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Appendix 1

Table A1. Variance-covariance matrix of the heterozygosity measures based on all SNPs (labelled $H_{O(allSNPs)}$), non-synonymous SNPs only (labelled $H_{O(AA)}$), synonymous SNPs (labelled $H_{O(sSNPs)}$) and the 12 putatively neutral microsatellite markers we studied in Vanpé et al. (2015) (labelled $H_{O(mic)}$).

	$H_{O(allSNPs)}$	$H_{O(AA)}$	$H_{O(sSNPs)}$	$H_{O(mic)}$
$H_{O(allSNPs)}$	0.1279	0.1164	0.1160	-0.0067
$H_{O(AA)}$		0.1853	0.1436	-0.0011
$H_{O(sSNPs)}$			0.2686	-0.0024
$H_{O(mic)}$				0.0500

Table A2. Dispersal and genotyping data.

ID	Sex	Capture year	Sector	Standardized body mass	Dispersing status	IBSDD	TLR2a	TLR2b	TLR5a	TLR5b	TLR4a	TLR4B	TLR3a	TLR3b	CMHDRBa	CMHDRBb
48	m	2002	closed	16.48	Disperser	-1.996	1	3	1	2	1	2	1	1	23	23
58	f	2002	closed	14.64	Sedentary	-1.898	2	2	6	2	1	2	2	1	23	23
70	f	2002	open	17.42	Disperser	1.322	1	2	1	3	1	2	1	1	23	38
94	f	2003	open	18.64	Sedentary	-0.986	1	1	1	4	1	1	3	1	23	23
118	m	2003	open	17.30	Disperser	2.497	1	2	1	2	1	1	1	1	23	23
164	f	2004	closed	17.66	Sedentary	-2.245	1	2	2	4	1	1	2	2	38	38
170	m	2004	closed	16.58	Sedentary	-0.733	2	2	1	2	1	4	2	1	23	33
172	m	2004	closed	18.50	Sedentary	-0.455	2	6	1	6	1	1	1	1	23	23
174	m	2004	closed	15.68	Sedentary	-1.776	1	3	2	4	3	4	2	2	23	38
180	m	2004	closed	17.28	Sedentary	-1.384	2	3	1	2	1	1	1	1	33	38
190	f	2005	open	17.29	Disperser	1.475	1	2	1	2	1	3	2	1	23	23
232	f	2005	open	17.54	Disperser	1.947	2	3	1	2	1	1	3	1	23	38
280	m	2006	open	19.23	Disperser	2.658	2	2	3	2	1	3	2	2	36	38
320	f	2007	open	16.94	Sedentary	-3.337	1	2	1	3	1	1	2	1	33	38
334	m	2007	open	17.90	Sedentary	-0.998	2	2	4	4	1	2	1	1	23	23
338	m	2007	open	16.72	Disperser	-0.806	1	3	3	2	1	1	3	3	23	38
344	f	2007	open	16.22	Sedentary	-0.005	2	3	3	2	1	1	3	1	23	38
350	m	2007	open	17.82	Disperser	2.978	1	2	1	4	1	1	2	1	23	33
352	m	2007	open	18.88	Disperser	2.498	1	2	1	2	1	1	1	1	23	38
368	f	2007	open	17.36	Sedentary	-1.062	1	1	1	1	1	1	1	1	23	23
378	m	2007	closed	12.42	Sedentary	-2.172	1	2	2	4	1	3	2	2	23	23
386	f	2007	open	16.03	Sedentary	-0.590	2	3	2	2	1	4	1	1	38	40
392	m	2008	open	16.71	Sedentary	-3.727	2	3	1	2	1	4	1	1	38	38
396	f	2008	open	14.82	Sedentary	-0.635	1	1	1	1	1	4	2	1	23	23
406	f	2008	open	18.95	Disperser	1.207	1	1	4	4	1	4	1	1	38	38
412	m	2008	open	14.63	Sedentary	-0.294	1	1	1	1	3	4	2	1	23	33
416	m	2008	open	13.76	Sedentary	-1.407	1	2	2	4	2	4	2	1	23	38
420	f	2008	open	17.66	Disperser	2.853	1	1	1	3	1	1	2	2	23	23
434	m	2008	open	15.92	Disperser	1.354	2	2	2	2	4	4	2	1	23	36
438	f	2008	open	14.22	Sedentary	-1.568	1	6	1	4	1	4	2	1	23	23
444	f	2008	open	16.04	Disperser	1.297	1	1	1	4	1	1	3	1	23	23
446	f	2008	open	19.10	Disperser	0.163	1	2	2	4	1	1	3	1	23	23
476	f	2009	open	15.33	Sedentary	-1.346	1	3	2	2	1	2	2	2	23	23

480	m	2009	open	17.77	Sedentary	-1.570	2	2	1	4	1	4	3	1	23	33
486	m	2009	open	18.59	Sedentary	0.103	1	2	2	4	1	1	1	1	23	23
494	m	2009	open	17.22	Disperser	2.433	1	2	2	4	1	2	2	1	36	36
504	f	2008	open	17.50	Sedentary	-1.740	1	2	1	4	1	4	1	1	33	38
510	f	2009	open	18.67	Disperser	2.902	1	2	2	4	1	4	2	1	23	33
516	m	2009	open	18.66	Disperser	-0.689	1	2	3	4	1	1	1	1	23	38
520	m	2009	open	17.67	Disperser	-0.437	2	2	1	6	1	1	2	1	23	23
530	f	2010	open	17.92	Sedentary	-0.364	2	2	1	2	1	1	2	1	23	36
F532	f	2009	open	19.31	Disperser	3.599	1	2	3	2	1	3	2	3	23	38
536	f	2010	open	16.82	Disperser	1.846	1	2	1	2	2	4	3	1	23	23
538	f	2010	open	16.39	Sedentary	-0.325	1	3	3	2	1	2	1	1	23	23
542	f	2009	open	17.91	Disperser	2.390	2	2	1	4	1	4	2	1	23	23
546	f	2010	closed	13.52	Sedentary	-0.312	1	1	1	3	1	4	1	1	23	36
550	m	2010	closed	16.72	Sedentary	-0.797	1	1	1	3	1	2	3	1	23	36
552	f	2010	closed	13.35	Sedentary	-1.349	2	3	1	1	1	4	2	1	23	38
F554	m	2011	open	18.91	Disperser	1.668	2	3	2	4	1	2	2	1	23	23
560	m	2010	closed	14.36	Sedentary	-0.689	1	2	1	6	1	4	2	3	23	38
F572	f	2010	open	17.64	Sedentary	-1.515	1	1	1	1	1	4	2	1	23	38
578	f	2010	open	14.84	Sedentary	-2.100	1	2	1	3	3	4	2	1	23	33
F582	f	2011	open	17.47	Disperser	3.465	1	2	1	4	1	4	1	1	23	23
F586	f	2011	closed	18.31	Disperser	0.872	1	2	1	1	1	4	2	1	36	36
610	m	2011	open	18.19	Sedentary	-0.399	1	2	1	1	4	4	1	1	23	23
632	f	2011	open	19.09	Sedentary	-0.485	1	1	2	4	1	1	2	1	23	23
634	m	2011	open	15.89	Disperser	0.805	2	2	1	2	1	3	2	1	33	36
636	m	2011	open	18.15	Sedentary	-0.572	2	3	3	2	1	1	1	1	23	33
660	f	2011	open	18.34	Disperser	2.033	2	2	1	2	1	2	3	1	38	38
664	f	2011	open	17.42	Disperser	1.947	2	2	1	2	3	4	2	2	23	23
666	f	2011	open	17.48	Sedentary	-0.073	1	2	2	4	3	2	2	1	36	38
696	f	2012	open	17.51	Sedentary	-2.974	1	2	1	1	1	4	1	1	23	38
698	f	2012	open	19.37	Sedentary	0.107	2	6	1	2	1	1	3	1	38	38
710	f	2012	open	19.29	Disperser	2.605	1	2	1	2	1	3	2	3	23	38
722	m	2012	closed	14.73	Sedentary	-1.272	1	2	1	2	1	4	1	1	23	23
726	m	2012	open	17.37	Sedentary	-0.090	1	1	2	2	1	3	2	2	23	38
736	m	2012	open	16.59	Disperser	3.707	1	2	2	2	2	4	2	1	36	38
738	m	2012	open	16.21	Sedentary	-2.206	2	2	1	2	1	1	3	1	23	38
760	m	2012	open	19.65	Disperser	3.738	1	2	2	2	1	4	3	1	23	23
F1062	f	2012	open	13.93	Disperser	1.538	2	2	1	2	1	1	3	1	23	23
F1064	f	2012	open	14.99	Disperser	1.494	1	1	1	1	1	4	3	1	23	38

Note:

ID: Identity of individuals.

Sex: sex of individuals with m: male and f: female.

Capture year: year of capture of individuals as juveniles.

Sector: habitat type of the capture site. We identified two sectors of contrasting landscape structure based on woodland extent: the closed sector (noted closed) included the two large forest blocks, whereas the open sector (noted open) included the remaining part of the landscape and was composed of a more open landscape of fragmented woodland (see Debeffe et al. 2012 for details).

Standardized body mass: body mass (in kg) controlled for capture date and standardized by adding the mean between-sex difference in body mass to the body mass of all females.

Dispersing status: dispersing status of juveniles as either disperser or philopatric (noted sedentary).

IBSDD: Individual Based Standardised Dispersal Distance calculated as the residual value from the linear regression of the Euclidean distance between juvenile and adult home range centres of gravity on the juvenile home range size (see Debeffe et al. 2012 for details).

TLR2a, TLR2b, TLR3a, TLR3b, TLR4a, TLR4b, TLR5a, TLR5b, CMH-DRBa, CMH-DRBb: genotyping data for TLR2, TLR3, TLR4, TLR5 and MHC-DRB. MHC-DRB haplotypes were obtained by 454 sequencing the exon 2 of the MHC-DRB gene. TLRs haplotypes were reconstructed from phased SNPs (see Quéméré et al. 2015 for details).

Table A3. Comparison of the performances of the generalized linear mixed-effect models (with binary response) testing the influence of standardized body mass (labelled BM_{std}) on heterozygosity at individual immune gene loci (labelled $H_{O(TLR2)}$, $H_{O(TLR3)}$, $H_{O(TLR4)}$, $H_{O(TLR5)}$ and $H_{O(MHC)}$, for TLR2, TLR3, TLR4, TLR5 and MHC, respectively) with the corresponding constant models (A) as well as the performances of the mixed linear models testing the influence of the individual effect of $H_{O(TLR2)}$, $H_{O(TLR3)}$, $H_{O(TLR4)}$, $H_{O(TLR5)}$ and $H_{O(MHC)}$ on BM_{std} with the corresponding constant models (B), with the year of capture as a random factor.

(A)

	K	AICc	$\Delta AICc$	wAIC
$H_{O(TLR2)} \sim BM_{std}$	3	100.39	1.90	0.28
$H_{O(TLR2)} \sim 1$	2	98.49	0.00	0.72
$H_{O(TLR3)} \sim BM_{std}$	3	102.79	1.90	0.28
$H_{O(TLR3)} \sim 1$	2	100.89	0.00	0.72
$H_{O(TLR4)} \sim BM_{std}$	3	93.43	0.00	0.87
$H_{O(TLR4)} \sim 1$	2	97.23	3.80	0.13
$H_{O(TLR5)} \sim BM_{std}$	3	83.93	1.91	0.28
$H_{O(TLR5)} \sim 1$	2	82.02	0.00	0.72
$H_{O(MHC)} \sim BM_{std}$	3	103.77	1.23	0.35
$H_{O(MHC)} \sim 1$	2	102.54	0.00	0.65

(B).

	K	AICc	$\Delta AICc$	wAIC
$BM_{std} \sim H_{O(TLR2)}$	4	277.70	2.19	0.25
$BM_{std} \sim 1$	3	275.52	0.00	0.75
$BM_{std} \sim H_{O(TLR3)}$	4	277.66	2.14	0.26
$BM_{std} \sim 1$	3	275.52	0.00	0.74
$BM_{std} \sim H_{O(TLR4)}$	4	272.26	0.00	0.84
$BM_{std} \sim 1$	3	275.52	3.25	0.16
$BM_{std} \sim H_{O(TLR5)}$	4	277.70	2.18	0.25
$BM_{std} \sim 1$	3	275.52	0.00	0.75
$BM_{std} \sim H_{O(MHC)}$	4	276.81	1.30	0.34
$BM_{std} \sim 1$	3	275.52	0.00	0.66

Note: Model selection was performed using the Akaike information criterion corrected for small sample size (AICc) as recommended by Burnham and Anderson (2002). ΔAICc is the AICc difference between the given model and the model with the lowest AICc. K is the number of parameters. $w\text{AICc}$ is the AICc weight that is a measure of the likelihood that the given model is the best among the set of fitted models. The best model (in bold) generally is the model with the lowest AICc value, reflecting the best compromise between precision and accuracy. However, according to the parsimony rule, when simpler models (with a lower number of parameters K) had an AICc which differed from the best model by < 2 , we retained the simplest model. In such cases, the model with the lowest AICc occurs in italics and the retained simplest model occurs in bold.

Table A4. Parameter estimates of the mixed linear regression model describing the relationship between dispersal distance (measured as individually-based standardized dispersal distance) of juvenile roe deer and individual standardized observed heterozygosity at the five immune gene loci when based on all SNPs (labelled $H_{O(allSNPs)}$), standardized body mass (labelled BM_{std}) and landscape sector (labelled Sector) as fixed effects, as well as the year of capture as a random effect.

	Estimate	SE	df	t	P
Intercept	5.495	6.811	57	0.807	-
$H_{O(allSNPs)}$	-11.638	6.128	57	-1.899	-
BM_{std}	-0.391	0.391	57	-0.998	-
Sector	1.005	0.525	57	1.914	0.061
$H_{O(allSNPs)} : BM_{std}$	0.717	0.354	57	2.025	0.048

Table A5. Parameter estimates of the mixed linear regression model describing the relationship between dispersal distance (measured as individually-based standardized dispersal distance) of juvenile roe deer and heterozygosity at TLR4 (labelled $H_{O(TLR4)}$), standardized body mass (labelled BM_{std}), and landscape sector (labelled Sector) as fixed effects, as well as the year of capture as a random effect.

	Estimate	SE	z	P
Intercept	1.583202	4.689955	0.3376	-
$H_{O(TLR4)}$	-11.94601	5.219584	-2.289	-
BM_{std}	-0.085841	0.265986	-0.323	-
$H_{O(TLR4)} : BM_{std}$	0.72021	0.299206	2.4071	0.0193

Table A6. Performance of the ten candidate mixed logistic regression and mixed linear regression models of variation in dispersal propensity and in dispersal distance (measured as individual-based standardized dispersal distance), respectively, for juvenile roe deer, including the effects of individual standardized observed heterozygosity at the five immune gene loci with haplotype reconstruction based on synonymous SNPs (labelled $H_{O(sSNPs)}$), standardized body mass (labelled BM_{std}) and landscape sector (labelled Sector) as fixed effects, as well as the year of capture as a random effect.

	Dispersal propensity			Dispersal distance				
	K	AICc	Δ AICc	wAICc	K	AICc	Δ AICc	wAICc
$H_{O(sSNPs)}$ * BM_{std} + Sector	6	93.66	0.00	0.26	7	284.05	1.90	0.15
$H_{O(sSNPs)}$ * BM_{std}	5	94.57	0.91	0.17	6	285.89	3.75	0.06
$H_{O(sSNPs)}$ + BM_{std} + Sector	5	96.10	2.44	0.08	6	284.10	1.95	0.15
$H_{O(sSNPs)}$ + BM_{std}	4	97.39	3.73	0.04	5	286.21	4.07	0.05
$H_{O(sSNPs)}$ + Sector	4	98.94	5.29	0.02	5	288.88	6.73	0.01
BM_{std} + Sector	4	93.80	0.14	0.25	5	282.15	0.00	0.39
$H_{O(sSNPs)}$	3	103.96	10.3	0.00	4	296.13	13.99	0.00
BM_{std}	3	95.15	1.49	0.12	4	284.03	1.88	0.15
Sector	3	96.70	3.04	0.06	4	286.82	4.67	0.04
Constant	2	101.89	8.23	0.00	3	293.89	11.74	0.00

Note: BM_{std} was centered around the mean for the mixed logistic regressions. Model selection was performed using the Akaike information criterion corrected for small sample size (AICc) as recommended by Burnham and Anderson (2002). Δ AICc is the AICc difference between the given model and the model with the lowest AICc. K is the number of parameters. wAICc is the AICc weight that is a measure of the likelihood that the given model is the best among the set of fitted models. The selected model (in bold) is generally the model with the lowest AICc value, reflecting the best compromise between precision and accuracy. However, according to the parsimony rule, when simpler models (with a lower number of parameters K) had an AICc which differed from the best model by < 2 , we retained the simplest model. In such cases, the model with the lowest AICc occurs in italics and the retained simplest model occurs in bold.

Table A7. Parameter estimates of the mixed logistic regression model describing the effects of individual standardized observed heterozygosity at the five immune gene loci with haplotype reconstruction based on synonymous SNPs (labelled $H_{O(sSNPs)}$) and standardized body mass (labelled BM_{std}) on dispersal propensity of juvenile roe deer, with the year of capture as a random effect.

	Estimate	SE	z	P
Intercept	-0.196	0.585	-0.335	-
$H_{O(sSNPs)}$	-0.050	0.513	-0.098	0.92
BM_{std}	0.476	0.176	2.705	0.007

Table A8. Parameter estimates of the mixed linear regression model describing the effects of individual standardized observed heterozygosity at the five immune gene loci with haplotype reconstruction based on synonymous SNPs (labelled $H_{O(sSNPs)}$) and standardized body mass (labelled BM_{std}) on dispersal distance (measured as individual-based standardized dispersal distance) of juvenile roe deer, with the year of capture as a random effect.

	Estimate	SE	df	t	P
Intercept	-7.499	2.185	59	-3.431	-
$H_{O(sSNPs)}$	0.146	0.409	59	0.356	0.72
BM_{std}	0.441	0.123	59	3.584	0.0007