

The influence of habitat structure on genetic differentiation in red fox populations in north-eastern Poland

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Supplementary Material

Table S1. Primers designed from *Vulpes vulpes* microsatellites available on GenBank

Acc_#	motif	bp	Locus	primer	PrimerID	Sequence 5-3	primer_Tm
JN831730.1	(GT)19	123	VVM39	F	VVM39F	TGTCCGTCTTAAATGCAAGGAT	61
			VVM39	R	VVM39R	CTTTGGAACACCAACACACAC	60
JN831737.1	(TG)17	136	VVM246	F	VVM246F	CATCCCCATCATATCTGGTTCT	60
			VVM246	R	VVM246R	ACTCTCCAAGTCACATCCCATC	60
JN831745.1	(GT)17	139	VVM81	F	VVM81F	GCTGAAATCCTGCTTAGAACTTG	61
			VVM81	R	VVM81R	GCTGAATGGATGAAAGGTTGAC	61
JN831734.1	(TG)12	142	VVM831	F	VVM831F	CTGTGTTTTGTGTGTGCTGCTA	60
			VVM831	R	VVM831R	GAAGTGTGTACTTTCCGCTCAA	59
JN831724.1	(AG)13	148	VVM33	F	VVM33F	CAATCAATCTGAGCACCACAAT	60
			VVM33	R	VVM33R	GATAGATGAGGGGAATGTGAGGA	60
JN831726.1	(AC)16	150	VVM85	F	VVM85F	AATTAAGTTTTCCCAGCTCCC	59
			VVM85	R	VVM85R	CCTATATTGAGACCATGAGGAGG	59
JN831742.1	(GT)11	165	VVM235	F	VVM235F	GTGTGTTTCGTGTTGTTTGTGTG	60

			VVM235	R	VVM235R	AATGACCTCCAAGTCTCCTGAA	60
JN831723.1	(TG)19	169	VVM219	F	VVM219F	GTTTCTTCACAAGGGGCATAAC	60
			VVM219	R	VVM219R	CACACTATTTCCATGTTTCCCA	60
JN831747.1	(AC)18	177	VVM213	F	VVM213F	TGCAGAGACAAACCTTCAAAAC	59
			VVM213	R	VVM213R	CGATCCTAAGAAACACATGGAA	59
JN831740.1	(GT)15	188	VVM529	F	VVM529F	AAAATGACTGTGAACTGCCCTC	61
			VVM529	R	VVM529R	AATGCTGAATCTTTGCTCTTCC	60
JN831731.1	(GT)17	197	VVM104	F	VVM104F	GTGATGCAAGAAACCAAGAACA	60
			VVM104	R	VVM104R	AAGAATCCAAAGGAAAAGCTCC	60
JN831735.1	(CA)17	204	VVM100	F	VVM100F	GATACACACACACTCCCCTGTG	60
			VVM100	R	VVM100R	TGCTGAAGGAAGAAAAGAGGTC	60
JN831738.1	(GT)18	212	VVM63	F	VVM63F	AGTCCTTTGCGTGGTTCTTCT	60
			VVM63	R	VVM63R	ACTGCACTCTAGCCAACTCTCC	60
JN831749.1	(TG)17	226	VVM828	F	VVM828F	AGAAGGCACTTGTAAGGTGGAT	59
			VVM828	R	VVM828R	GCACACAGACACACATGGAATA	59
JN831729.1	(CA)14	234	VVM828	F	VVM828F	TGGAAGACCTGGAAGAGGTAGA	60
			VVM828	R	VVM828R	ATTCCTTCACCTGTATTGCTC	59
JN831739.1	(TG)16	240	VVM128	F	VVM128F	CATTTCTATCCTACTGCTGGC	60
			VVM128	R	VVM128R	GGGAAGCCTCACATCCTTTAG	60
JN831741.1	(GT)19	240	VVM189	F	VVM189F	GATCTGTGAGCATAAGGGTTTT	57
			VVM189	R	VVM189R	TTATCCAGTCCCAAAGTCTGTC	58
JN831736.1	(TG)17	244	VVM190	F	VVM190F	GCACATTTGAGGGTCAGTGTA	60
			VVM190	R	VVM190R	CTCCTTCCCTTCTCACCAGTAA	60
JN831748.1	(CA)12	244	VVM124	F	VVM124F	CTCTGCTACACGGCCAACT	60
			VVM124	R	VVM124R	GGTATTCCTGTGCCTCTTGTTT	60
JN831722.1	(TG)11	252	VVM148	F	VVM148F	GCCTAACTTCCAACCTGAAATACT	59
			VVM148	R	VVM148R	TTGTAGAGGGCATGGCAG	60
JN831744.1	(CA)16	252	VVM238	F	VVM238F	AAATTGGAAGTCAGCTCTTGC	60
			VVM238	R	VVM238R	CAAGCAACCCATGTCAAGTAAA	60
JN831733.1	(CA)18	257	VVM25	F	VVM25F	AAATCCTCTTATGCCTTCCGAT	60
			VVM25	R	VVM25R	CCATGTTGTAGCAAATAGCAGG	60
JN831725.1	(AC)18	260	VVM812	F	VVM812F	CTCCTTGTGGTTATGGCTGAGT	61
			VVM812	R	VVM812R	TTTACCCAGAGAACGATGAAGG	60
JN831746.1	(TG)20	261	VVM844	F	VVM844F	CTGGGTCTTGTTTTGTCTCCA	60

			VVM844	R	VVM844R	GCCTCAGTAAATGCTTCCTGTT	60
JN831728.1	(AC)15	264	VVM192	F	VVM192F	CCAGGATAATGAACAGCTTG	56
			VVM192	R	VVM192R	GTTTAAGCCACCTTTAGATGAG	55
JN831727.1	(AC)9	267	VVM509	F	VVM509F	GCATCCCTTCATTCCTGTAAAT	59
			VVM509	R	VVM509R	GTGAGTG GGGAGTAGAGTGCTT	60
JN831732.1	(TG)14	278	VVM838	F	VVM838F	AGAAATGGAAAGAGCAAGCAAG	60
			VVM838	R	VVM838R	AAGAAGAGGGCAGGATGTATCA	60

Table S2. Pilot study of 12 microsatellites in adult foxes from Augustów Forest (N = 23)

Locus	A	H_O	H_E	HWE-p	Nf
FH2088	7	0.43	0.77	< 0.01	0.182
C466	6	0.78	0.79	ns	0
FH2010	4	0.74	0.66	ns	0
FH2054	13	0.83	0.88	ns	0.017
C250	9	0.65	0.75	ns	0.046
FH2096	3	0.43	0.57	ns	0.081
FH2137	9	0.96	0.84	ns	0
VVM189	10	0.96	0.85	ns	0
VVM81	9	0.39	0.83	< 0.01	0.230
VVM828	9	0.78	0.83	ns	0.017
VVM33	11	0.62	0.91	< 0.01	0.278
VVM124	7	0.65	0.69	ns	0.011

A: Number of alleles

H_O : Observed heterozygosity

H_E : Expected heterozygosity

HWE- p : HWE test p -value

Nf: Null allele frequency estimate

ns: not significant ($p > 0.05$)

Table S3. Proportion of different habitats on Euclidean distances (for description of habitats see Material and methods) and its influence on genetic differentiation between red fox populations in north-eastern Poland. Correlation between proportion of a given habitat and genetic distance is given at the bottom of the table

Pairs of populations	Euclidian distance (m)	Forest		Forest edge (300 m)		Grasslands, wastelands, wetlands and extensive agriculture		Villages and scattered settlements	
		m	%	m	%	m	%	m	%
AUG-BIA	142995.06	33428.41	23.38	26691.34	18.67	35899.20	25.11	5488.82	3.84
AUG-DRY	84692.39	21120.37	24.94	16162.45	19.08	6785.61	8.01	2275.88	2.69
AUG-JED	179366.83	55228.89	30.79	37460.63	20.88	25577.08	14.26	6543.58	3.65
AUG-KNY	98278.40	26021.94	26.48	13346.14	13.58	20177.14	20.53	7635.02	7.77
AUG-LOM	125187.55	37088.44	29.63	24615.02	19.66	35597.21	28.44	4373.77	3.49
BIA-DRY	163725.96	17453.96	10.66	27229.49	16.63	40077.20	24.48	6207.08	3.79
BIA-JED	211758.85	40704.18	19.22	45609.68	21.54	41529.51	19.61	8163.52	3.86
BIA-KNY	46793.29	11228.41	24.00	7343.23	15.69	12667.07	27.07	1389.36	2.97
BIA-LOM	109478.37	13695.39	12.51	18633.64	17.02	12062.94	11.02	5941.48	5.43
DRY-JED	95794.91	39143.42	40.86	21196.65	22.13	14694.32	15.34	1746.22	1.82
DRY-KNY	134933.55	42803.31	31.72	21102.85	15.64	33804.72	25.05	3376.29	2.50
DRY-LOM	81915.21	16353.46	19.96	16611.01	20.28	17801.83	21.73	3190.21	3.89
JED-KNY	201412.15	33167.87	16.47	38164.23	18.95	60695.13	30.13	9034.75	4.49
JED-LOM	102301.69	24252.38	23.71	19646.23	19.20	32169.03	31.45	989.09	0.97
KNY-LOM	104717.48	17699.81	16.90	16495.03	15.75	24416.36	23.32	5284.93	5.05
Correlation with genetic distance		$r^2=0.272$; $p=0.046$		$r^2=0.115$; $p=0.217$		$r^2=0.026$; $p=0.564$		$r^2=0.112$; $p=0.223$	

Table S3. continued

Pairs of populations	Urban development		Arable land		Arable land edges (300 m)		Water		Forest + water
	m	%	m	%	m	%	m	%	%
AUG-BIA	1803.53	1.26	9327.90	6.52	30355.86	21.23	0.00	0.00	23.377
AUG-DRY	2184.80	2.58	10016.85	11.83	14886.70	17.58	11259.73	13.29	38.233
AUG-JED	3273.28	1.82	15626.94	8.71	19140.02	10.67	16516.40	9.21	39.999
AUG-KNY	1734.82	1.77	4512.52	4.59	24584.77	25.02	266.05	0.27	26.748
AUG-LOM	0.00	0.00	5000.42	3.99	18391.26	14.69	121.43	0.10	29.723
BIA-DRY	0.00	0.00	17992.07	10.99	54766.17	33.45	0.00	0.00	10.660
BIA-JED	173.68	0.08	23147.06	10.93	52251.73	24.68	179.50	0.08	19.307
BIA-KNY	4508.02	9.63	1558.84	3.33	8098.36	17.31	0.00	0.00	23.996
BIA-LOM	424.60	0.39	21659.57	19.78	37060.74	33.85	0.00	0.00	12.510
DRY-JED	0.00	0.00	1403.01	1.46	12341.00	12.88	5270.29	5.50	46.363
DRY-KNY	0.00	0.00	4833.31	3.58	28601.12	21.20	411.96	0.31	32.027
DRY-LOM	3084.55	3.77	4081.98	4.98	20792.17	25.38	0.00	0.00	19.964
JED-KNY	8729.61	4.33	6301.02	3.13	43487.79	21.59	1831.74	0.91	17.377
JED-LOM	0.00	0.00	5975.66	5.84	19117.92	18.69	151.38	0.15	23.855
KNY-LOM	0.00	0.00	6612.91	6.32	34208.43	32.67	0.00	0.00	16.902
Correlation with genetic distance	$r^2=0.005$ $p=0.797$		$r^2=0.217$; $p=0.080$		$r^2=0.121$; $p=0.204$		$r^2=0.152$; $p=0.150$		$r^2=0.311$; $p=0.031$

Figure S1. Statistical power of the nine microsatellite loci used in this study to detect genetic differentiation.

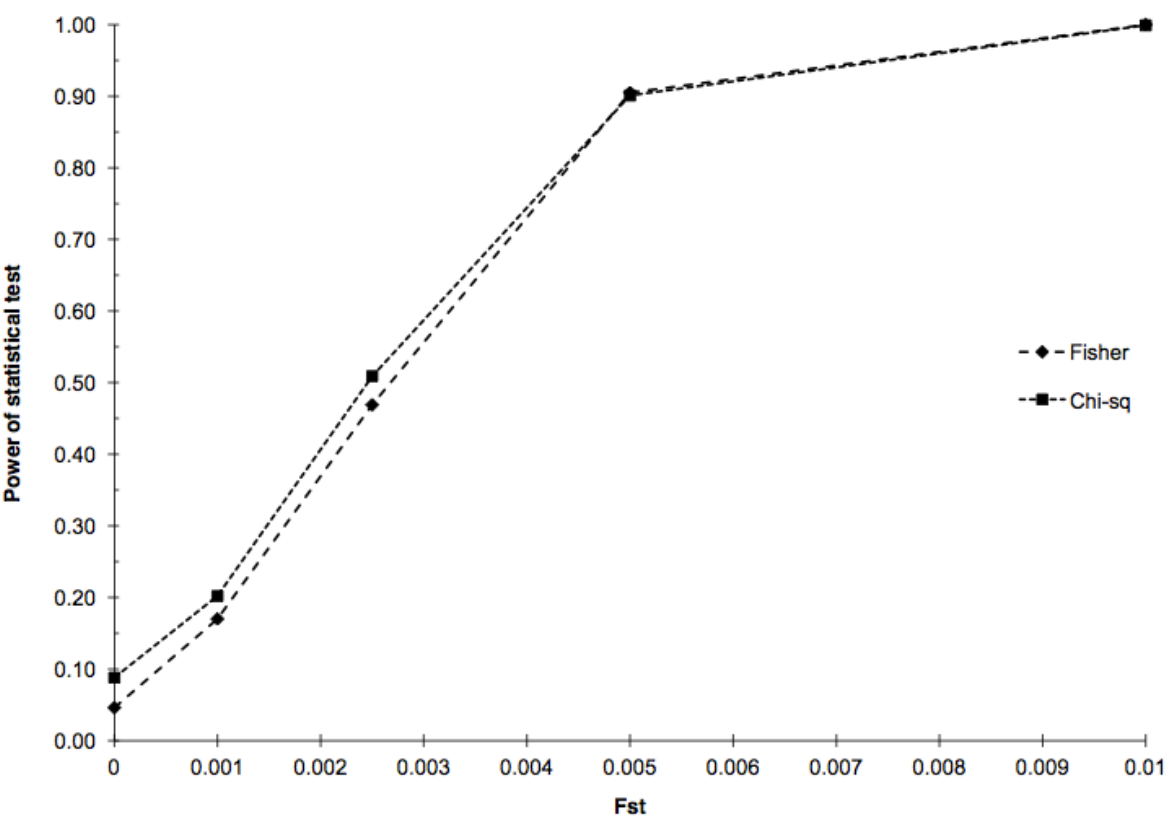


Figure S2. The average posterior log-likelihood probability (LnPr) of the data for each K was averaged over five replicates in STRUCTURE.

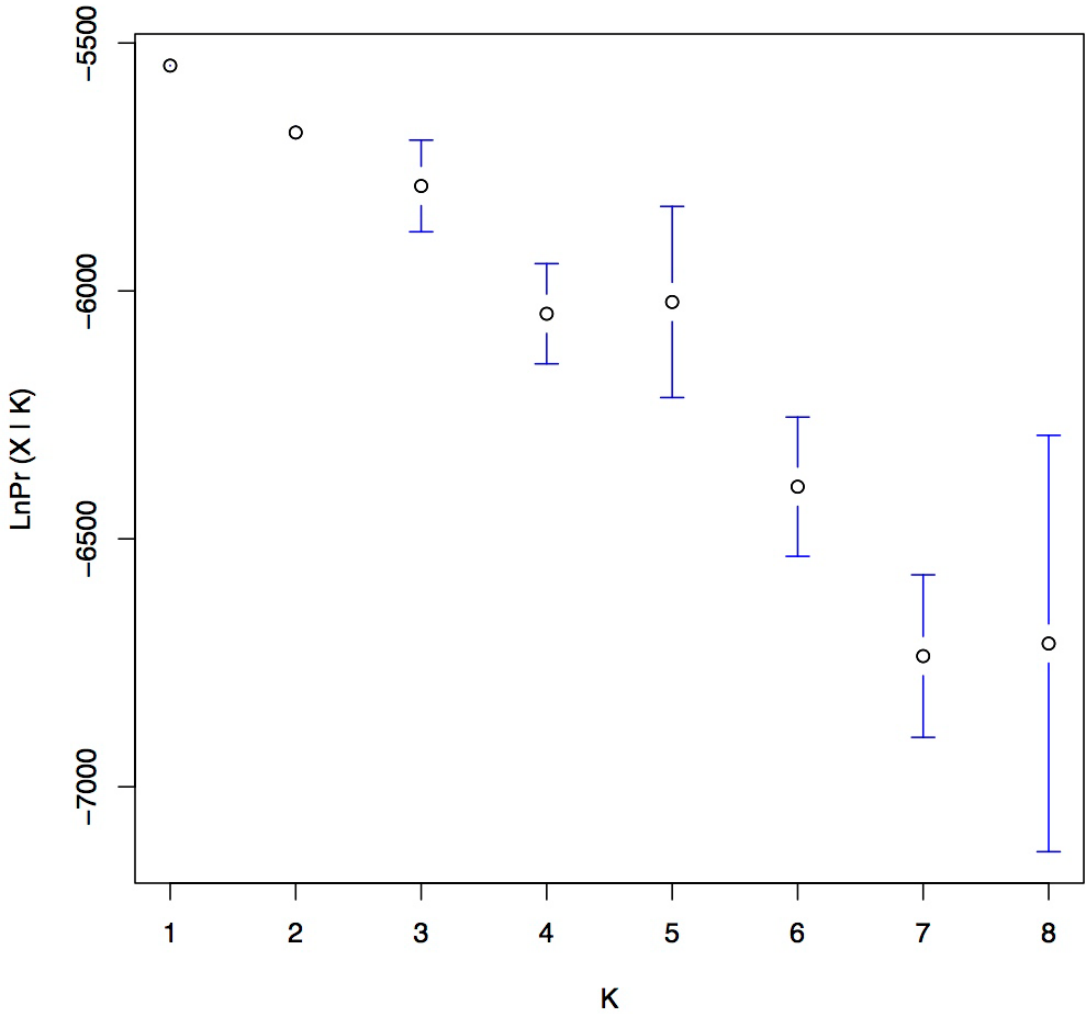


Figure S3. Spatial autocorrelation analysis for each sex separately. Variable distance class intervals were used to ensure sufficient sample size (>100) within each class.

