

Occidentalist

The end logic of equality is the overcoming of all life boundaries, all distinctions, and all separations until Singularity or death

Did Sarich Get It Right?

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Lewontin's 7% of between race genetic variance is often cited as proof of the insignificance racial differences [9]. This 7%, of course, should be 10%; [when averaged across studies](#) and markers, the median value is at least ~10% [see: 8,11]. Rarely is it explained what this 10% implies. When it comes to population differences, it implies moderate genetic differentiation within a species [7]:

"0 to 0.05 indicates little genetic differentiation.

"0.05 to 0.15 indicates moderate genetic differentiation.

0.15 to 0.25 indicates great genetic differentiation.

0.25 indicate very great genetic differentiation.

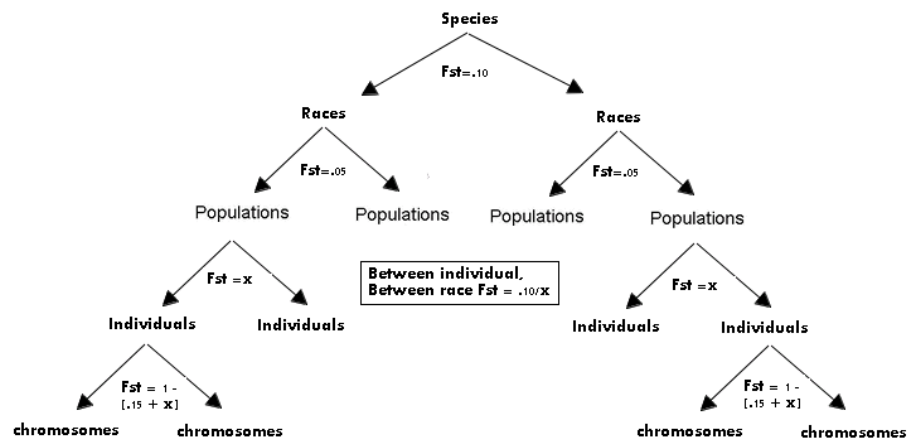
(Wright, S. 1978. Evolution and the genetics of populations)"

Were we to take the difference at face value, it would also imply moderate heritable phenotypic differences between racial populations [12]. Now, when it comes to phenotypic differences, Sarich and Miele [6] have argued that the 10% (or 15% if we are talking about populations) represents a deflated value:

Yet the world had to wait until 2002 for someone to explain the basic problems with Lewontin's famous 15 percent. It was Henry Harpending replying to a question from Frank Salter. Lewontin had noted that 85 percent of the genetic variability was among individuals within populations, and only an additional 15 percent was added when individuals in different populations were compared. However, this analysis omits a third level of variability—the within-individual one. The point is that we are diploid organisms, getting one set of chromosomes from one parent and a second from the other. To the extent that your mother and father are not especially closely related, then, those two sets of chromosomes will come close to being a random sample of the chromosomes in your population. And the sets present in some randomly chosen member of yours will also be about as different from your two sets as they are from one another. So how much of the variability will be distributed where?

*First is the 15 percent that is interpopulational. The other 85 percent will then split half and half (42.5 percent) between the intra- and interindividual within-population comparisons. **The increase in variability in between-population comparisons is thus 15 percent against the 42.5 percent that is between-individual within-population. Thus, $15/42.5 = 32.5$ percent [This should be 35%], a much more impressive and, more important, more legitimate value than 15 percent.***

Basically, according to them, the 10%/15% refers to the between race/population genetic variance and not to the between individual, between race/population genetic variance. The between race/population variance, they argue, includes both within individual variance and between individual variance — and the latter is the only relevant variance when it comes to the issue of heritable phenotypic differences. The partitioning of the variance would look as follows:



Sarich and Miele cite Henry Harpending who first brought up the issue. This point, however, has been criticized. In “Sarich Got it Wrong”, Anthropologist Jim Bidon [1] makes three counter points:

1) Parents would not be completely unrelated, since every one is related.

“If my parents were completely unrelated, and their parents were completely unrelated, and their parents parents were completely unrelated, going on back into history”

2) The Y chromosome and mtDNA do not come in pairs, so the variance is not split equally within and between individuals.

“Since Y chromosomes and mtDNA do not come in double copies, they would reduce by some theoretically quantifiable amount the 1/2 of the within population variation that can be attributed to intra-individual variation.”

3) The within group variance already contains the within individual variance

In a hierarchical partitioning like this, each lower level is fully contained by the variation explained by the succeeding level. That is, intra-individual variation is a fraction of the inter-individual (within population) variation

The first point clearly demonstrates a misunderstanding of the meaning of genetic variance and relatedness. Genetic difference and relatedness are defined as the correlation between the gametes with respect to the population. Within an ethny, if the pairing off is random, the correlation will be random. The second point is valid. But blood group proteins, RFLP loci, enzymes, SNPs, etc. all show 4-17% differentiation (median 10%); as it is, the Y and MtDNA population variance range much higher [11], so there would be no reduction, relative to Sarich’s figure, on that account. As best I can tell, the third point represents a misunderstanding of how genetic variance/relatedness is measured [8].

For those interested, Salter (2008) [5] explains the logic of this point:

Appendix: The Apportionment of Variation Within and Among Families p.337-338.

[Henry Harpending’s derivation of within-family variation is unpublished as I write. Following is his derivation, received as a personal communication.]

If we choose an allele A at some locus that has frequency p in a randomly mixed population, and if we pick a single gene from this population from this locus, the probability that it is A is just p. The variance of this frequency is just the variance of a single Bernoulli trial, $p(1-p)$ or pq if we let $q=1-p$

If our population of genes is grouped in certain ways, we can partition this variance into

within-group and between-group components. We are doing precisely what Lewontin (1972) and others have done, partitioning diversity (variance) into within-and between-group parts.

First consider diploid individuals in a random mating population. What is the variance of the frequency of A in diploid individuals. Since mating is random, diploids are simply random alleles taken 2 at a time. The variance of the frequency of A in samples of 2 is binomial, $pq/2$. This shows that half the variance is among diploid individuals.

Now consider the variance within an individual. Call the frequency in an individual $p(i)$. The variance of the frequency of A in a single gene chosen from an individual is $p(i)(1-p(i))$, and this figure averaged over all individuals is:

$$\begin{aligned} & \text{Average}(p(i)(1-p(i))) \\ &= \text{Average}(p(i) - (p(i) \times p(i))) \\ &= p - p^2 - \text{Var}(p(i)) \\ &= pq - pq/2 \\ &= pq/2 \end{aligned}$$

since the average of the square of any random variable is the mean of that variable squared plus the variance of that variable. This shows that half the variance of a gene frequency is within any individual member of a random mating population. We have partitioned the variance into between and within individual components as 1/2 within and 1/2 between. (Once stated, this result is obvious, but I cannot find an earlier reference to it. Perhaps it was considered too obvious to publish

So based on 650,000 single-nucleotide polymorphisms, Li et al., (2008) found a between-region variance of ~10% [2]. So, we would have: 10% between region/45% intra-individual + 45% interindividual or roughly $10/45 = 22\%$. The above doesn't mean much (apart from calculations of inclusive fitness and quantifications of population diversity), because F_{st} isn't a good measure of genetic-phenotypic mediation. As a case example, Long and Kittles (2003) found a between human population F_{st} of 11% based on their sample; when they added chimpanzees, the between population F_{st} increased only to 18% [3]. Mountain and Risch (2004), citing this example, note that "a low F_{ST} estimate implies little about the degree to which genes contribute to between-group differences." [4]

While this between individual versus between population F_{st} difference might not mean much, for an entrepreneurial academic, it might make for an easy paper. These days, nothing is too obvious to publish.

[1] Bidon, Sarich Got it Wrong. <http://anthropology.ua.edu/race/index.php?title=Sarich%20Got%20It%20Wrong>

[2] Li, et al., 2008. Worldwide human relationships inferred from genome-wide patterns of variation

[3] Long and Kittles, 2003. Human Genetic Diversity and the Nonexistence of Biological Races

[4] Mountain and Risch, 2004. Assessing genetic contributions to phenotypic differences among 'racial' and 'ethnic' groups

[5] Salter, 2008. Misunderstandings of Kin Selection with Reference to the Immortality of Values and the Delay in Quantifying Ethnic Kinship

[6] Sarich and Miele, 2004. Race: The Reality of Human Difference:

[7] See, for example: de Oliveira, et al., 2007. Structure and genetic relationships between Brazilian naturalized and exotic purebred goat domestic goat (*Capra hircus*) breeds based on microsatellites

"The F_{ST} value measures the degree of genetic differentiation between populations. Considering the

interpretation of F_{ST} , it can be presumed that a value lying in the range 0 to 0.05 indicates little genetic differentiation, 0.05 to 0.15 indicates moderate differentiation, 0.15 to 0.25 a large degree of differentiation and values above 0.25 very great differentiation (Wright 1978; Hartl and Clark, 1997)."

**Lewontin (1972) didn't use F_{ST} ; rather he used Shannon information measure. The result are often assumed to be equivalent. I will follow the conventional practice here.

[8] refer to: Holsinger and Weir, 2009. Genetics in geographically structured populations: defining, estimating and interpreting F_{ST}

Estimate 5-10% between populations

[9] Konigsberg, et al., 2009. Estimation and Evidence in Forensic Anthropology: Sex and Race

[10] Campbell and Trishkoff, 2008. AFRICAN GENETIC DIVERSITY: Implications for Human Demographic History, Modern Human Origins, and Complex Disease Mapping

Estimate 10-16% between major populations

[11] Jorde, 2000. The distribution of human genetic diversity: a comparison of mitochondrial, autosomal, and Y-chromosome data

[12] Imagine some trait for which there is a 1:1 phenotypic/geneotypic relation and for which the within population SDs are 15; assuming equally numerous populations, if the genes for that trait were randomly dispersed throughout the genetic variance, a 10% between group variance would be equivalent to a .67 SD difference.

$$\begin{aligned} \text{between trait variance} &= a(b)/w = y \\ &= 2(\sqrt{y}) = z \end{aligned}$$

a=within group trait variance
b=between group genetic variance
w= within group genetic variance
y= between group trait variance
z=between group trait difference

$$\begin{aligned} \text{between trait variance} &= 225(.10)/.90 = 25 \\ &= 2(\sqrt{25}) = 10 = .67 \text{ SD} \end{aligned}$$



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