

1. Below are the major electrophoretic genotypes at the *ApoE* locus and their average serum cholesterol levels:

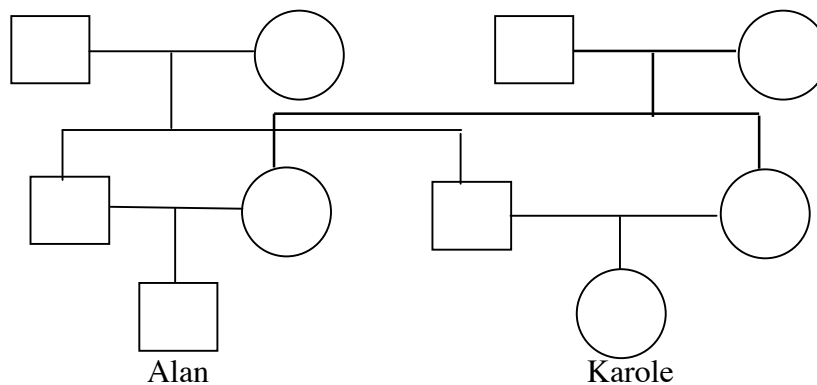
Genotype	$\epsilon 2/\epsilon 2$	$\epsilon 2/\epsilon 3$	$\epsilon 3/\epsilon 3$	$\epsilon 2/\epsilon 4$	$\epsilon 3/\epsilon 4$	$\epsilon 4/\epsilon 4$
Ave. Chol. Level (mg/dl)	136.0	161.4	173.8	178.1	183.5	180.3

The allele frequencies in a randomly mating population are 0.4, 0.1 and 0.5 for the $\epsilon 2$, $\epsilon 3$ and $\epsilon 4$ alleles respectively. The variance of serum cholesterol level in this population is $800 \text{ mg}^2/\text{dl}^2$. What are the broad-sense and narrow sense heritabilities for serum cholesterol as determined by this locus?

Genotypes:	$\epsilon 2/\epsilon 2$	$\epsilon 2/\epsilon 3$	$\epsilon 3/\epsilon 3$	$\epsilon 2/\epsilon 4$	$\epsilon 3/\epsilon 4$	$\epsilon 4/\epsilon 4$	Sum/Ave/Var
HW genotype	0.160	0.080	0.010	0.400	0.100	0.250	1
Genotypic Mean	136	161.4	173.8	178.1	183.5	180.3	Ave.=171.1
Genotypic Dev.	-35.075	-9.675	2.725	7.025	12.425	9.225	Var.=260.9
Average Ex.	-11.485	2.615	8.665				
BV.	-22.970	-8.870	5.230	-2.820	11.280	17.330	Var.=182.0
dom. dev.	-12.105	-0.805	-2.505	9.845	1.145	-8.105	Var.= 78.9
heritabilities	broad:	0.326					
	narrow	0.227					

20 points: 2 pts for HW, 1 pt for phenotypic mean, 3 pts for genotypic deviations, 3 pts for average excesses, 3 pts. for breeding values, 2 pt. for genetic variance, 2 pts. for broad-sense heritability, 2 pts. for additive variance, 2 pts for narrow sense heritability.

2. Half sibs share $\frac{1}{4}$ of their genes due to a shared parent. Double cousins also share $\frac{1}{4}$ of their genes. In case you do not know what a double cousin is, here is an example pedigree, in which Alan and Karole are double cousins:



Suppose a polygenic trait is such that there is both an additive and dominance variance and that all environmental deviations are independent and identically distributed for all individuals. Which relationship would have a greater phenotypic correlation, half-sibs or double-cousins, and why?

Both half sibs and double cousins would share the same additive variance component as they both share $\frac{1}{4}$ of their genes. However, double cousins also share some of their genotypes, so the dominance

genotypic variance would also contribute to their phenotypic correlation (5 pts). Hence, the phenotypic correlation of double-cousins is greater than that of half-sibs (5 pts).