Wheaten Genetics for Dummies Like Me
Jim Andrews

Since few of us are geneticists, including myself, I thought I might be helpful to show a few simple examples of inheritance without using the "genetic" language that so many of us find confusing. I am a programmer, and since genetics is really just the ultimate representation of binary probabilities, I thought it might be easier to understand if I just use "ones" ● and "zeros" ◐ to represent genes.

Simple Recessive or Simple Dominant Traits

A single gene pair is represented as two symbols - There are two possibilities for each gene, a solid symbol ● and a striped symbol ◐. For example a simple recessive trait would require both symbols to be solid ●● for the trait to be present. Only one symbol would have to be solid for a dominant trait to be present. A dog with one solid symbol ◐● is considered a carrier for a recessive trait while having both symbols striped ◐◐ is considered clear. We commonly refer to a recessive trait being present as being affected even though recessive traits are not necessarily bad. However, since breeding *for* simple recessive traits and *against* simple dominant traits is a very easy, single generation process, we are usually faced with the problem of eliminating recessive traits or increasing the probability of dominant traits.

The classic single gene pair combination rules are:

◐◐ x ◐◐ = 100% ◐◐.
◐● x ◐◐ = 50% ◐●, 50% ◐◐.
●● x ◐◐ = 100% ◐●.
◐● x ◐● = 25% ●●, 50% ◐●, 25% ◐◐.
●● x ●● = 100% ●● (It is easy to breed for a recessive trait.)

Test Breeding to Determine Carrier Status

If a recessive trait is not present there is no physical way of knowing, without DNA testing, if the pair contains one or zero solid symbols. If the trait has a fairly early onset and does not prevent breeding there is a fairly simple test to determine if one the dog (or other organism) is a carrier.

Using our symbols an affected dog is ●●. When breeding to an affected dog we would expect 50% of the offspring to have the trait present if the mate is ◐● and none of the offspring to have the trait if the mate is ◐◐. Therefore, if seven offspring of this mating do not have the trait present then we can say there is a 99%+ probability the other dog is clear. (1 - 0.5^7 = 1 - 0.0078125 = 99.21875%) If the trait is present in any of the offspring then there is a 100% chance the mate is a carrier.

Polygenic Traits

Polygenic traits are controlled by two or more gene pairs. There are many modes of inheritance. In the simplest case, all the symbols could be thought of as the same color with the effect based on a simple count of the solid symbols. This has been identified as the mode of inheritance for human skin color. There are three pairs of symbols, all with an equal contribution. You get three from your mother and three from your father and the total number of solid color symbols determines the skin color.

 (Pure Black) x  (Pure White) = 100%  . All of the children of this breeding are identical in color. (This is a good example hybrid consistency.)

But the next generation of  x 

1.5%  (Pure Black)
9.4%  (Much darker than parents)
23.4%  (Darker than parents)
31.2%  (Same as parents)
23.4%  (Lighter than parents)
9.4% (Much lighter than parents)
1.5%  (Pure White)

These examples are just shown as total numbers of the symbols. Actual distribution into pairs would vary. For example, the combination show as  could actually be:  or  or  or  or  or  . Although these possible combinations would have the same color or phenotype they do affect the results of subsequent breedings.

Now lets look at another hypothetical mode. Two gene pairs control the trait. It is only manifested if at least one solid symbol is present in each pair. To show this I will use two different colored symbols, Red and Blue, to represent the two different pairs. Now lets look at a hypothetical breeding from two different "lines". If this article has been reproduced in black and white the first pair is the red pair and the second one is the blue pair.

One comes from a line that is 100%  . With no  in the line there are no affected dogs so the line is considered clear. The other comes from a line that is 100%  . There are no  in this line so it is also considered clear.

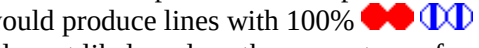
 x  produces 100%  so 100% of the offspring would be affected and the disease would "come out of nowhere". Of course the problem would be with "their" line because you know you never had any problems and "your" line is clear.

The next generation or  x  would produce 56.25% affected dogs as follows.

6.25% 
12.5% 
6.25% 
12.5% 
25%  (Affected)
12.5%  (Affected)
6.25% 
12.5%  (Affected)
6.25%  (Affected)

We face a very difficult situation with the most common genetic problems in Wheatens. Even if PLE / PLN were simple recessive traits, the late onset and the possibility that the trait may not always manifest itself make test breeding to determine carriers impossible.

We don't know the mode of inheritance of PLE or PLN. Breeding two clear lines theoretically COULD cause problems. Depending on the mode of inheritance there is even a small chance that two affected dogs COULD produce a clear offspring.

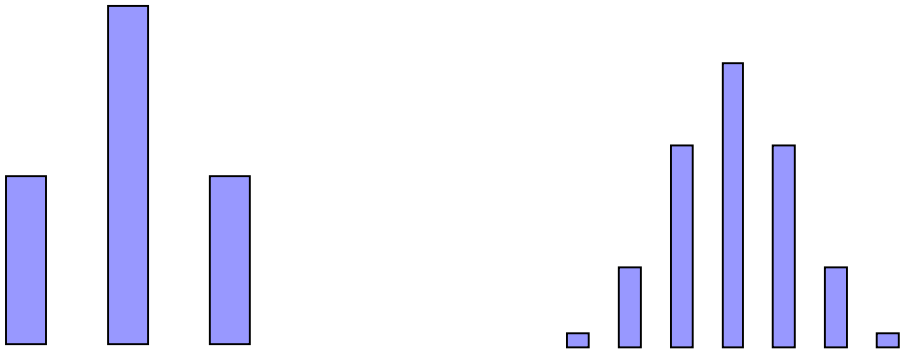
The "disease out of nowhere"  example is of course possible but not likely as there is no identified method of selection that would produce lines with 100%  or 100 %  . Therefore, out-crossing to "clear" lines will most likely reduce the percentage of problem genes but, without knowledge of the mode of inheritance, there is no guarantee.

So since there is nothing we can do to guarantee we won't have problems we might as well go ahead and breed known carriers and their descendents and just hope for the best.

WRONG!!!

What is true in all cases and for all modes of inheritance is offspring of affected dogs and their decendents have a greater probability of being carriers or affected.

The simple recessive trait has three combinations while polygenic traits have additional possibilities but all genetic combinations produce "bell shaped" results. Polygenic traits just have more possibilities.



Yes, the polygenic example I used does have a 1.5% "clear"  column so just because two of the grandparents were affected that doesn't mean that any particular dog couldn't be  . They, however, have the same chance of being  as they do of being what might be called "super" affected, or  . But, even despite the trait being polygenic, the projected average of vs. in the gene pool of the offspring will always equal the average percentage of the parents.

The general health of any breed depends on the overall gene pool. Unfortunately the past practice of matador breeding dogs that are later diagnosed as affected or identified as strong carriers has severely polluted our gene pool.

What can we do?

1. Avoid breeding dogs with high risk factors.

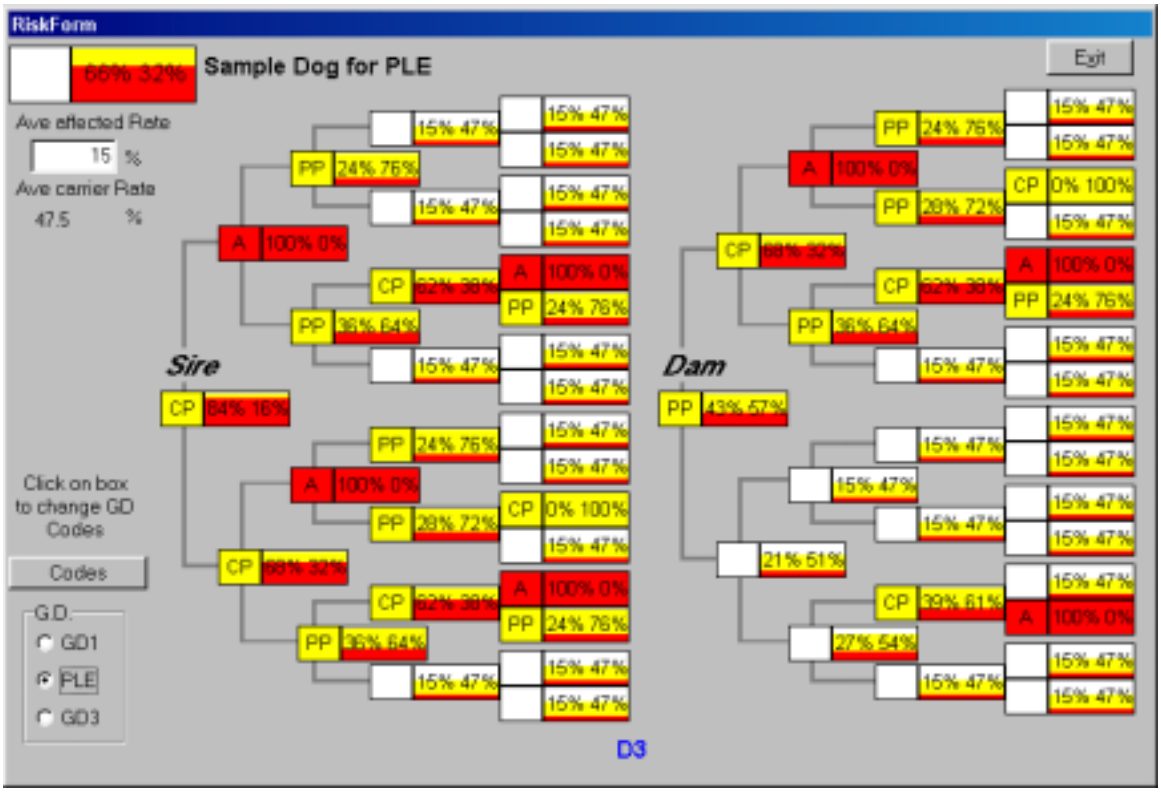
2. Avoid matador breeding! This isn't a good idea in popular breeds like Labs or Cockers but it can be a real disaster when the gene pool is smaller.

3. Freeze the sperm from all active stud dogs. Breed a reasonable number of litters. Wait two or three generations and then only use the sperm from the dogs that produced lower than average affected offspring.

4. If and when reliable genetic markers become available, breed to clear dogs and use the frozen sperm from clear dogs.

Determining Risk Factors

Since the probability formulas for simple recessive represent a close approximation of most polygenic inheritance modes we can use the existing tools. A good example is in Dr. Padgett's book. Parents of affected dogs are listed as "Producing" and offspring of affected dogs as carriers. K9-Ped and PedRisk also allowed for an average rate to be used when no information is known. These values are used to calculate the risk factors of the offspring of each successive generation. The calculated value is used unless specific Affected, Produced, or Clear data is known.



In the graphical example from K9-Ped shown above, the first percentage is the chance the dog is affected and is represented by the amount of red. The second percentage is the chance the dog is a carrier and is shown by the amount of yellow. K9-Ped "propagates" the information for affected dogs and make the parents at least producers and make the offspring at least carriers. A sample of the risk factor screen is shown here. The status of a dog is never reduced by this propagated data.

If an affected dog's sire is also affected the program recognizes that affected is "worse" than produced so it does not change this value. The program calculates the average carrier rate based on the user supplied average affected rate. An interesting thing to observe is that using an average affected rate of 15% means there is a corresponding average carrier rate of 47% with only the remaining 38% clear.

These calculations can also be done using the free "Risk Factor" calculator available at http://azdogs.com/pedrisk.html but since this program does not have pedigree data affected dogs do not propagate information to ancestors or offspring.

The open registry data is available to open registry members as a text file that K9-Ped can read directly into the database. K9-Ped can be downloaded from http://k9ped.com and includes a free Wheaten starter database of over 16,000 dogs.