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ERRATUM

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Population genetic structure and the effect of founder events on the genetic variability of introduced sika deer, *Cervus nippon*, in Germany and Austria

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Table 1 in this article was published without the legend and the footnote. The complete table is shown below.

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Table 1 Characteristics and distribution of mtDNA haplotypes at each sampled location, number of individuals (N), haplotype diversity (*h*), and nucleotide diversity (π) within sika deer populations (OA = Ostangel, HDB = Hüttener and Duvenstedter Berge, WB = Weserbergland, MS = Möhnesee, HR = Hochrhein, PO = Persenbeug-Ostrong and TD = Tullner Donauauen)

	variable sites‡	no.of repeats	population							

haplotype	`23334445567888999991111111111111111111111111222222222222223333333333334444`
	`01792370783578134590111223334444555566667779005566666679990012245667883333`
	`                   2048070680127167814683676177913456712567833905780493467`
			OA	HDB	WB	MS	HR	PO	TD	N

A1	`CAATACCTTAGACCTTGCTTAAACTTCGGGTGCATAGCTTTAAAATTTCGTTATTATGCGAACGGAATAAGATC`	4				43				43
A11	`.................................................A....C....A..T..........T`	4			1					1
A3	`.................................................A....C....A..T........G.T`	4		8	3					11
A4	`.................................................A.........A..T.......A..T`	4					9		54	63
A7	`.................................................A.........A..T......CA..T`	4	1							1
A17	`.................................................A.........A..T.......A...`	4	1							1
A8	`.................................................A.....G...A..T..........T`	4				2		9		11
A9	`T................................................A.....G...A..T..........T`	4						1		1
A10	`.................................................A.....G...A..T.......A..T`	4						3		3
B2	`T.....-.C.A..T.CA..C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GC....C.`	8	19		1		16		1	37
B12	`T.....-.C.A..T.CA..C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GCG...C.`	8	1							1
B13	`T.CA..-.C.A..T.CA..C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GC....C.`	8	1							1
B14	`TC....-.C.A..T.CA..C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GC....C.`	8	1							1
B16	`T...C.-.C.A..T.CA..C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GC....C.`	7					1			1
B18	`T.....-.C.AC.T.CA..C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GC....C.`	8	1							1
B15	`T.....-.C.A..T.C...C..GT.C.AA.C-.GCGATC.CGGGGCC..ACC..C..A....TA..GC....C.`	8					1			1
B5	`T.....-.C.A.TT.CA..C..GT.C.AA.C-.GCGATC..G.GGCCCAACC..CG.AT...TA...C....C.`	7			34		1			35
B6	`T.....-.C.A.TT.CA..C..GT.C.AA.C-.GCGATC..G.GGCCCAACC..CG.AT...TAA..C....C.`	7			1					1
Sika viet	`.....TTCCGAG..C..TC.-G.TC-T.AA.AT......C....G....A..GC.GCA.AGG...G.C...G..`									
N			25	8	40	45	28	13	55	∑214
h(%)			43.0	0.0	23.3	8.7	58.7	50.0	3.6	
π(%)			1.4	0.0	1.6	0.1	3.9	0.1	0.3	

[1] The sequenced fragments correspond to positions 15494-15893 in the control region of the complete *Munticus muntjak* mitochondrial genome (AY225986). Letters designate base substitutions. Nucleotide position numbers correspond to positions in the alignment

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