

Genetic Fidelity

Keith T. Weber, LadyHawke Great Pyrenees

Many dog fanciers reading this will already have heard the term "back massing". For those unfamiliar with the term, it refers to the potential for relatively distant ancestors of a given dog –we'll call him Fido, to have substantial genetic influence on Fido because the distant ancestor –let's call him Spot, appears a multitude of times in Fido's pedigree. The way it works goes like this: genetically, we know that 50% of Fido's genes were contributed from his sire while the balance was contributed by his dam. But these genes came from somewhere and the source was the grandparents. Since there are four grandparents to carry the generation forward to Fido's parents, each is believed to have a 25% genetic contribution. It may be obvious that we now have genetic contributions totaling 200% but that is not a problem¹. The problem lies, not in the math, but in the logic. You see we have made an assumption regarding gene flow that flies in the face of what we *know* about genetics.

The genes contributed to Fido's parents by Fido's grandparents are not marked and bundled as a package. Rather, they simply become part of the genetic makeup of Fido's parents. Then, during cell division (producing sperm (or egg)), 50% of Fido's parent's genes are copied and stored within the sperm (or egg). Since this process follows random assortment there is no guarantee that the genes added to the sperm (or egg) represent Fido's grandparents equally.

To better understand what is happening, try this simple experiment. Take out your box of Chinese checkers and select 10 black marbles and 10 white marbles. These 20 marbles will represent Fido's father's genetic makeup. The black marbles were contributed by Fido's grandfather while

the white marbles were contributed by Fido's grandmother. Next, place all 20 marbles in a paper bag and shake them up. Without looking, reach inside and draw 10 marbles (50%). These marbles represent the genes that will be contributed to Fido from his sire. Under nearly all individual instances, you will not select five black marbles and five white marbles. However, if you repeat the experiment numerous times, you will average five black marbles and five white marbles.

This is an important observation and it is where the assumption we are discussing came from. That is, is back massing a real consideration? The answer is that it matters if you are a breeder or a population geneticist. If today's kennels contained hundreds of dogs each then the answer *may* be yes. However, breeders deal with individuals (or small numbers of dogs at best) and calculating time-consuming back massing percentages –which operate on averages within populations-- may be a waste of time. Breeders deal with individuals –like Fido– while population geneticists deal with –you guessed it-- populations.

The simple experiment we performed earlier (the black and white marbles) helped illustrate genetic assortment and flow from grandparent, to parent, and ultimately to Fido. Back massing is actually a bit more complicated in that it deals with the potential for *distant* ancestors (10 or more generations removed) to influence Fido today. To add an additional layer of complexity, we consider that Spot (the distant ancestor) appears numerous times within Fido's 10 generation pedigree. Attempting to illustrate this with bags of black and white marbles would be sheer folly. We would need thousands of bags of marbles and impeccable record keeping. Luckily, we can solve this problem using computer simulations to quickly and accurately illustrate genetic assortment and flow from Great-grand-daddy Spot to Fido.

A CASE STUDY

While preparing to breed Fido, owners Mr. and Mrs. Smith reconstructed Fido's pedigree backward 20 generations. When finished, they discovered that Spot (a famous show dog and hall of fame producer) appeared many times between the 10th and 15th generation. In fact, Spot appeared 2322 times in Fido pedigree². Knowing this, the Smith's wondered how important Spot's genetic contribution really was. After all, Spot was a very famous dog in their breed and documenting direct –and substantial-- lineage back to him would be very good indeed.

¹ Since each generation contributes 100% of the genes appearing in the next generation, percent contribution can be normalized (made to fit within the range of 0-100%) by dividing it by (number of generations assessed * 100).

² There are over 32,000 names in a 15 generation pedigree and over one million in a 20 generation pedigree.

The Smith's read various articles and books and learned how to calculate percent contribution (a back massing statistic). The results were staggering. Apparently, 49% of Fido's genes could be traced directly back to Spot. Normalized for 15 generations, the result was still an impressive 0.4% genetic contribution.

The Smith's continued their work using computer software (<http://www.sdk-weber.com/shop>) designed to simulate random gene assortment and calculate genetic fidelity³. The way this software works is very similar to the black and white marble experiment described earlier. However, the computer simulation makes a few important strides to provide a better estimate of genetic fidelity. The simulation accounts for the possibility that Spot's puppies may be breeding to Spot's puppies, thereby multiplying Spot's genetic prepotency. It also allows the general breeding program to be specified (for example, linebreeding, outcrossing, etc.) which can have important consequences (see the sidebar).

The results of the Smith's various analyses were quite different (see table 1 for all results). The question now was which is correct? And why are they different?

Table 1. Results of various genetic back massing estimates.

	Percent contribution	Normalized Percent Contribution	Genetic Fidelity (computer simulation)*
Spot's prepotency (at 15 generations)	49.00%	0.36%	0.08%

* These results used the following inputs; N=2322, G=15, R=1:4.

INTERPRETING THE RESULTS

We can tackle the questions posed above best, by first addressing the second question (Why are the results different?). The results of the various estimates are different because, on one hand percent contribution *may* overestimate genetic prepotency by assuming that genes flow from one generation to another as equally proportioned bundles. On the other hand, genetic fidelity *may* underestimate genetic prepotency because it assumes genes are contributed to later generations in a completely random fashion. Within an individual this is true. But most breeders do not employ random breeding practices as they develop their lines. Rather, successful breeders tend to be *very* selective about their breeding program and "selection" is certainly not random. Since breeders are selecting for specific traits it stands to reason that Spot's genes—which are ultimately responsible for many (but not all) of Spot's award winning traits—have been similarly selected for.

Which estimate is correct? I would say neither! The correct answer probably lies somewhere between the two estimates. Both provide useful pieces of information to assist breeders and for that reason, both are valuable.

ADDITIONAL READING

Armstrong, John. 2002. Significant Relations. The Canine Diversity Project.

GENETIC DILUTION

While using the genetic fidelity simulations I have learned a very important lesson. If breeders wish to maintain or amplify a sire's prepotency they need to "double-up" on those genes fairly frequently. In fact, without this "doubling-up" using the important sire (or his finest progeny) his genetic effect will be extinguished within five generations. The flip-side of this same coin is that it will take equally as long to extinguish the genetic aftermath of a serious breeding mistake.

Another lesson that was made clear is that when looking at the prepotency of sires 15 generations removed the only ones that will have *any* real influence on today's dogs are those sires appearing at least 15,000 times in the pedigree (under a linebreeding program). That's really an inbreeding scenario since there is only slightly over 16,000 sires at the 15th generation! Now that's food for thought.

³ Genetic fidelity refers to the proportion of genes found in a contemporary dog that are identical to those found in an ancestor of that dog.