

FOR THE RECORD

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Allele Frequencies for Three STR Loci RT24, RT09, and BM1225 in Northern New England White-tailed Deer*

POPULATION: White-tailed deer (*Odocoileus virginianus*) from Vermont, New Hampshire, and Maine.

KEYWORDS: forensic science, DNA typing, *Odocoileus virginianus*, BM1225, RT09, RT24, wildlife, short tandem repeats, non-human DNA evidence

Muscle samples (~1 cm³) were obtained from harvested animals in four distinct locations in each state (total sample size = 362). Maine samples were collected during the 1998 deer hunting season (November 1–31, 1998), New Hampshire samples were collected during the 1999 hunt (November 13–19, 1999), and Vermont samples were collected during the 1999 hunt (November 13–19, 1999). DNA was extracted using the QIAmpTM tissue kit (Quiagen, Valencia, CA) as per the manufacturer's instructions (1). One to two μ L of extracted DNA was used in a 25 μ L multiplex PCR reaction containing 10 mM KCl, 20 mM Tris pH 9.5, 10 mM (NH₄)₂SO₄, 1 mM MgCl, 4 mM dNTP's (Promega, Madison, WI), 0.75 units of Taq DNA Polymerase (GibcoBRL, Grand Island, NY), and 0.3 μ M of each primer (Operon, Alameda, CA). Three STR loci were examined: BM1225 [(2), primers: BM1225f ttt ctc aac aga ggt gtc cac BM1225r acc cct atc acc atg ctc tg], RT09 [(3), primers: RT9f tga agt tta att tcc act ct, RT9r cag tea ctt tea tcc cac at] and RT24 [(3), primers: RT24f tgt atc cat ctg gaa gat ttc ag, RT24r cag ttt aac cag tcc tct gtg]. PCR was performed in a HYBAid OMN-E Personal Thermal CyclerTM (HYBAid, Middlesex, UK) for 30 cycles (94°C, 30s; 54°C, 45 s; 70°C, 2 min) and a final extension (72°C, 10 min). PCR products were electrophoresed and analyzed with an ABI

377TM automated DNA sequencer as per the manufacturer's instructions (Applied Biosystems International, Foster City, CA). Electropherograms were interpreted using GenescanTM (ver. 3.1) and GenotyperTM (ver. 2.1) software (Applied Biosystems International, Foster City, CA). Allele frequencies and heterozygosities were calculated with Genepop (ver. 3.1c) (4) and Hardy Weinberg tests were performed with GDA (ver. 1.0d16c) (5).

The complete dataset can be accessed at: <http://nature.umesci.maine.edu/forensics/data.htm>

Acknowledgments

The authors are grateful for funding from the Maine Outdoor Heritage Fund and the Vice Provost for Research and Graduate Studies at the University of Maine. The Maine Department of Inland Fisheries and Wildlife, New Hampshire Fish and Game Department, and Vermont Department of Fish and Wildlife generously contributed samples to this study. The authors benefitted from conversations with J. Coffin and J. Ruth.

References

1. Greenspoon SA, Scarpetta MA, Drayton ML, Turek SA. QIAamp spin columns as a method of DNA isolation for forensic casework. *J Forensic Sci* 1998;43:1024–30.
2. Bishop MD, Kappes SM, Keele JW, Stone RT, Sunden SL, et al. A genetic linkage map for cattle. *Genetics* 1994;136:619–39.
3. Wilson GA, Strobeck C, Wu L, Coffin JW. Characterization of microsatellite loci in caribou *Rangifer tarandus*, and their use in other artiodactyls. *Mol Ecol* 1997;6:697–99.
4. Raymond M, Rousset F. GENEPOP(version 1.2): Population genetics software for exact test and ecumenicism. *J Heredity* 1995;86:248–49.
5. Lewis PO, Zaykin D. Genetic data analysis: software for the analysis of discrete genetic data. 2000.

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* Presented at the 53rd annual meeting of the American Academy of Forensic Sciences, February 2001, Seattle, WA.

TABLE 1—Allele frequencies of three STR loci in 12 samples of white-tailed deer.

Locus	Allele	N-ME (37)	C-ME (50)	E-ME (34)	W-ME (48)	N-NH (25)	E-NH (23)	SE-NH (21)	W-NH (23)	NW-VT (24)	C-VT (27)	SE-VT (24)	SW-VT (28)
RT24	204	0.014	0.020	...	0.042	0.100	0.045	0.083	0.060	0.031	0.058
	208	0.041	0.030	0.059	0.031	0.020	0.023	0.100	0.024	0.063	0.060	0.094	0.115
	210	...	0.040	...	0.010	0.040	0.023
	212	0.149	0.150	0.132	0.063	0.080	0.114	0.067	...	0.063	0.280	0.125	0.231
	214	0.432	0.300	0.338	0.458	0.240	0.318	0.233	0.262	0.354	0.300	0.344	0.135
	216	0.108	0.080	0.044	0.073	0.020	0.136	0.133	0.048	...	0.060	0.094	0.077
	218	...	0.020	0.015	0.042	0.060	...	0.067	0.119	0.104	0.096
	220	0.027	0.040	...	0.021	0.020	0.091	0.067	0.071	0.021	...	0.125	0.077
	222	0.027	0.020	0.118	0.023	0.067	0.024	0.021	0.040	0.000	0.038
	224	0.135	0.170	0.176	0.198	0.280	0.114	0.033	0.143	0.250	0.100	0.031	0.058
	226	0.027	0.070	0.088	0.010	...	0.023	0.031	...
	228	...	0.010	...	0.010	0.024	0.021	0.020	0.063	...
	230*	0.023
	232	0.041	0.020	0.029	...	0.020	0.068	0.021	0.019
	234	0.024	0.019
	236*	0.024
	238	...	0.030	...	0.042	0.120	...	0.233	0.214	...	0.080	0.063	0.077
	240*	0.024
	A		10	14	9	12	11	12	9	12	10	9	10
He		0.676	0.780	0.882	0.646	0.840	0.864	0.733	0.857	0.875	0.840	0.813	0.885
Ho		0.766	0.849	0.821	0.742	0.843	0.856	0.874	0.861	0.801	0.819	0.849	0.897
P		0.206	0.052	0.943	0.143	0.498	0.782	0.522	0.077	0.696	0.680	0.355	0.483
RT09	103	0.068	0.082	0.015	0.064	0.040	0.095	0.050	0.075	0.125	0.175	0.179	0.096
	105	0.095	0.041	0.088	0.011	0.040	...	0.050	0.025	0.042	0.125	0.036	0.019
	107	0.043	0.075	0.025	0.036	0.077
	109	0.270	0.184	0.162	0.160	0.320	0.095	0.150	0.100	0.229	0.075	...	0.115
	111	0.284	0.347	0.412	0.426	0.320	0.452	0.400	0.550	0.375	0.375	0.357	0.404
	113	...	0.071	0.044	0.075	0.083	...	0.036	0.077
	115	0.014	0.025
	117	0.068	0.112	0.074	0.011	0.140	0.048	0.025	...	0.021	...	0.036	0.038
	119	0.081	0.020	0.029	0.085	0.040	0.119	0.150	0.050	0.021	0.025	0.179	0.019
	121	...	0.020	...	0.074	0.040	0.071	...	0.075	...	0.075	0.036	0.077

TABLE 1—(Continued)

	123*	0.014
	125	0.108	0.122	0.176	0.128	0.060	0.095	0.100	0.025	0.083	0.125	0.107	0.058
	129	0.021	0.019
	139*	0.024
A		9	9	8	9	8	8	8	9	9	8	9	11
He		0.730	0.776	0.735	0.723	0.840	0.905	0.850	0.650	0.833	0.900	0.929	0.731
Ho		0.821	0.812	0.768	0.766	0.781	0.764	0.794	0.683	0.791	0.805	0.820	0.806
P		0.031	0.100	0.062	0.876	0.929	0.989	0.655	0.461	0.702	0.704	0.987	0.150
BM1225	224*	0.045
	226	0.081	0.071	...	0.250	0.080	0.318	0.381	0.174	...	0.167	0.146	0.196
	228*	...	0.010
	230	0.081	0.122	0.015	0.167	0.180	0.205	0.262	0.239	0.167	0.167	0.146	0.161
	232	0.392	0.469	0.794	0.156	0.360	0.182	0.143	0.152	0.292	0.130	0.167	0.143
	234	0.149	0.122	0.044	0.240	0.200	0.182	0.095	0.217	0.292	0.259	0.188	0.214
	236	0.081	0.020	...	0.104	0.048	0.043	0.063	0.056	0.104	0.018
	238	0.095	0.061	0.132	0.063	0.020	0.023	0.024	0.065	...	0.019	0.021	...
	240*	0.019
	244	0.068	0.071	0.015	...	0.020	0.023	0.037	0.042	0.036
	246	0.054	0.051	...	0.021	0.140	0.023	0.048	0.109	0.146	0.111	0.042	0.143
	250	0.042	0.037	0.146	0.089
A		8	9	5	7	7	8	7	7	6	10	9	8
He		0.838	0.694	0.382	0.833	0.640	0.652	0.810	0.783	0.708	0.778	0.875	0.857
Ho		0.799	0.740	0.355	0.821	0.787	0.794	0.770	0.843	0.792	0.857	0.877	0.855
P		0.900	0.219	0.238	0.269	0.321	0.017	0.611	0.140	0.528	0.317	0.855	0.597

NOTE: Sample size given in parentheses. A: number of alleles observed. He: expected heterozygosity. Ho: observed heterozygosity. P: Hardy Weinberg probability (3200 shufflings). Average Power of Exclusion for entire dataset >0.999995.

* Indicates a unique, subpopulation specific allele.