Haplotypes Impacting Fertility

With our growing knowledge about the bovine genome, experts have predicted for some time that we'd likely discover numerous cattle genetic defects. Human genetic researchers estimate that we each carry four or five genetic defects. It is reasonable to expect that these exist at a similar level in cattle.

Recently USDA announced the discovery of five haplotypes that appear to cause embryo loss when they exist in the homozygous state. A haplotype is a stretch of chromosome or DNA that is transmitted as a unit from one generation to the next. In this case, we are talking about a set of single-nucleotide polymorphisms (SNPs) on a single chromosome that is inherited together. We often think about genes or SNPs as individual units but SNPs that are located next to each other on an individual chromosome are almost always inherited together as a unit.

These genetic conditions resulting from the five haplotypes discovered by USDA have not been directly observed and the exact genetic or biological cause is unknown. Because of this, they've been given simple names of Holstein Haplotype 1 (HH1), Holstein Haplotype 2 (HH2), Holstein Haplotype 3 (HH3), Jersey Haplotype 1 (JH1) and Brown Swiss Haplotype 1 (BH1). These haplotypes appear to have a recessive mode of inheritance where animals with zero or one copy of the haplotype are completely normal. Those that inherit two copies of the haplotype are lost as embryos most likely early in gestation.

The impact these haplotypes have on fertility, which largely determines their economic impact, is dependent on their frequency in the population. JH1 has the highest frequency (23.4%) and animals that are heterozygous for this haplotype could have conception rates that are reduced by 2.6 percentage points. HH1, HH2 and HH3 all have similar frequencies (4.5%, 4.6% and 4.7%, respectively) and the impact on fertility is less than 0.5 percentage points. BH1 exists at a frequency of 14 percent. It is important to realize that the negative impact of these haplotypes is already accounted for in the routinely published sire conception rate (SCR) evaluations and daughter pregnancy rate (DPR) genomic evaluations. So, if you are using these traits in selecting A.I. sires you are already avoiding or compensating for these new genetic conditions.

Select Mating Service™ (SMS™) is an excellent tool for managing these genetic conditions as well as for avoiding inbreeding which may result in recessive conditions. By using the SMS program, herds with at least one generation of pedigree information on their cows can include heterozygous bulls in their breeding program with less than a 1 percent chance of lost pregnancies from known genetic conditions.

7HO7615	COLBY	HH2C
7HO8165	MILLION	HH2C
7HO8351	LUCIUS	HH1C
7HO8559	BOGART	HH3C
7HO8659	SILVA	HH1C
7HO8747	BRONCO	HH3C
7HO8777	GENERAL	HH1C
7HO8847	RICECREST	HH3C
7HO8866	CARUSO	HH3C
7HO9021	A L H DUKE	HH3C
7HO9069	INGLES	HH3C
7HO9107	DURABLE	HH2C
7HO9281	BIGSHOT	HH3C
7HO9321	CROWN	HH3C
7HO9393	EZEKIEL	HH1C
7HO9424	GONE-GOLD	HH3C
7HO9502	OMAR	HH1C
7HO10356	WATSON	HH3C
7HO10653	DAMASCUS	HH2C
7HO10723	SPUR	HH3C
7HO10782	TEXIERA	HH2C
7HO10834	CENA	HH2C
7HO10839	BENNIE	HH3C
7HO10853	COBRA	HH3C
7HO10884	AVERY	HH3C
7HO10989	KRAMER	HH3C
7HO11100	MONTAGE	HH1C
7JE738	LOUIE	JH1C
7JE840	BELVEDERE	JH1C
7JE1038	VALENTINO	JH1C
7JE1104	SPIRIT	JH1C
7JE1110	IMPRESS	JH1C
7BS843	PEPPER	BH1C