Match-A-Yak a tool to minimize inbreeding in North American Yaks

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The domesticated yak (*Bos grunniens*) arrived in North America in the late 1890's. There were a few animals imported into Canada and North American zoos which became the foundation of the North American genetic pool. Research was conducted in Alaska hybridizing them with Highland cattle in the early 1900's. A very limited number of yaks were imported into the United States in the early 1900's and again later in the 1980's. However, the genetic diversity of the North American yak is limited necessitating a need to manage breeding programs to reduce inbreeding.

Figure 1. First yak at the National Zoo in the United States. Reported to be taken December 23, 1898 with the bull dying January 14, 1912. Source: posted on Yak History Channel Facebook from William Bartels of New York City.



Organized breeding association of *Bos grunniens* recognized the importance of maintaining genetic diversity. Registration of animals now requires DNA testing which reveals the degree of cattle introgression as well as the genetic coefficient of inbreeding (COI) based on the expected degree of heterozygosity. This information along with pedigree can assist in reducing inbreeding.

The next step to assist in conserving genetic diversity was the development of an online software tool which is available to members of the US Yaks association (USYAKS). The program is called Match-A-Yak. Users enter a proposed mating between a sire and dam. The software then calculates an average COI and the number of heterozygous SNPs for the progeny. These results are based on the single nucleotide polymorphisms (SNPs) currently being reported for the animals registered in USYAKS.

Using the software, a breeder seeking to replace a bull for mating with their current herd of females can run each female and potential replacement bull to identify the bull that would provide the greatest degree of heterozygosity in the SNPs monitored. In this situation, heterozygosity refers to SNPs having differing alleles (ie. G/C, A/T, G/T, etc.) while having the same alleles (ie. A/A, G/G, T/T, C/C) at the SNP is referred to as homozygous. An example report for an individual yak SNP profile and calculated COI is shown in Figure 2. As inbreeding increases, there will be decrease in the heterozygosity or increase in homozygosity at these SNPs. To illustrate how this tool can be utilized to estimate the COI of a bull in a

small herd. Table 1 reports modeled matings for a herd of females and several bulls with the expected COI and number of heterozygous SNPs of the progeny from these matings.

Figure 2. Example of the single nucleotide polymorphism (SNP) profile reported for a yak registered in with United States Yaks association.

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COI = 1.0 - heterozygoteTotal/(Nsites * ExpectedHets)
ExpectedHets = 0.3946
COI = 1.0 - 41/(94 * 0.3946)
COI = -0.1053
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SNP #	Genotype	24	C/G	48	G/T	72	A/G
1	G/G	25	C/C	49	A/A	73	A/G
2	C/C	26	T/T	50	C/C	74	C/C
3	G/T	27	A/G	51	T/T	75	A/G
4	C/C	28	C/T	52	G/G	76	G/T
5	A/A	29	C/G	53	C/G	77	T/T
6	G/T	30	T/T	54	C/C	78	C/G
7	T/T	31	G/G	55	T/T	79	T/T
8	A/A	32	C/C	56	C/C	80	C/C
9	A/G	33	A/A	57	C/C	81	G/T
10	C/G	34	G/G	58	C/C	82	C/T
11	T/T	35	C/T	59	T/T	83	A/A
12	G/G	36	C/C	60	G/C	84	C/T
13	C/G	37	G/G	61	A/C	85	G/T
14	C/T	38	A/G	62	C/C	86	G/G
15	C/C	39	A/A	63	A/G	87	G/T
16	A/A	40	A/C	64	G/T	88	C/T
17	C/C	41	A/C	65	C/T	89	C/T
18	G/G	42		66	G/G	90	G/G
19	C/C	43	T/T	67	A/T	91	G/T
20	A/T	44	A/A	68	A/A	92	G/T
21	C/C	45	A/G	69	C/C	93	T/T
22	A/T	46	C/T	70	C/T	94	G/G
23	C/C	47	C/C	71	G/G	95	A/A

Running the model for the five bulls in this group of females, Duke would be expected to yield the least number of homozygosity of the SNPs and lowest COI an average. However, as is the case in most herds, a few individuals are likely to have similar alleles for several of the SNPs reported and may not result in the greatest degree of heterozygosity. In this scenario, Audry mated to Duke is expected to yield progeny with greater homozygosity than if she were mated to any of the other bulls. Looking at the pedigrees for these two individuals, a common ancestor SBR Dreadlock is found. Further investigating the expected number of heterozygous SNPs, the mating of Dr. Who and Smash is observed to yield the fewest heterozygous SNPs and highest COI at 0.301. Again, investigating the pedigrees, these two are half-siblings sharing the same dam.

In an effort to maintain genetic diversity and limit inbreeding, the Match-A-Yak tool can assist breeders in making mating decisions to reduce the degree of homozygosity. Granted, the number of SNPs currently being monitored is limited. Even with the few SNPs reported, the tool can still be used to quickly determine the expected COI outcome. As new bulls are sought to be introduced to herds, the Match-A-Yak program is another tool in the toolbox for selection.

Table 1. Results of Match-A-Yak for five different bulls mated to 14 female yaks and the resulting expected Coefficient of Inbreeding and the number of heterozygous SNP's. Scaled color coding for ease of viewing where green results in the greatest and red is the fewest heterozygous SNPs within each mating.

Bull ID / Reg. #	Powerball	13D17	Dr. Who	17A07	Phantom	19B51	Mohair Sam	18D09	Duke	20A05
Bull COI	0.018		0.1103		-0.1053		0.057		0.095	
Female	COI	No. Hets	COI	No. Hets	COI	No. Hets	COI	No. Hets	COI	No. Hets
Lexiberry 09A12	-0.007	33.5	0.119	30	0.064	31.5	0.15	28.5	-0.082	36
Marigold 14A19	-0.027	33.75	0.049	32	0.068	31	-0.097	36.5	-0.072	35.25
Re'em 14A17	0.061	31.25	0.148	29	0.079	31	0.2	27	-0.082	36
Jersey Girl 13A25	-0.024	33.25	0.083	30.5	0.163	27.5	0.019	32.25	0	32.5
Audry 12A13	0.016	32.75	0.105	30.5	0.035	32.5	0.012	33.25	0.113	29.5
Smash 14A16	0.088	19.5	0.301	15.5	0.166	18.5	0.082	20	0.036	21
Tuffy 14A14	0.061	31.25	0.134	29.5	0.079	31	0.057	31.75	-0.037	34.5
Aurora 14A18	0.061	31.25	0.156	28.75	-0.017	34.25	0.057	31.75	-0.022	34
Showgirl 04A21	0.143	28.5	0.398	20.5	0.139	29	0.072	31.25	0	33.25
Comet 17A08	0.061	31.25	0.237	26	0.079	31	0.235	25.75	-0.052	35
Nikita 17A09	0.046	31.75	0.031	33	0.183	27.5	0.228	26	-0.082	36
Latifah 14C75	0.011	32.5	0.124	29.5	0.068	31	0.233	25.5	-0.022	34
Agni 07A22	-0.029	34.25	0.075	31.5	-0.01	37	-0.032	34.75	-0.142	38
Nala 18D10	0.016	32.75	0.163	28.5	0.168	28	0.2	27	-0.037	34.5