GENOTYPE RECONSTRUCTIONS

This is a term that is used by our lab and maybe different from what others use. This method can be costly and every effort should be made to test the animal while it is still alive or at least keep a hair sample for every animal in the herd. (Even if the breeder does not think at the time that testing will be needed).

REQUIREMENT OVERVIEW

1. 5 offspring and the available parent.
2. Test all these animals for STR's.
3. The test animal's parents can also be very helpful if available.

The basis of this test is to use the STR (microsatellite) genotypes for 5 of the test animal's offspring, along with the other parent. We are able to use 4 offspring if that is all that is available. With 3 animals, we are only able to produce a "PARTIAL RECONSTRUCTION", which can have some limitations and will likely be missing some alleles. We cannot run this test with 2 offspring. It can also be very useful to have the genotype for the test animal's parents.

LIMITATIONS

1. Reconstruction cannot be produced from siblings of the missing animal.
2. While the parents of the reconstruction animals can add additional information to a genotype, they cannot be used alone to generate the reconstruction.

(See below if you are interested in specifics of the reconstruction.)

ANIMAL	OS1	OS1	P1	P1	OS2	OS2	P2	P2	OS3	OS3	P3	P3	OS4	OS4	P4	P4	OS5	OS5	P5	P5	RECON	
ALLELE	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
MARKER 1	180	180	180	182	182	188	182	188	178	180	178	178	182	188	182	190	188	188	178	188	180	188
MARKER 2	127	127	125	127	127	139	135	139	127	127	127	131	127	131	127	131	127	141	141	141	127	
MARKER 3	163	163	163	173	163	173	163	179	163	173	163	173	163	185	185	185	173	173	173	185	163	173

This shows an example of how we produce the reconstructions. The parents of the offspring must each give one allele. We look at what the available parent has given to the offspring and the reconstruction animal must give the other. With Marker 1/Offspring 1, the parent gives a 180, meaning the reconstruction must give the 180. You continue with this process for all markers and all offspring.

ANIMAL	OS1	OS1	P1	P1	RECON	
ALLELE	1	2	1	2	1	2
MARKER 1	180	180	180	182	180	188

The reason that we use STR's only, is that if there is a problem with the parentage of one of the offspring, there is no way with SNP's to realize there is an issue.

ANIMAL	OS1	OS1	P1	P1	OS2	OS2	P2	P2	OS3	OS3	P3	P3	OS4	OS4	P4	P4	OS5	OS5	P5	P5	RECON		
ALLELE	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	3
MARKER 1	180	180	180	182	182	188	182	188	178	180	180	182	182	188	182	190	188	188	178	188	178	180	188
MARKER 2	127	127	125	127	127	139	135	139	127	127	127	131	127	131	127	131	127	141	141	141	127		
MARKER 3	163	163	163	173	163	173	163	179	163	179	163	173	163	185	185	185	173	173	173	185	163	173	179

Notice that the reconstruction using the above 5 offspring, is showing that there are 3 alleles for two markers. This is not possible, so there is a problem with parentage.

ANIMAL	OS1	OS1	P1	P1	OS2	OS2	P2	P2	OS3	OS3	P3	P3	OS4	OS4	P4	P4	OS5	OS5	P5	P5	RECON		
ALLELE	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	3
MARKER 1	180	180	180	182	182	188	182	188	178	180	180	182	182	188	182	190	188	188	178	188	178	180	188
MARKER 2	127	127	125	127	127	139	135	139	127	127	127	131	127	131	127	131	127	141	141	141	127		
MARKER 3	163	163	163	173	163	173	163	179	163	179	163	173	163	185	185	185	173	173	173	185	163	173	179

We will then go through a process of elimination to determine which offspring does not fit the reconstructed parent. In the example above, Offspring 3 is the one adding the extra alleles and removing it from the reconstruction will produce a good result, as shown below.

ANIMAL	OS1	OS1	P1	P1	OS2	OS2	P2	P2	OS4	OS4	P4	P4	OS5	OS5	P5	P5	RECON	
ALLELE	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
MARKER 1	180	180	180	182	182	188	182	188	182	188	182	190	188	188	178	188	180	188
MARKER 2	127	127	125	127	127	139	135	139	127	131	127	131	127	141	141	141	127	
MARKER 3	163	163	163	173	163	173	163	179	163	185	185	185	173	173	173	185	163	173

There are often times when there is a marker where we know there is going to be a second allele, but there is not enough information to determine what the exact number is. In these cases we place a note, indicating that other alleles are likely. If in the future, if more animals are tested, we can update the reconstructed genotype to include this new information.