ID-273

Cooperative Extension Service

Match-a-Yak: a Tool to Minimize Inbreeding in North American Yaks

Jeff Lehmkuhler, Darrh Bullock, Mary McCarty, and Les Anderson, Animal and Food Sciences, and Ted Kalbfleisch, Veterinary Sciences

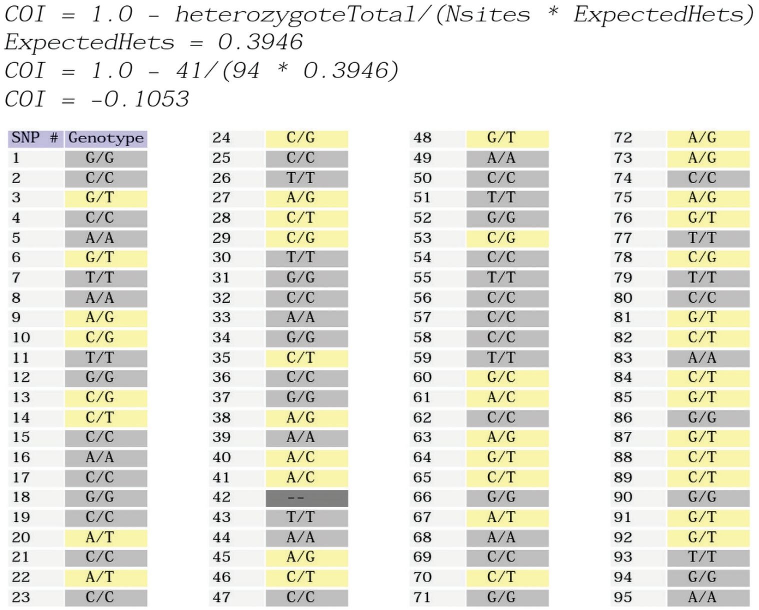
Figure 1. The first yak at the National Zoo in Washington, D.C., was photographed on December 23, 1898. The bull, a gift to the zoo from William Bartels of New York, died January 14, 1912. Source: Smithsonian Institution Archives

The domesticated yak (*Bos grunniens*) arrived in North America in the late 1890s. A few animals were imported into Canada and North American zoos and became the foundation of the North American genetic pool (Figure 1). Research was conducted in Alaska hybridizing them with Highland cattle in the early 1900s. A handful of yaks were imported into the United States in the early 1900s and again later in the 1980s. However, the genetic diversity of the North American yak is limited, necessitating a need to manage breeding programs to reduce inbreeding.

Organized breeding associations of *Bos grunniens* recognized the importance of maintaining genetic diversity. Most of the yak associations now require DNA testing for registration of animals, which reveals the degree of cattle introgression as well as the genetic coefficient of inbreeding (COI) based on the estimated 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 that 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 single nucleotide polymorphisms (SNPs) for the progeny. These results are based on a subset of SNPs being reported for the animals registered in USYAKS.

Using the software, a breeder seeking to replace a bull for mating with their female herd can run each female yak 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 (i.e. G/C, A/T, G/T, etc.), while having the same alleles (i.e. 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.



```
COI = 1.0 - heterozygoteTotal/(Nsites * ExpectedHets)
ExpectedHets = 0.3946
COI = 1.0 - 41/(94 * 0.3946)
COI = -0.1053
```

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

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

Cooperative Extension Service | Agriculture and Natural Resources | Family and Consumer Sciences | 4-H Youth Development | Community and Economic Development

Table 1. Results of Match-a-Yak for five bulls mated to 14 female yaks and the resulting estimated coefficient of inbreeding and the number of heterozygous SNPs. Scaled color coding for ease of viewing where green results in the greatest and red 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

As inbreeding increases, heterozygosity will decrease and homozygosity will increase in these SNPs. A scenario using cows representing a small herd was modeled using different bulls. The outcome of these matings with the estimated COI and number of heterozygous SNPs of the progeny are shown in Table 1.

Running the model for the five bulls in this group of female yaks, Duke is estimated to yield the fewest homozygotes for the SNPs and lowest COI on average. However, the amount of heterozygosity in individual matings varies across the herd, as would be expected. Some individuals mated to the overall "best" bull are likely to have similar alleles for several of the SNPs reported and may have less heterozygosity than if they were mated to a different bull. In this scenario, Audry mated to Duke is estimated 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 estimated 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, it is found that these two are half-siblings sharing the same dam.

Using Match-a-Yak

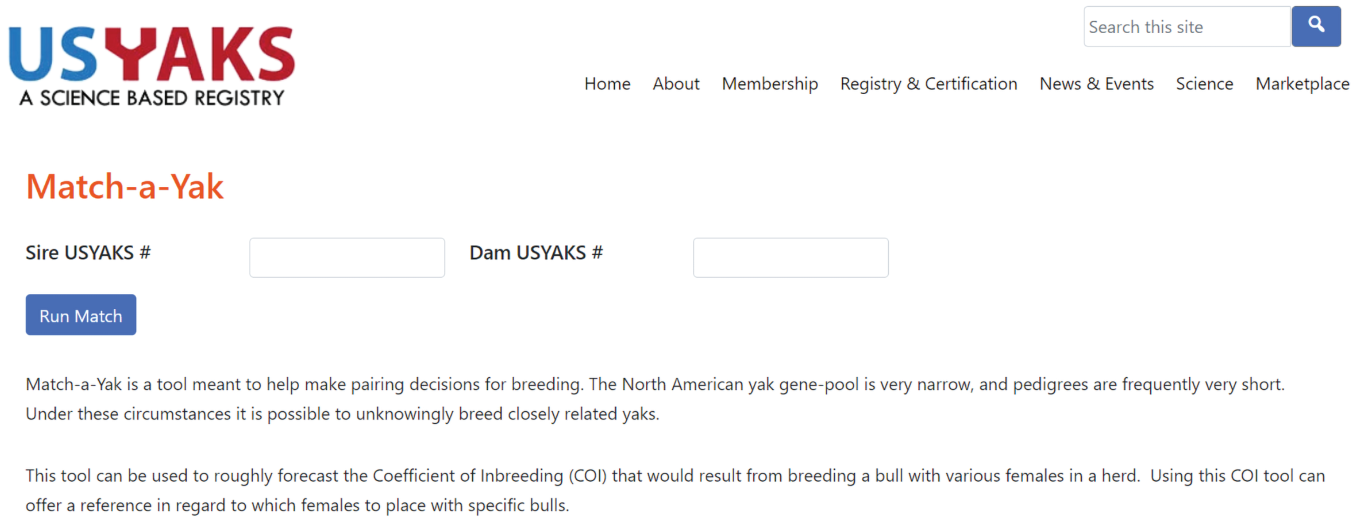
To use the Match-a-Yak tool, one must be a registered member of USYAKS. After logging in with one's username and password, scrolling under "Membership" and hovering over "Membership Benefits" the "Match a Yak" tool becomes accessible.

Clicking on "Match a Yak," takes one to the tool landing page (Figure 3). On this page, one can enter the registration number of the sire and dam registered in USYAKS to obtain estimated COI and number of heterogeneous SNPs. Each mating must be conducted for each animal of interest. If the DNA information has not been added to the registry database, the computation cannot be performed.

Once the sire and dam numbers are entered, click the "Run Match" button (Figure 4). The predicted heterozygous SNPs or "hetsites" are shown. The number of useable sites refers to the number of SNPs that were used in the analysis as some animals may not have the full 95 SNPs reported. The Expected Heterozygote proportion is a constant based on animals assessed when the initial DNA tests were assembled. A coefficient of inbreeding (COI) is calculated. In theory, COI values range between -1.0 and +1.0 where 0 is the average level of inbreeding. The actual observed COI lies between -0.45 and +0.45. The more positive the calculated COI, the greater the degree of inbreeding while a more negative number would indicate less inbreeding than the average. The estimated number of cattle alleles are also calculated for the progeny.

The alleles passed on are random and the software generates a bell-shaped curve (Figure 5). This provides a degree of confidence for the actual number of hetsites and COI of the mating.

Figure 3. USYAKS landing page.



Match-a-Yak

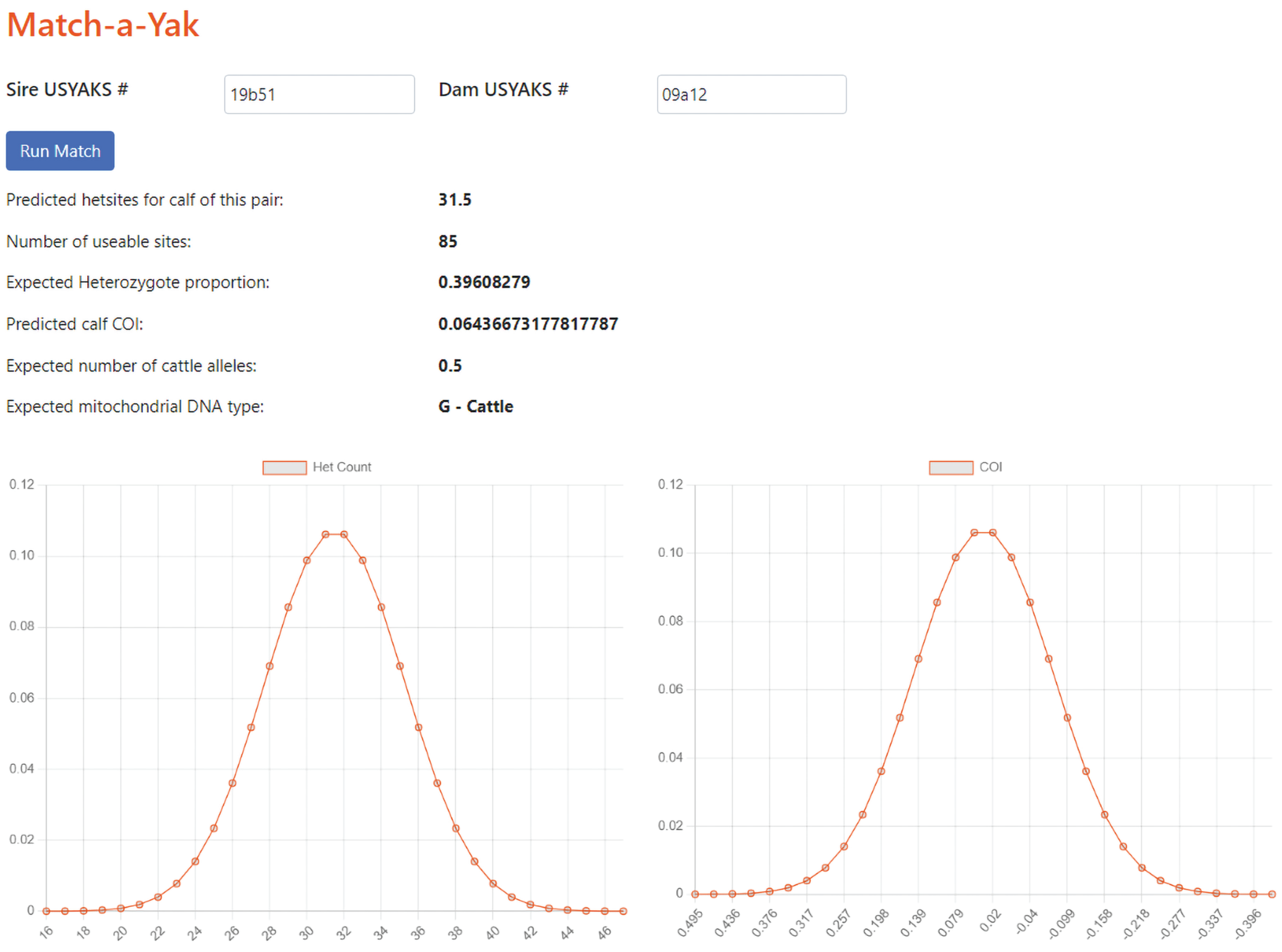
Sire USYAKS #

Dam USYAKS #

Match-a-Yak is a tool meant to help make pairing decisions for breeding. The North American yak gene-pool is very narrow, and pedigrees are frequently very short. Under these circumstances it is possible to unknowingly breed closely related yaks.

This tool can be used to roughly forecast the Coefficient of Inbreeding (COI) that would result from breeding a bull with various females in a herd. Using this COI tool can offer a reference in regard to which females to place with specific bulls.

Figure 4. Enter sire and dam registration numbers on the Match-a-Yak page to obtain estimated COI and number of heterogeneous SNPs.



Match-a-Yak

Sire USYAKS # 19b51

Dam USYAKS # 09a12

Predicted hetsites for calf of this pair:	**31.5**
Number of useable sites:	**85**
Expected Heterozygote proportion:	**0.39608279**
Predicted calf COI:	**0.06436673177817787**
Expected number of cattle alleles:	**0.5**
Expected mitochondrial DNA type:	**G - Cattle**

Figure 5. The results of Match-a-Yak generate a bell-shaped curve.

Yak breeders are increasing their ability to make improved breeding decisions with increased registration of animals. Having access to tools such as Match-a-Yak has the potential to reduce the level of homozygosity and aid in managing the genetic diversity of the narrow gene pool of the North American yak population.

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 an estimated COI outcome. As new bulls are sought to be introduced to herds, the Match-a-Yak program is another tool in the toolbox to assist in selection decisions to increase genetic diversity, or at least minimize homozygosity.

Additional Information

USYAKS: http://usyaks.org

Acknowledgement

The authors wish to thank Mr. Gregor Dike of Shi-bah Shing-ga Yaks for permitting us to use the female yaks in the simulations ran in the Match-a-Yak program.

Cooperative Extension Service

Agriculture and Natural Resources
Family and Consumer Sciences
4-H Youth Development
Community and Economic Development

MARTIN-GATTON COLLEGE OF AGRICULTURE, FOOD AND ENVIRONMENT

Lexington, KY 40506 Issued 09-2023