A note about double first cousins

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If your sibling marries your spouse's sibling, then your child and your sibling's child are double first cousins. Clark (2023) made use of the correlation between double first cousins, expected if genetics is the only source of familial resemblance, to argue that certain genealogical complications do not substantially affect the expected correlations between other types of relatives.

It turns out that the literature on the correlation between double first cousins is somewhat unsettled. Nagylaki (1992) and Yengo and Visscher (2018) reviewed the history. This note will try to justify the best solution to this puzzle to date. It should be emphasized at the outset that the precise expression for this correlation has a negligible quantitative impact on Clark's argument.

Let h^2 be the heritability of the trait and m the correlation between the genetic values of spouses. Fisher (1918) gave the correlation between double first cousins as

$$r^{\rm DFC} = \left(\frac{1+3m}{4}\right)h^2,\tag{1}$$

neglecting a possible contribution from non-additive genetic variance. It is widely agreed that this expression will be accurate for small values of m, but not for large values. The reason is that as m increases, double first cousins occur more frequently in the population and become more unrepresentative.¹

Gimelfarb (1981) accounted for these difficulties and found the covariance between the genetic values of double first cousins to be

$$\operatorname{Cov}_{g}^{\mathrm{DFC}} = \frac{\frac{1}{4}(1+m)^{3}}{1-\frac{1}{4}(1+m)^{2}m^{2}}v,$$
(2)

where v is the additive genetic variance in the entire population. To obtain the correlation between double first cousins, we must divide this expression by the phenotypic

¹Clark (2023) noted a pair of brothers marrying a pair of sisters in his own family tree.

variance in double first cousins (*not* the phenotypic variance in the population at large). Gimelfarb (1981) did not give an expression for the variance in double first cousins, but we can deduce it from other results in his paper.

Gimelfarb (1981) gave the covariance between the genetic values of the parents of a double first cousin as

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$$\operatorname{Cov}_{g}^{\text{parents of DFC}} = \frac{m + \frac{1}{4}m(1+m)^{2}}{1 - \frac{1}{4}m^{2}(1+m)^{2}}v$$
(3)

and the variance of their genetic values as

$$v^{\text{parents of DFC}} = \frac{1 + \frac{1}{4}m^2(1+m)^2}{1 - \frac{1}{4}m^2(1+m)^2}v.$$
(4)

The genetic value of the offspring is equal to the average genetic value of the parents plus a deviation resulting from Mendelian segregation. This deviation has a variance equal to half of the additive genetic variance that would be observed in a randommating population, v(1-m). Let A stand for the genetic value of an individual (i.e., the A in the ACE model of behavioral genetics). We then have

$$v^{\text{DFC}} = \text{Var}\left(\frac{A^{\text{father}} + A^{\text{mother}}}{2}\right) + \frac{(1-m)v}{2}$$
$$= \frac{1}{2}v^{\text{parents of DFC}} + \frac{1}{2}\text{Cov}_{g}^{\text{parents of DFC}} + \frac{(1-m)v}{2}$$
$$= \frac{1 + \frac{1}{8}m(1+m)^{2}(1+m^{2})}{1 - \frac{1}{4}m^{2}(1+m)^{2}}v.$$
(5)

Now we can compute the phenotypic correlation between double first cousins as

$$r^{\text{DFC}} = \frac{\text{Cov}_g^{\text{DFC}}}{v^{\text{DFC}} + v\left(\frac{1}{h^2} - 1\right)}$$

= $\frac{\text{Cov}_g^{\text{DFC}}h^2}{h^2 v^{\text{DFC}} + v\left(1 - h^2\right)}$
= $\frac{\frac{1}{4}(1+m)^3h^2}{1 + \frac{1}{8}h^2m(1+m)^2(1+m^2) - \frac{1}{4}m^2(1+m)^2(1-h^2)}.$ (6)

As $m \to 0$, we recover Fisher's $h^2(1+3m)/4$.

I thank Loic Yengo for invaluable conversations and correspondence. If anyone wishes to cite the result in this note, for now refer to Gimelfarb (1981) or Nagylaki (1992) or Yengo and Visscher (2018), although none of these works gave the result in this form.

References

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