim will generate an output file that contains any matching segments between the 500,000 cousin pairs for a particular degree. Matching segments will be measured in cMs. All cM values in this study will be reported based on the genetic map of 23andMe. Output files will contain some small segments that are not above the matching thresholds of 23andMe. Although all of the output segments from Ped-sim are identical-by-descent (IBD), segments below the thresholds will be removed in order to provide a more accurate comparison to DNA matching databases.

For each segment in the output files, an approximate conversion will be made from the Bhérer et al. genetic map[5] to the 23andMe genetic map[1]. This conversion will be based on the proportionate differences in total autosomal cMs for reported atDNA segments and the proportionate differences in total X Chromosome cMs for X-DNA segments.

The low-cM thresholds at 23andMe are as follows: 7 cMs for the first autosomal segment and 5 cMs for any additional autosomal segments for the same match;

6 cMs for X-DNA segments when one or more testers is female, and 1 cM for X-DNA segments when both testers are male[6].

Then I will test Question 2, the easier to test of the two questions in the Introduction. After that, I will build the tool that can answer Question 1, which means that anyone else will be able to answer Question 1 from then on.

Question 2: Do distant cousins share more X-DNA or more atDNA?

After applying the autosomal and X-DNA cutoff values used at 23andMe, I will sum the cMs from all remaining segments between any cousin pairs who share DNA.

I will then compare the total amount of atDNA to the total X-DNA for each degree of cousins. If X-DNA turns out to not be typically more distant than atDNA, I will investigate whether or not X-DNA is typically from a more distant common ancestor than any autosomes. If X-DNA turns out to be typically more distant than Chromosome 1 DNA, then that would likely be true when compared to other autosomes.

Question 1: Is the most probable shared ancestor or ancestor pair for a given amount of shared X-DNA farther back than an atDNA match who shares the same amount?

Specifically to answer this question, I will build a relationship prediction tool that only considers X-DNA shared between two matches. Autosomal-only relationship predictors already exist[7]. Neither of the two relationship predictors in this study will employ population weights, although those typically make relationship predictions more accurate. Since the purpose of this study is only to compare the two relationship predictors by using the same methodology, the methodology should be kept as simple as possible.

For the X-DNA-only predictor, there will be no requirement that two DNA testers share no atDNA. Instead, any shared atDNA will be ignored and the predictor will be built based on the amount of shared X-DNA, if any.

Results

Question 2: Do distant cousins share more X-DNA or more atDNA?

Distant cousin pairs rarely share DNA. Fewer than 0.3% of 8th cousin pairs shared any IBD segment above the matching thresholds at 23andMe. No 15th cousins shared DNA and only four 14th cousin pairs shared DNA above the

matching thresholds at 23andMe. Table 2 shows that the ratio of atDNA to X-DNA decreases with genetic distance, as expected. While 500,000 trials per relationship type is not enough to always show a monotonically decreasing relationship, that correlation is still clear. Thus, atDNA on the whole is typically more distant than X-DNA. This is even true in cases with two female DNA testers, as shown in Table 2.

Relationship	Total atDNA (cMs)	Total X-DNA (cMs)	atDNA / X-DNA	# of Matching Cousins	# of Matches w/ 2 Segments	# of Matches w/ 3 Segments	# of Matches w/ 4 Segments
15C	0	0	-	0 (0)	0	0	0
14C	42.3	7.2	5.88	4 (4)	0	0	0
13C	35.0	0	-	3 (10)	0	0	0
12C	99.0	23.6	4.19	12 (31)	0	0	0
11C	232	58.6	3.96	22 (103)	0	0	0
10C	948	81.3	11.7	91 (369)	0	0	0
9C	4,210	396	10.6	390 (1,396)	0	0	0
8C	16,700	1,590	10.5	1,470 (4,873)	19	0	0
7C	78,000	6,570	11.9	6,260 (17,100)	173	7	0
6C	327,000	26,600	12.3	24,000 (56,800)	2,810	213	16
...	...	...	...				
Mother/Child*	3,540	182	19.5				

Table 2. X-DNA vs. atDNA for distant female cousins summed across a population. A comparison of total X-DNA vs. total atDNA amounts for 500,000 female cousin pairs of each degree is shown. All reported values are for cM sums after applying 23andMe low cM cutoff values with one exception: The number of matching cousin pairs in parentheses indicates the number of matching cousins before applying the low cM thresholds. Chr., chromosome; cMs, centiMorgans; 6C, 6th cousin, etc. *Statistics are added for one mother/child pair to show the trend of atDNA / X-DNA with varying degree of relationship.

This study treats atDNA and X-DNA separately. While some cousin pairs might have shared both atDNA and X-DNA, the counts in table columns only include the respective amounts for either. The trend of decreasing atDNA to X-DNA could eventually result in more X-DNA than atDNA at a certain distance. However, the tendency to share no DNA whatsoever appears to come before the point that X-DNA can become more prevalent. There was no degree of cousins for which 500,000 simulated DNA testers shared more X-DNA than atDNA in this study.

If two female testers can be expected to share more atDNA than X-DNA, it may be possible that they will not typically share more X-DNA than DNA from Chromosome 1. We know that X-DNA would usually outlast the DNA from Chromosome 7, which has a similar size, because X-DNA has fewer opportunities for recombination. The interesting question is if any of the autosomes can outlast X-DNA on their own. If there is an autosome that can do

so, it would be the largest one. Table 3 provides a comparison of Chromosome 1 to X-DNA.

Relationship	Total Chr. 1 DNA (cMs)	Total X-DNA (cMs)	Chr. 1 DNA / X-DNA
15C	0	0	-
14C	0	7.2	0
13C	11.2	0	-
12C	17.0	23.6	0.720
11C	24.8	58.6	0.423
10C	31.4	81.3	0.386
9C	390	396	0.985
8C	1,390	1,590	0.874
7C	6,330	6,570	0.963
6C	25,800	26,600	0.970
...	...	...	...
Mother/Child*	284	182	1.56

Table 3. X-DNA vs. Chromosome 1 DNA for distant female cousins summed across a population. A comparison of total X-DNA vs. total Chromosome 1 amounts for 500,000 female cousin pairs of each degree is shown. All reported values are for cM sums after applying 23andMe low cM cutoff values with one exception: The number of matching cousin pairs in parentheses indicates the number of matching cousins before applying the low cM thresholds. Chr., chromosome; cMs, centiMorgans; 6C, 6th cousin, etc. *Statistics are added for one mother and daughter pair to show the trend of Chr. 1 DNA / X-DNA with varying degree of relationship.

For all relationships in Table 3 except 13th cousins, more X-DNA was shared than Chromosome 1 DNA between two female DNA testers. Like with combined atDNA in Table 3, 500,000 trials is not enough for the ratio of Chromosome 1 DNA to X-DNA to always be monotonically decreasing with increasing generational distance. But again there is a clear correlation. These results show that X-DNA is usually passed down in greater quantities than DNA from Chromosome 1 for two females who are 6th cousins or more distant. This means that X-DNA will usually outlast any one autosomal chromosome for two female relatives who share DNA.

This effect might be diminished if using empirical data. Since Chromosome 1 contains a known pile-up region (region with excess IBD sharing)[8], DNA matches from the same founding populations might share more Chromosome 1 DNA, on average, than X-DNA. But the important point is that X-DNA has the potential to outlast individual autosomes, while not outlasting atDNA as a whole.

If two female DNA testers can be expected to share more atDNA than X-DNA, then that will also be true for two male DNA testers, who have half of the X-DNA and half of the potential X-DNA ancestors. Table 4 shows that, for every relationship type tested and where some DNA was shared, the population of male cousins shared more atDNA than X-DNA.

Relationship	Total atDNA (cMs)	Total X-DNA (cMs)	atDNA / X-DNA	# of Matching Cousins	# of Matches w/ 2 Segments	# of Matches w/ 3 Segments	# of Matches w/ 4 Segments
15C	0	0	-	0 (0)	0	0	0
14C	8.1	0	-	1 (3)	0	0	0
13C	35.0	2.2	15.9	4 (10)	0	0	0
12C	60.1	13.6	4.42	6 (19)	0	0	0
11C	217	7.7	28.2	20 (119)	0	0	0
10C	991	52.5	18.9	94 (368)	0	0	0
9C	3,800	123	30.9	336 (1,280)	10	0	0
8C	17,400	531	32.8	1,460 (4,650)	38	0	0
7C	75,600	2,190	34.5	5,860 (16,300)	318	6	0
6C	322,000	7,820	41.2	22,900 (54,700)	2,600	180	8
…	…	…	…				
Maternal Half-Siblings*	142	90.42	1.57				

Table 4. X-DNA vs. atDNA for distant male cousins summed across a population. A comparison of total X-DNA vs. total atDNA amounts for 500,000 male cousin pairs of each degree is shown. All reported values are for cM sums after applying 23andMe low cM cutoff values with one exception: The number of matching cousin pairs in parentheses indicates the number of matching cousins before applying the low cM thresholds. Chr., chromosome; cMs, centiMorgans; 6C, 6th cousin, etc.*Statistics are added for pair of maternal half-brothers to show the trend of atDNA / X-DNA with varying degree of relationship.

This raises another question. If two DNA testers are males, will matches on the X Chromosome typically be more distant than matches on Chromosome 1, as was true for two female testers?

Table 5 shows what may be inconclusive results. There are only two degrees of cousinship for which the population shared more X-DNA than Chromosome 1 DNA: 11th and 12th cousins. The trend of Chromosome 1 DNA divided by X-DNA appears to decrease to unity and below with increasing genetic distance, however for 13th cousins the total for Chromosome 1 DNA is higher than the X-DNA total. This may be because of one or more anomalous data points

anywhere in the range 11th to 13th cousins, but we will not know for exactly which degree.

Relationship	Total Chr. 1 DNA (cMs)	Total X-DNA (cMs)	Chr. 1 DNA / X-DNA
15C	0	0	-
14C	0	0	-
13C	11.2	2.2	5.05
12C	10.0	13.6	0.74
11C	0	7.7	0
10C	69.2	52.5	1.32
9C	314	123	2.55
8C	1,390	531	2.62
7C	5,820	2,190	2.66
6C	24,600	7,820	3.15
...	...	...	...
Maternal Half-Siblings*	142	90.42	1.57

Table 5. X-DNA vs. Chromosome 1 DNA for distant female cousins summed across a population. A comparison of total X-DNA vs. total Chromosome 1 amounts for 500,000 female cousin pairs of each degree is shown. All reported values are for cM sums after applying 23andMe low cM cutoff values with one exception: The number of matching cousin pairs in parentheses indicates the number of matching cousins before applying the low cM thresholds. Chr., chromosome; cMs, centiMorgans; 6C, 6th cousin, etc. *Statistics are added for a pair of maternal half-brothers to show the trend of Chr. 1 DNA / X-DNA with varying degree of relationship.

If the anomalies are in the data for 11th and 12th cousins, then it may be that Chromosome 1 DNA outlasts X-DNA for two distant male cousins, in contrast to that for two female cousins. It seems more likely, though, that the anomaly is for 13th cousins because the ratio of Chromosome 1 DNA to X-DNA is higher for 13th cousins than even that of 6th cousins. In that case, the table would appear to show that X-DNA does outlast Chromosome 1 DNA for two distant male cousins as it did for two female cousins. But the only way to get a clearer picture would be to simulate more than 500,000 cousin pairs for each relationship type.

One idea to keep in mind is that X-DNA has an advantage over atDNA for two male testers at 23andMe because the low-cM cutoff in that case is only 1 cM. If the cutoffs were equal, it is very likely that Chromosome 1 could show a clear tendency to outlast X-DNA for two male cousins, in contrast to that for two female cousins.

Total atDNA was higher than X-DNA whether DNA testers were male or female. For two female testers, X-DNA was more prevalent than Chromosome 1 DNA for all degrees of relationship from 6th cousins to 15th cousins. While this would not be the case for a mother/child match, the transition would occur somewhere between close family members and 6th cousins. The results of X-DNA versus Chromosome 1 DNA for two male testers were inconclusive, but probably show that Chromosome 1 DNA outlasts X-DNA given the advantage that X-DNA has from the lower cutoff value at 23andMe.

Question 1: Is the most probable shared ancestor or ancestor pair for a given amount of shared X-DNA farther back than an atDNA match who shares the same amount?

A new tool (located here: https://dna-sci.com/tools/orogen-x-unw/) calculates probabilities for relationships based on only the X-DNA that two matches share, including close family to 8th cousins once removed. A relationship predictor (located here: https://dna-sci.com/tools/orogen-unw/) that is traditional but without population weights allows for atDNA-only predictions based on cM inputs. Using an X-DNA predictor without population weights and an atDNA predictor that also excludes population weights allows for an unbiased comparison.

The methodology for the two relationship predictors is described in Nicholson (2022)[7]. This article provided validation with empirical data. Additional, anyone can enter theoretical averages or reasonable cM values for a given relationship into either predictor in order to verify that that relationship is given a high probability.

One does not need to have access to empirical data to enter data into these predictors; the result will be the same whether a person enters 100 cMs as a randomly chosen value or whether they enter it because they have a DNA match with that value. The important test is whether or not any integer cM value entered into both predictors will show more distant common ancestors for the X-DNA predictor. The results show that entering any cM input into these tools ranging from 8 cMs to over 364 cMs, the latter of which is the highest possible value for full-sisters at 23andMe, an X-DNA match of a given cM value is likely

more recent than an atDNA match of the same cM value. This defies our intuition that X-DNA matches share a farther-back ancestor.

Discussion

Whether comparing atDNA and X-DNA matches for a given cM value or whether analyzing the amounts of both types of DNA that would be found in a population of matches at a given degree of cousinship, the results are clear. The evidence is to the contrary of the idea that large segments of X-DNA will be shared between distant relatives as compared to atDNA.

From close family members to 15th cousins, DNA matches can expect to share more atDNA than X-DNA. A 15th cousin is a *very* distant relative, sharing ancestors far outside of the timeframe in which we could reasonably identify a genealogical connection with a DNA match. If X-DNA cannot overtake atDNA before that distant of a relationship, at which point it is extremely unlikely for cousins to share any DNA, then it would be of no use to say that X-DNA is usually farther back than atDNA. If 20th cousins are likely to share more X-DNA than atDNA, we will likely not ever be able to prove it. Genetic genealogists need information that can actually help them with their X-DNA matches rather than theories that would be true if DNA could be shared over more distant relationships.

There is one more conclusion that we can draw from these results. Since the vast majority of distant cousin matches only share one segment of DNA, the results also apply to single segments for distant cousin matches. That is, a segment of shared X-DNA between distant cousin matches is likely to come from a more recent ancestor or ancestor pair than a single segment of atDNA.

Our intuition told us that X-DNA should typically be more distant than atDNA from a particular chromosome. But it failed us when it told us that that should apply to atDNA on the whole. It is true that X-DNA is typically more distant than DNA from an autosome of a similar size because of fewer opportunities for the X Chromosome to recombine. But we could not expect that property to carry on indefinitely. Ped-sim, along with the refined genetic map of Bhérer et al., suggest that our intuition will have to be revised. According to the findings of this study, an X-DNA match of a given number of cMs will usually come from a more recent common ancestor than an atDNA match of the same number of cMs.

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