Genetic relations between people via the X/Y chromosome pair

Günther P. Können, Soest, The Netherlands

Private Document 2010/02
21 Feb 2010 (Dutch); updated English version 30 Dec 2010

Abstract

The genetic relation between humans via their sex chromosomes differs from that via the other chromosomes. One of the consequences is that sisters are genetically more closely related with each others than with their mother or with their own daughters.

1. Background

The formula for genetic relationship [Eq (2) in Können (2010)]

$$Fract = Rel = \sum_{all.strings} \left(\frac{1}{2}\right)^{n} \qquad (1)$$

(where n is the number of genetic steps) holds for all 22 not-sexlinked pairs of chromosomes (the so-called autosomes). I call that quantity Rel_{auto}. Then, one has for the total:

$$Rel = \frac{22}{23} Rel_{auto} + \frac{1}{23} Rel_{sex} \qquad (2)$$

where Rel_{sex} represents the relationship via the pair of sex chromosomes.

2. Application

a. Woman-woman (relationship via X chromosomes)

Women posses only X chromosomes. From the standpoint of a woman, the father is only haploid, as he possesses only one X chromosome. That is the same situation as if he were (in that pair of chromosomes) the result of inbreed, so homozygote in his sex chromosomes. The count along the genetic strings is the same as in case of autosomes, but:
1. a genetic step that passes a man is skipped (as he has only one X chromosome, and that X chromosome is directly passed on to a daughter)
2. a string with two consecutive men in it is omitted – hence yielding $Rel_{sex} = 0$ *(a man can never transfer his X chromosome via a son to a descendant. So a female descendant via such a string is never related with her female ancestor via her sex chromosomes).*

Example 1: Mother/daughter: $n = 1$, as in the in the normal case (so $Rel_{sex} = Rel_{auto} = ½$).
Example 2: Sister/sisters A,B. Via their mother one has the usual count, as there is no man in that string. So two genetic steps (hence $n = 2$): $Rel_{sex} = ¼$. Via the father there is one step less as Dad does not take part in the counting, as he is haploid in his X chromosome: $Rel_{sex} = ½$. So, in total (the sum of the two strings) yields $Rel_{sex} = ¾$.
The startling consequence is that via the sex chromosomes sisters are genetically closer related with each other than with their own mother or daughters, for which the genetic relationship has the normal (autosomic) value of ½.

In the word of the bees this effect is even more prominent, as males are haploid in all their chromosomes – and not just in their X chromosome. Sisters (the workers) are therefore closer related with each other than with an own daughter. So the best strategy to transmit their genes to the next generation is to refrain from own offspring, and instead to promote her mother (the queen) to produce more (female) offspring, in particular next queens. This evolutionary argument forms the basis of the social behavior of bees (and some ants), including the fact that workers are sterile (see e.g. Hartl (1980), p. 357-358).

b. Man-woman (relationship via the X chromosomes)

Here also one has only to deal with the X chromosome, as in the sex chromosomes only via the X chromosome genetic relationship between male and female family members can exists. *The count in the genetic strings are therefore the same as in case of woman-woman*, because:
- a man has only one X chromosome, and that chromosome is unchanged transmitted to its daughter.
- a man can never transmit the X chromosome, required for female offspring, via his son.

Of course is the first step from the male endpoint of a string to his mother or a male starting point to daughter is counted – but steps via man within are skipped in the counts. Ann, as in case of woman-woman, strings containing two consecutive men are entirely omitted (all yielding by definition $Rel_{sex} = 0$).

Example 1*:* Father/daughter or mother/son: $n = 1$, just like in the normal case (so $Rel_{sex} = Rel_{auto} = ½$).
Example 2: Brother/sister A,B. Via the mother the normal counting applies, as their is no man in the string. Hence two steps: $Rel_{sex} = ¼$. The string via the father is omitted, as it contains two consecutive men. So: $Rel_{sex} = ¼$; two times less than Rel_{auto}.
Example 3: Great-grandfather/great-granddaughter (W = woman, M = man):
String M-W-W-W : $n = 3$, like by all other pair of chromosomes (so $Rel_{sex} = Rel_{auto} = ⅛$).
String M-W-M-W: $n = 2$ ($Rel_{sex} = ¼$), as the step via M in the string is skipped. So the value is the same as in case of grandfather/granddaughter in the string M-W-W.
String M-M-W-W (or M-M-M-W): Is omitted ($Rel_{sex} = 0$) since it is impossible to transmit via this string a X chromosome from starting point to its endpoint.

c. Man-man

Genetic relation can here materialize in two ways: either by transmission of the X chromosome, or via the transmission of the Y chromosome. For the first mechanism the same rules hold as for the woman/woman (en hence the man/woman) case; for the second mechanism one has to take into account that the Y chromosome is directly and unchanged transmitted through the direct male line. This results in the following modification of the counting-rules:
1. Via his X chromosome as before: a step via a man is skipped (he has only one X chromosome, and that one is transmitted unchanged)
2. Via his Y chromosome: a string with two consecutive men is omitted, ***unless*** *the string consists of men only. In the latter case,* ***regardless*** *of the length of the string, $Rel_{sex} = ½$ (the Y chromosome is transmitted unchanged)*

Example 1*:* Father/son: $n = 1$, just like in the normal case (so $Rel_{sex} = Rel_{auto} = ½$).
Example 2: Brother/brother A,B. Via the mother one has the normal count, as there is a woman in the string – so it is the relationship via the X chromosome that counts. Hence two

steps: Rel_{sex} = ¼. The string via father yields Rel_{sex} = ½ (transmission Y chromosome); Added up: Rel_{sex} = ¾, just like in case of sister/sister.
Example 3: Great-grandfather/great-grandson (W = woman, M = man):
Via string M-W-W-M : $n = 3$, like by all other pairs of chromosomes (so $Rel_{sex} = Rel_{auto}$ = ⅛).
Via string M-M-M-M: $n = 1$ (Rel_{sex} = ½), as the Y chromosome is transmitted unchanged
Via string M-M-W-M (or M-W-M-M): is omitted ($Rel_{sex} = 0$) since it is impossible to transmit via this string neither a X chromosome nor a Y chromosome from starting point to its endpoint.

Remark 1:
The variation in the total number of Y chromosomes in the world is very smal. In first approximation one can assume that men in a given country all share the same Y chromosome, irrespective if they are family or not. Between two men in such an community – family members or not – one has minimally Rel_{sex} *= ½. In how far* Rel_{sex} *has a larger vlue than ½ should be determined from other strings than the direct male lines. From this point of view is the genetic relationship between two men according to Eqs (2) and (4) van Können (2010) minimally* ${}^{2}\log 46 = 5.5$*, whereas it is infinitely (remote) between two arbitrary women (*$Rel_{sex} = 0$ *).*

Remark 2:
On the other hand contains the Y chromosome hardly genes. If we consider relationship on the level of genes, the Y chromosome hardly contributes. It is therefore be maintained to consider the Y chromosome as a dummy that plays no significant role in genetic relationship. In this approximation, men can be regarded to be haploid in his sex chromosome. Relationship via the Y chromosome (father and son) can be excluded. The count is then exactly the same as in case of woman-woman. The result in the three examples above changes than as follows:

Example 1: father/son: *no relationship via the sex chromosomen* (so $Rel_{sex} = 0$)
Example 2: brother/brother A,B. Via the mother one has Rel_{sex} = ¼, as before. Via the father on has $Rel_{sex} = 0$; Added up gives Rel_{sex} = ¼, three times less than before.
Example 3: Great-grandfather/great-grandson (W = woman, M = man):
Via string M-W-W-M : $n = 3$, as before (so $Rel_{sex} = Rel_{auto}$ = ⅛).
Via string M-M-M-M: *no relationship* ($Rel_{sex} =0$).
Via string M-M-W-M (or M-W-M-M): $Rel_{sex} = 0$, as before.

References:

Hartl, Daniel L. (1980), *Principles of Population Genetics,* Sinauer Associates Inc., Sunderland Mass, ISBN 0-87893-272-0.
Können, G.P. (2010), *When does the genetic relationship between relatives end*?, Private Document 2010/01, http://www.guntherkonnen.com/downloads/2010_Verwandtschaft.pdf