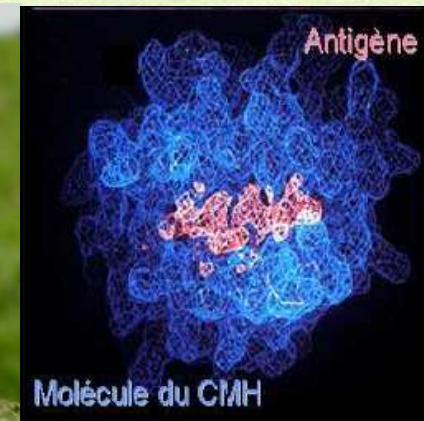


Mise en évidence de la sélection au gène majeur d'histo-compatibilité chez le campagnol terrestre

Quelques méthodes directes et indirectes de détection de la sélection



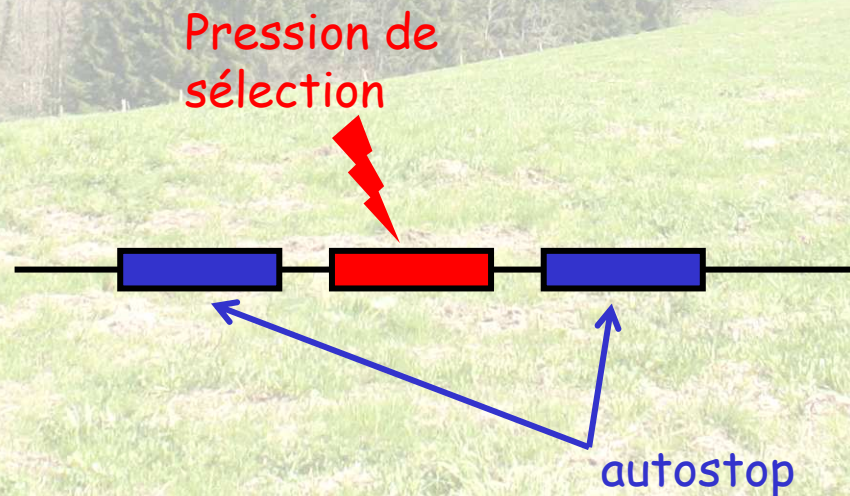
Cibles de la sélection:

- * gènes codants sous pression sélective

- * gènes neutres en DL (déséquilibre de liaison)

avec une région sélectionnée (sélection par autostop)

des évaluations sur les vertébrés indiquent que 5-15%
des locus microsatellites présentent des signatures de sélection



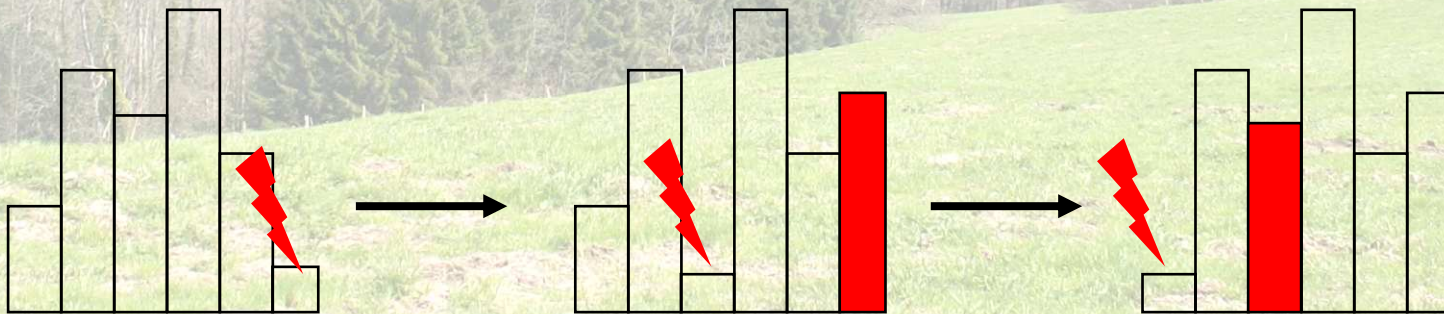
Différents types de sélection:

* **sélection balancée**: maintient du polymorphisme
sous différents mécanismes de sélection:

° avantage aux hétérozygotes (surdominance)

Aa >> AA, aa

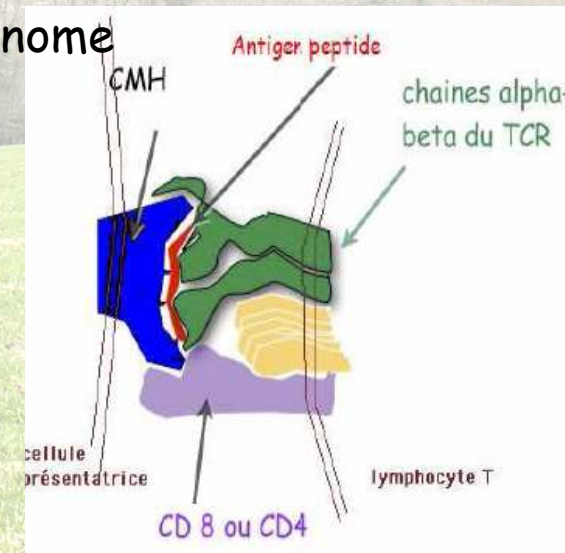
° avantage du rare (fréquence-dépendance)



* **sélection purifiante**: région conservée

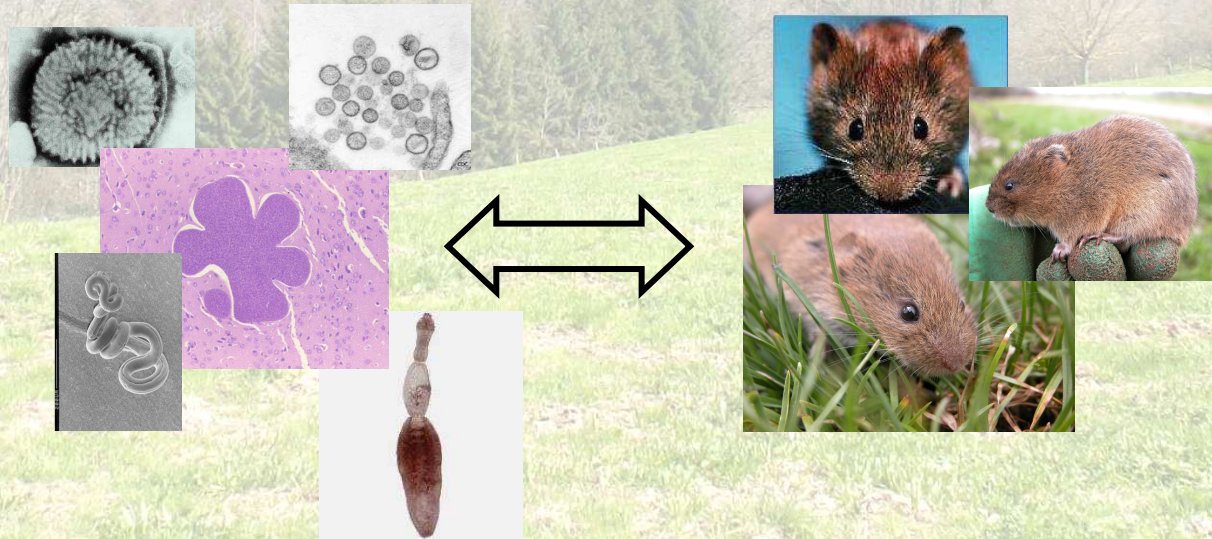
Les gènes du complexe majeur d'histo-compatibilité (MHC)

- * système de reconnaissance des antigènes
codent pour protéines de surface qui présentent les peptides étrangers aux lymphocytes T
- * gènes les plus polymorphes du génome
- * pression de sélection : parasites



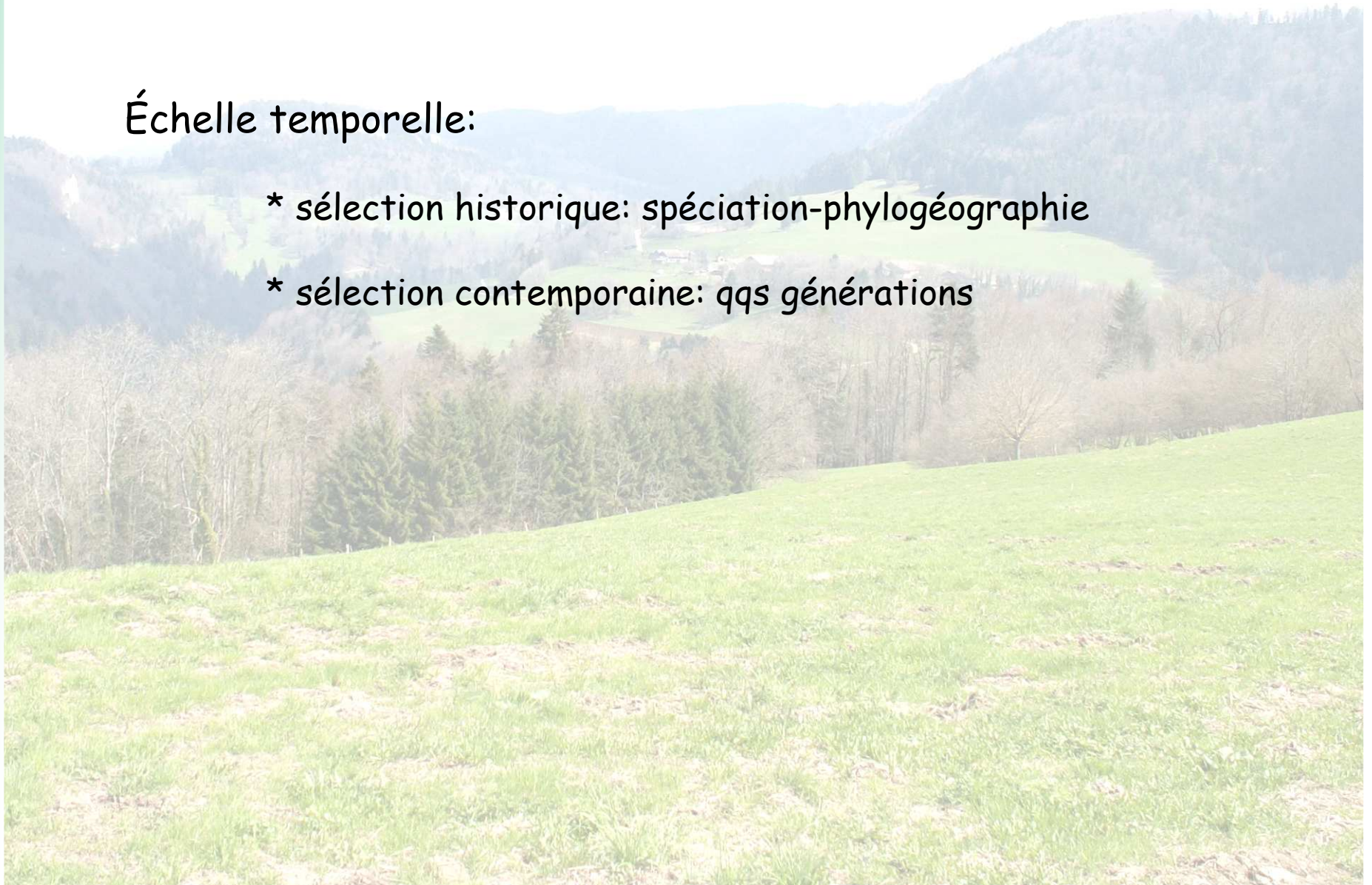
Impact des parasites sur les hôtes

- * pression de sélection: affecte la fitness individuelle
impact sur la survie, la fécondité ...
- * immunité innée: protection contre les parasites



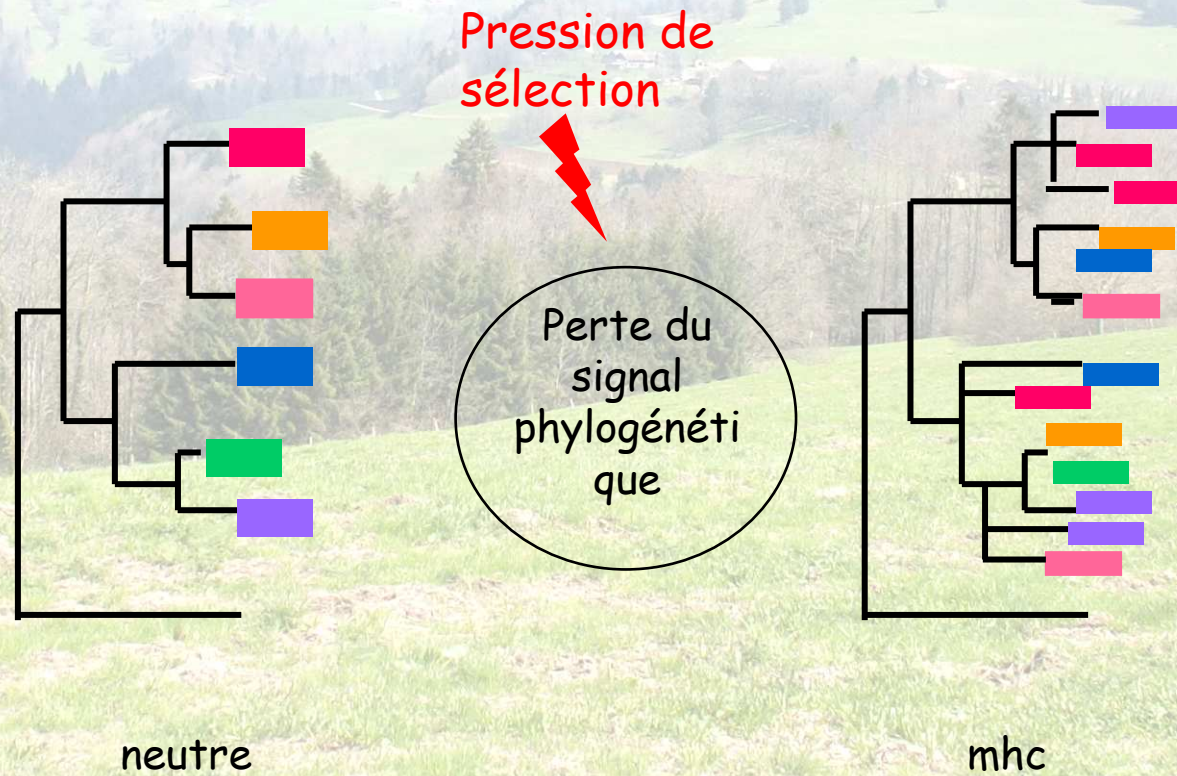
Échelle temporelle:

- * sélection historique: spéciation-phylogéographie
- * sélection contemporaine: qqs générations

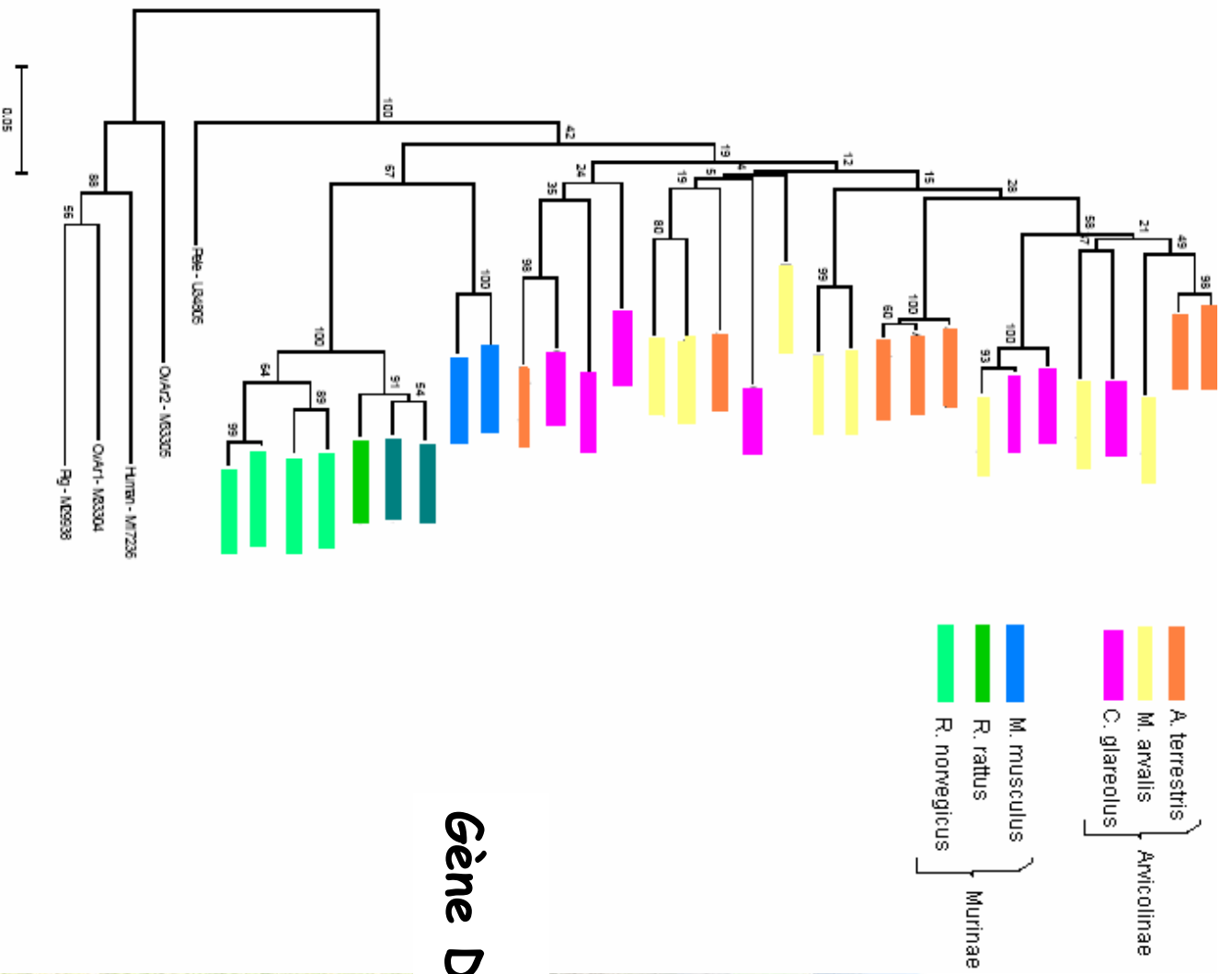


Sélection à l'échelle historique:

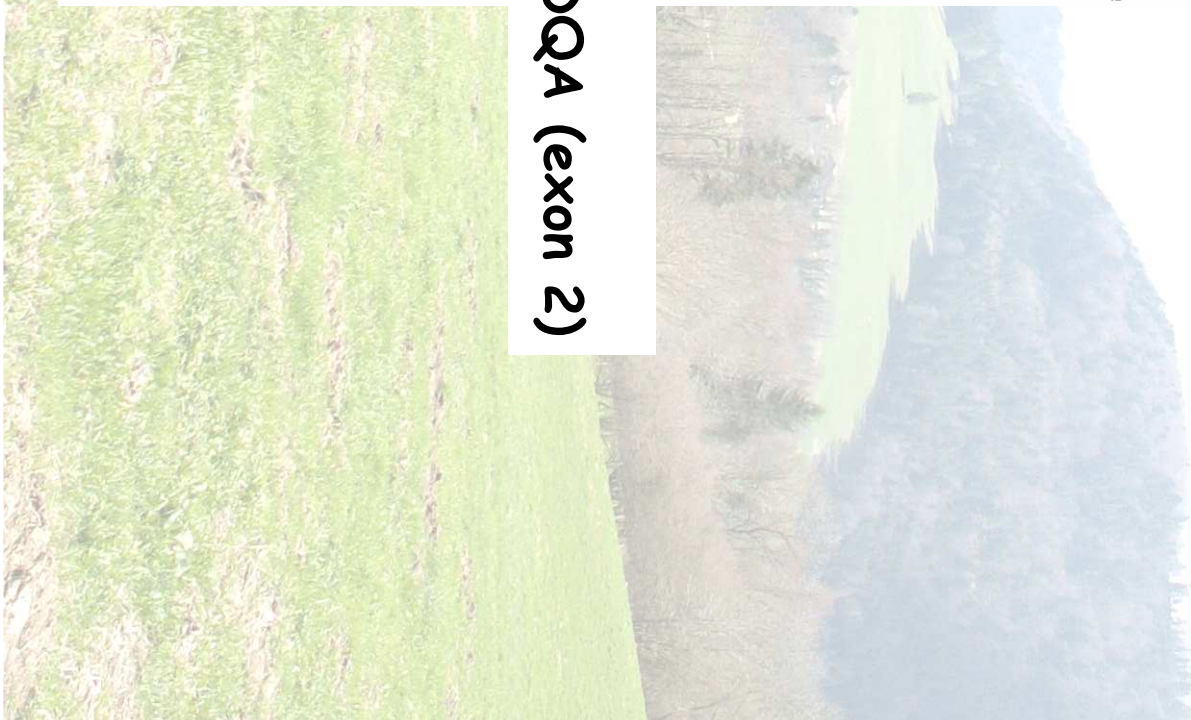
* phylogénie de gènes neutre vs. sélectionné



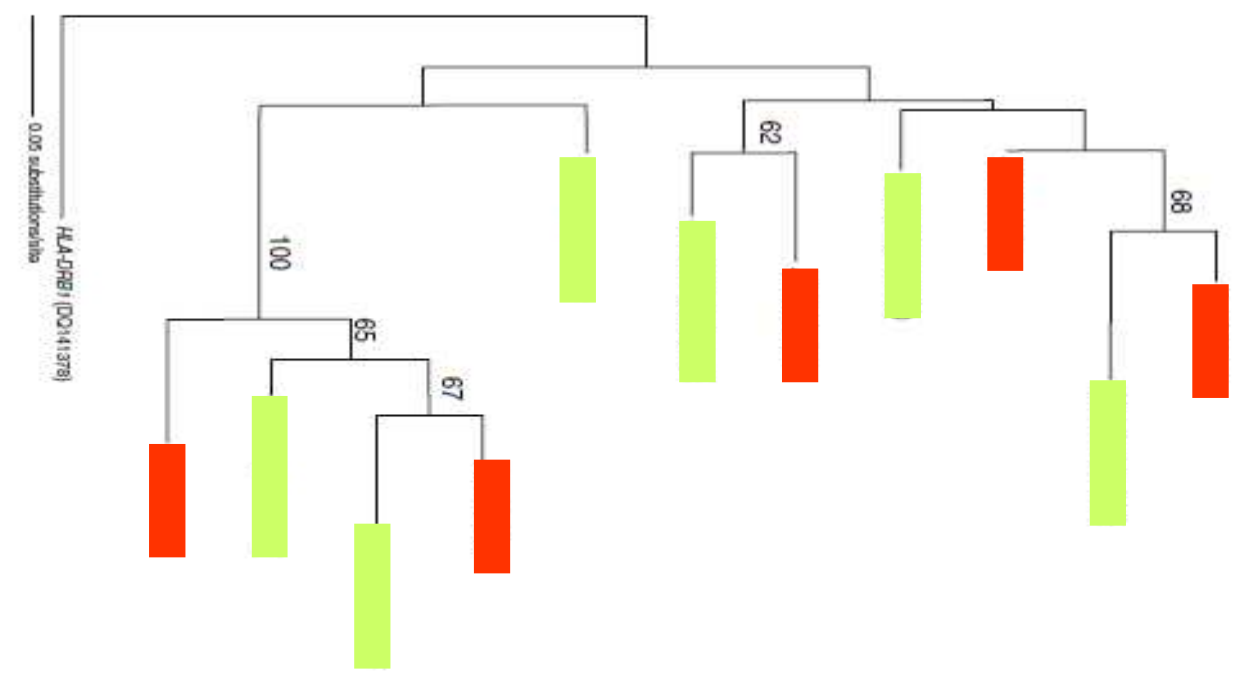
Mise en évidence de la sélection aux gènes du MHC



Gène DQA (exon 2)

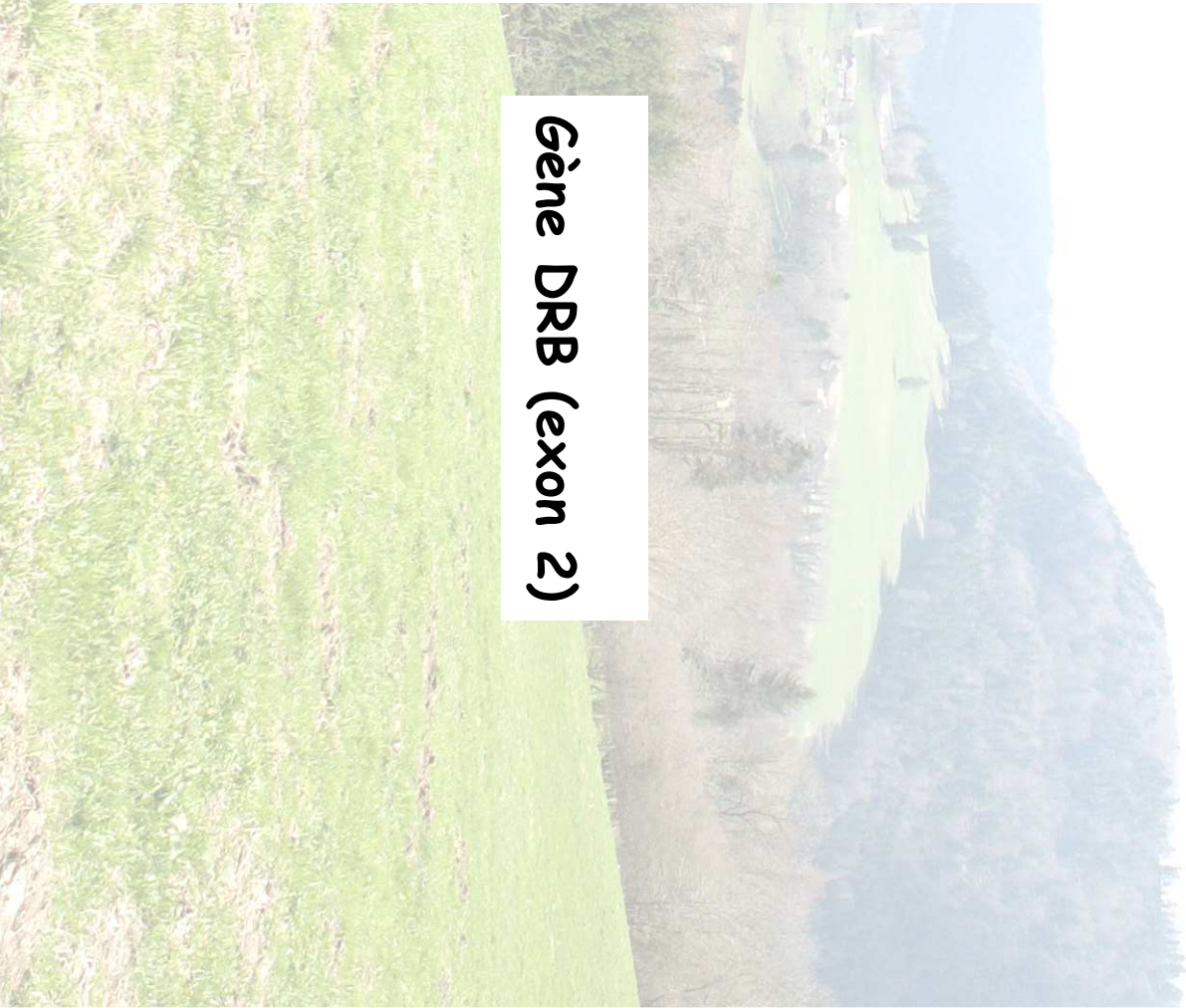


Mise en évidence de la sélection aux gènes du MHC



Arvicolinae
Murinae

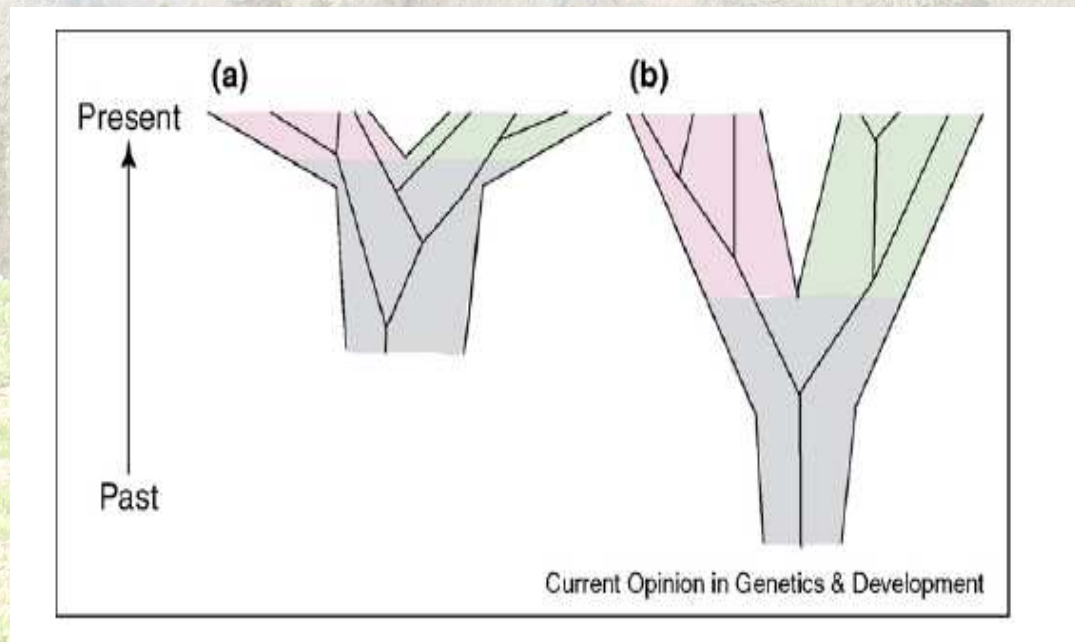
Gène DRB (exon 2)



Polymorphisme trans-spécifique:

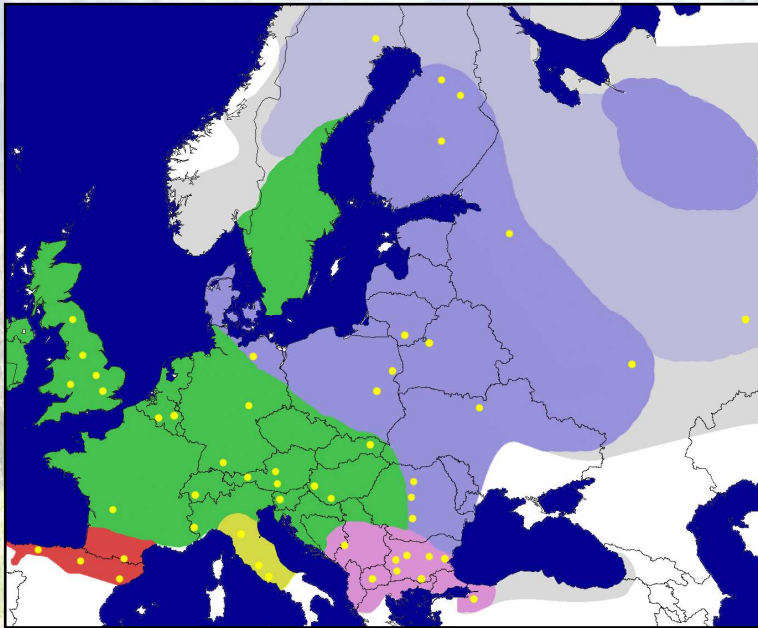
sélection balancée: maintient du polymorphisme allélique par sélection au cours de la spéciation

sélection fréquence-dépendante (avantage du rare) permet d'éviter l'extinction des lignées

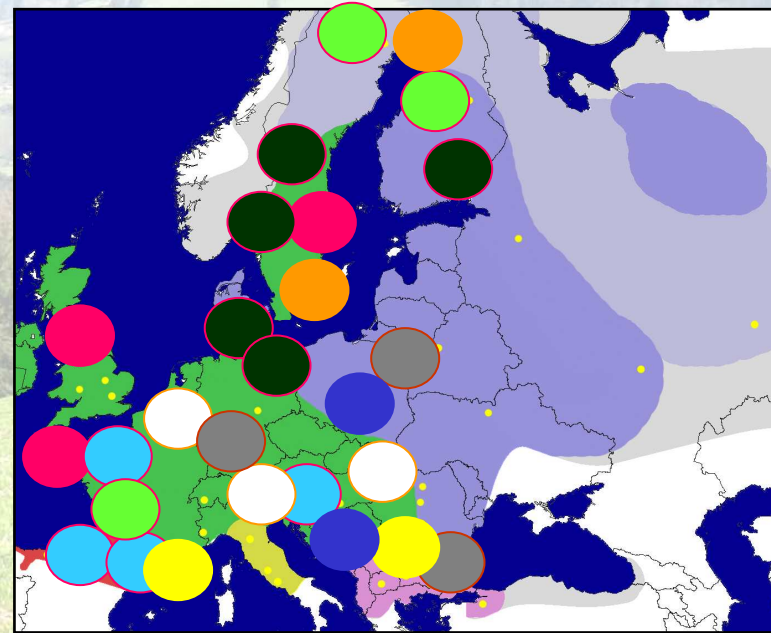


Sélection balancée:

perte du signal phylogéographique à l'échelle européenne



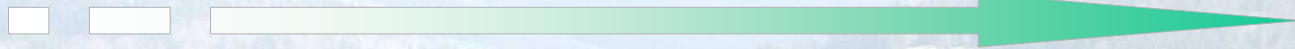
neutre



mhc

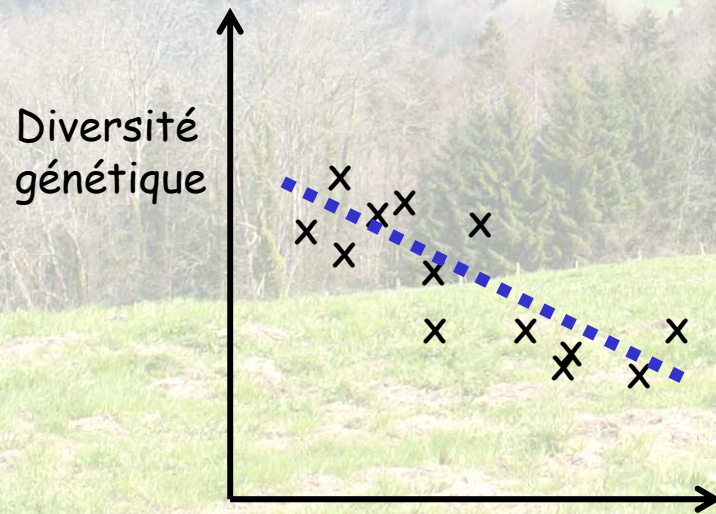
Sélection balancée:

maintient de la diversité lors des invasion (lignées phylogeog; introduction)

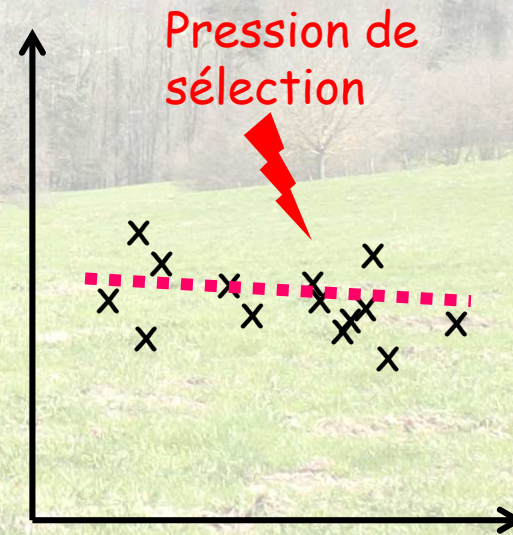


Gradient de colonisation (expansion d'aire)

Gradient de taille efficace (introduction)



neutre



mhc

Mise en évidence par l'analyse des séquences:

- * code génétique dégénéré : à un Acide Aminé correspond plusieurs codons
- * mutation synonyme : même AA
- * mutation non synonyme : AA différent
- * tests sur deux gènes MHC de classe II: DQA et DRB

Une chaîne d'AA

* un ensemble de sites conservés, neutres et sous sélection positive

	1	1111111112	2222222223	3333333334	4444444445	5555555556	6666666667	7777777778	8888
Arte-DQA*01	DHVGSYGI	TTYQSYGPNQ	QFTPEFDGDE	LLYVDLDKKE	TWRLPEFAQ	LRRFDPQGGI	QNIATGKHNL	DILTKRSNFT	PATN
Arte-DQA*02	..I.....	.V.....	.Y....D..I..G.	.G.L.....	R...A....T....
Arte-DQA*03	..I.....	.V.....	.Y....D..I..G.	...L.....	R...A....V...T....
Arte-DQA*04E....V.....
Arte-DQA*05	..I.....	.VN.....	.Y....D..I..G.	.G.L.....	R...A....V...T....
Arte-DQA*06F..	DP..T.ES..	.Y.....	EF....G..	...I..G.	.TT.....	RE..SS.Y..	..MI....S.
Arte-DQA*07	..I..F..	IVC....S..	.Y.M.....	.F.....	...I..GH	.AS....I..	.E..GA.Y..	.LM....S.	QV..
Miar-DQA*01	..I.....	NV....S..	.Y.M.....	E....G..	...I.G.G.	..S.....VA....	.MWI.E....
Miar-DQA*02	..I.....	NV....S..	.Y.M.....	KF....G..	...I..GK	.TS.....	.E..RA.F..	...I.ET.S.	.T..
Miar-DQA*03	..I.....	EL.....	.Y.....	.F....G..	...I..GH	.AS.....	.EM..A....V.....S.
Miar-DQA*04F.T	VV.....	.YIM.....I..GK	.ASL...S..	.Q...A....V...M..S.	.V..
Miar-DQA*05TF.T	VV.....	.V.C.....I..GK	.ASL.....	.Q...A.F..V.....S.	.V..
Miar-DQA*06I...	E.....	...K...S.	...L.....	R...M.Y..S.	L...
Miar-DQA*07	N.....	E.....	...I..G.	.ITV.....V.....
Miar-DQA*08T...S..	...M..N..	E....G..	...I..G.	..SY.....VE.F..L.....
Clg1-DQA*01	..IA....	K.....R.	...I..D.	.IT.....S..F..V.I.Q..S.
Clg1-DQA*02A...	IVC.....D	.Y.M.....	.F...S...	...I..G.	.AS.....	.Q...A....VI....S.	.T..
Clg1-DQA*03F..	DP....S..	.Y.....	EF...F..	...I..G.	.TS.....	.E..LS.QD.	..MI....S.
Clg1-DQA*04L	SPS..HQ...	.Y.....	.F...S...	...I..G.	.TS.....	.S..IE....NMI.W..S.
Clg1-DQA*05	N.I.....	IV.....	.Y.....	EF.....	...I..G.	.LY...N..	HD..IV.QY.P.....S.
Clg1-DQA*06T...S..	...M.....	E....G..	...I..G.	..SY.....VE.F..L.....
Clg1-DQA*07T...S..	...M.....	E....G..	.I..I..G.	..S.....A..F..L.....

Fig. 1 Alignment of seven expressed amino acid sequences of the complete *DQA* exon 2 of the water voles (*Arte-DQA*), eight sequences of the common voles (*Miar-DQA*) and seven sequences of the bank voles (*Clg1-DQA*). Dots indicate identity in the amino acid sequence of the *Arte-DQA**01. Numbering of amino acid residues is according to Brown et al. (1993)



Un excès de mutation non synonymes (dN) sur les sites fonctionnels (ABS)

Table 2 Synonymous and non-synonymous distances for antigen-binding sites (ABS) and non-ABS in *DQA* sequences

	<i>N</i>	ABS			Non-ABS		
		dS	dN	dN/dS	dS	dN	dN/dS
All rodents	32	0.28±0.10	0.39±0.07	1.40	0.30±0.06	0.09±0.02	0.31
Murinae (5 spp.)	9	0.22±0.16	0.21±0.05	0.95	0.16±0.05	0.08±0.02	0.53
Arvicolinae (3 spp.)	22	0.21±0.08	0.43±0.07	2.02	0.20±0.04	0.07±0.02	0.36
<i>Clethrionomys</i>	7	0.28±0.16	0.49±0.09	1.74	0.20±0.05	0.08±0.02	0.37
<i>Microtus</i>	7	0.19±0.09	0.45±0.10	2.40	0.18±0.05	0.08±0.02	0.42
<i>Arvicola</i>	8	0.11±0.07	0.36±0.07	3.16	0.17±0.05	0.06±0.01	0.33

Synonymous (dS) and non-synonymous (dN) distances were calculated using the Nei–Gojobori method with a Jukes–Cantor correction. Standard errors were estimated by bootstrap with 1,000 replicates
N Number of analysed sequences

Kumar S, Tamura K, Nei M (2004) MEGA 3: integrated software for molecular evolutionary genetics analysis and sequence alignment. *Briefings in Bioinformatics*, 5, 150–163.

Test de rapport de vraisemblance (PALM)

* modèles « avec » vs. « sans » sites sous sélection positive

Table 3 Summary of test statistics for the likelihood-ratio tests of exon 2 of the *DQA* gene in three species of voles

Models compared	<i>df</i>	Test statistic	Significance
M1a vs M2a	2	19.794	$p < 0.001$
M3 vs M0	4	82.860	$p < 0.001$
M8 vs M7	2	22.665	$p < 0.001$

Test statistic was computed as $2(L_b - L_a)$, where L_a and L_b are log-likelihood values for each of the nested models being compared

Détection des sites sous sélection positive (approche Bayésienne, PAML)

Table 4 Results of maximum likelihood models of exon 2 of the *DQA* gene in three species of voles

Model code	<i>P</i>	Log-likelihood	Parameter estimates	Positively selected sites
M0 (one ratio)	1	-1764.296	$\omega=0.861$	None
M1a (NearlyNeutral)	1	-1701.588	$p_0=0.551, p_1=0.450$	Not allowed
M2a (PositiveSelection)	3	-1681.795	$p_0=0.502, p_1=0.304, p_2=0.195, \omega_2=3.312$	24, 31, 52, 53, 65, 66, 68, 72
M3 (discrete)	5	-1681.436	$p_0=0.542, p_1=0.292, p_2=0.167, \omega_0=0.110, \omega_1=1.297, \omega_2=3.653$	Not analysed
M7 (beta)	2	-1705.451	$p=0.149, q=0.151$	Not allowed
M8 (beta and omega)	4	-1682.785	$p_0=0.792, p_1=0.208, p=0.211, q=0.300, \omega=3.231$	11, 24, 31, 52, 53, 62, 65, 66, 68, 72, 76

Alignment of 22 sequences from three vole species was used as input for the program CodeML (included in the PAML 3.14 program suite). Positively selected sites were identified in models M2a and M8 by the Bayes empirical Bayes procedure (Yang et al. 2005). Sites inferred under selection at the 99% level are listed in bold, and those at the 95% level are in italic
P Number of parameters in the ω distribution, ω selection parameter, p_n proportion of sites that fall into the ω_n site class, p, q shape parameters of the β function (for models M7 and M8)

Détection des sites sous sélection positive (approche Bayésienne, PAML)

* probabilité postérieure pour w à chaque site (modèle M8)

197

$\omega > 1$ =
sélection
positive

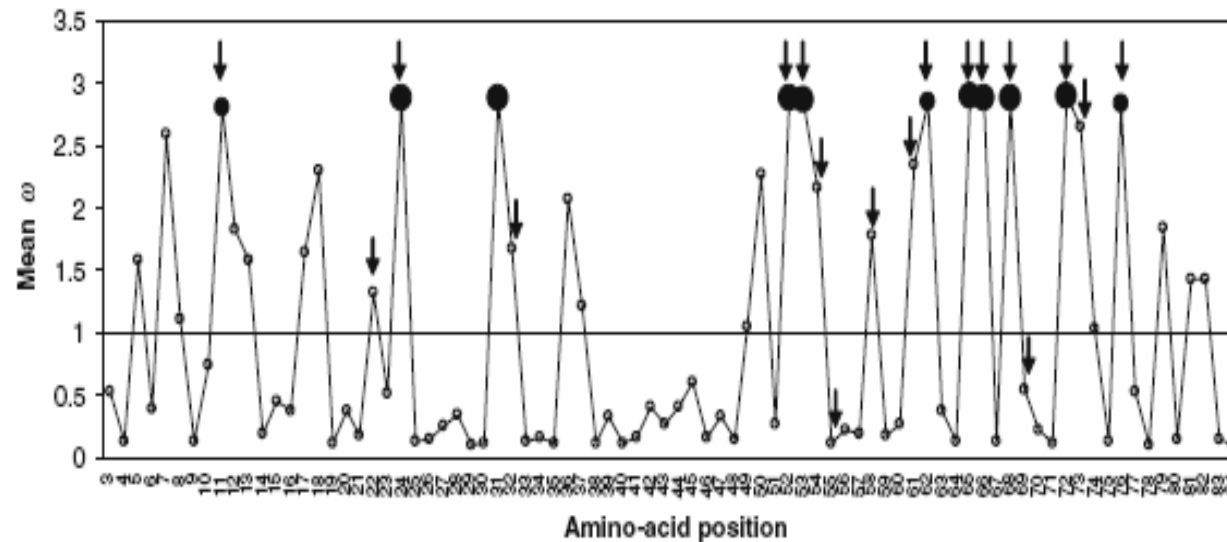


Fig. 2 Posterior means of ω , calculated as the average of ω over the 11 site classes, weighted by the posterior probabilities under the random-sites model M8 (β and ω). The posterior probabilities were computed by the Bayes empirical Bayes procedure in the program CodeML implemented in the PAML3.14 package. The amino acid numbering is according to Brown et al. (1993). Arrows indicate the ABS positions identified on the basis of the crystal structure of the I-A proteins (details in the text). Sites inferred to be under positive selection at the 99% level are indicated by *large black circles* and those at the 95% level by the *medium black circles*

Une alternative = effet de la recombinaison entre allèle

* ne peut être rejetée mais probabilités faibles

Table 5 Estimates of the amount of population mutation (Waterson's $\theta=4N\mu$) and population recombination rate ($\rho=4Nr$) obtained using the programme LDhat (McVean et al. 2002)

Species	n	θ	ρ	$p(\rho)$	r^2	$p(r^2)$
<i>A. terrestris</i>	55	23	3	0.019	-0.078	0.015
<i>C. glareolus</i>	61	25	35	0.071	-0.021	0.166
<i>M. arvalis</i>	68	26	99	0.017	-0.037	0.056
All three species	88	24	88	0.001	-0.034	0.029

Significance values of ρ and r^2 are based on 1,000 permutations and values of $p < 0.05$ are in bold
 n Number of segregating sites, r^2 correlation of pairwise linkage disequilibrium with nucleotide distance

McVean G, Awadalla P, Fearnhead P (2002) A coalescent-based method for detecting and estimating recombination from gene sequences. *Genetics* 160:1231-1241

Mêmes résultats pour un autre gène MHC classe II : DRB (exon 2)

```

          * * * *   **           *           * * * *   * * * *   * *
Arte-DRB*06  QRVRFLVRDIYNRBEVVRPDSVGEFRAVTELGPRDAEYFNSLKDFLEQKRAEVDY
Arte-DRB*07  .....Y.....F.....H.....GI..N...R.EL..RT..A...V
Arte-DRB*08  ...Y...F...Y...E...Y.....RS...W..Q..V..R...I..V
Arte-DRB*09  .....D.YFF...Y.....GI..NL..Q..I..RL.....V
Arte-DRB*10  .....D.Y.H.Q..F.....H.....GI...W..Q..I..R...A...
Arte-DRB*11  ...Y...V.H...Y.....Y.....GI...L.....M.....A...
Arte-DRB*12  .....D.Y.H.Q..FM.....H.....GI...W..Q..I..R...A...
Arte-DRB*13  ...L.D.YFF.Q..YL.....Y.....M.DR..A...
Arte-DRB*14  ...Y.....L.....Y.....W...A..R..A...V
Arte-DRB*15  ...L.D.V.....Y.....RS...R.....I..L..S...
Arte-DRB*16  .....E.YF...Y.....Y.E...GI..NL..R.EL.....I...
Arte-DRB*17  ...Y.....L.....Y.....GI...W...A..R...A...V
Arte-DRB*18  .....D.YFF...Y.....Y.....RS...W..Q..EL..NR.....V
Arte-DRB*19  ...L.....I..F
Arte-DRB*20  .....D.Y.H.Q..F.....H.....GI...W..Q..EL..R...A...
Arte-DRB*21  ...L.D.YFF.Q..Y.....Y.....M.DR..A...
    
```

Fig.2 Alignment of 16 expressed amino-acid sequences (corresponding to amino-acid residues 22–78 from Brown *et al.* 1993) of the partial DRB exon 2 from water voles. Dots indicate identity with the nucleotide sequence of Arte-DRB*06. Asterisks identify sites in the putative peptide-binding region of the human DRB molecule (according to Brown *et al.* 1993).



Gène MHC classe II : DRB (exon 2)

Table 1 Results of maximum-likelihood models for exon 2 of the DRB gene in water voles

Model code	P	Likelihood	Parameter estimates	Positively selected sites
M0 (one ratio)	1	-858,410	$w = 1,782$	None
M1a (nearly neutral)	1	-800,013	$p0 = 0,598$ ($p1 = 0,402$)	Not allowed
M2a (positive selection)	3	-782,798	$p0 = 0,524$, $p1 = 0,123$ $(p2 = 0,353)$, $w2 = 8,274$	26, 28, 32, 37, 47, 56, 57, 61, 64, 67, 70, 71, 74, 75, 78
M3 (discrete)	5	-767,079	$p0 = 0,605$, $p1 = 0,360$ $(p2 = 0,035)$, $w0 = 0,092$, $w1 = 9,651$, $w2 = 18,297$	Not analysed
M7 (beta)	2	-900,186	$p = 0,016$, $q = 0,021$	Not allowed
M8 (beta and omega)	4	-782,741	$p0 = 0,642$ ($p1 = 0,358$), $p = 0,005$, $q = 0,020$, $w = 8,934$	26, 28, 30, 31, 32, 34, 37, 47, 56, 57, 60, 61, 64, 67, 68, 70, 71, 74, 75, 78

An alignment of 16 DRB sequences (171 bp) from water vole was used as the input for CodeML (included in the PAM3.14 program suite). P is the number of parameters in the ω distribution, ω is the selection parameter and P_n is the proportion of sites falling into the ω_n site class. For models M7 and M8, p and q are the shape parameters of the β function.

Positively selected sites were identified in models M2a and M8 by the Bayes empirical Bayes procedure (Yang *et al.* 2005). Sites inferred under selection at the 99% level are listed in bold, and those inferred at the 95% level are shown in italics.

Mise en évidence de la sélection aux gènes du MHC



Mise en évidence de la sélection aux gènes du MHC

Pour en savoir plus

Immunogenetics (2006) 58: 191–202
DOI 10.1007/s00251-006-0085-6

ORIGINAL PAPER

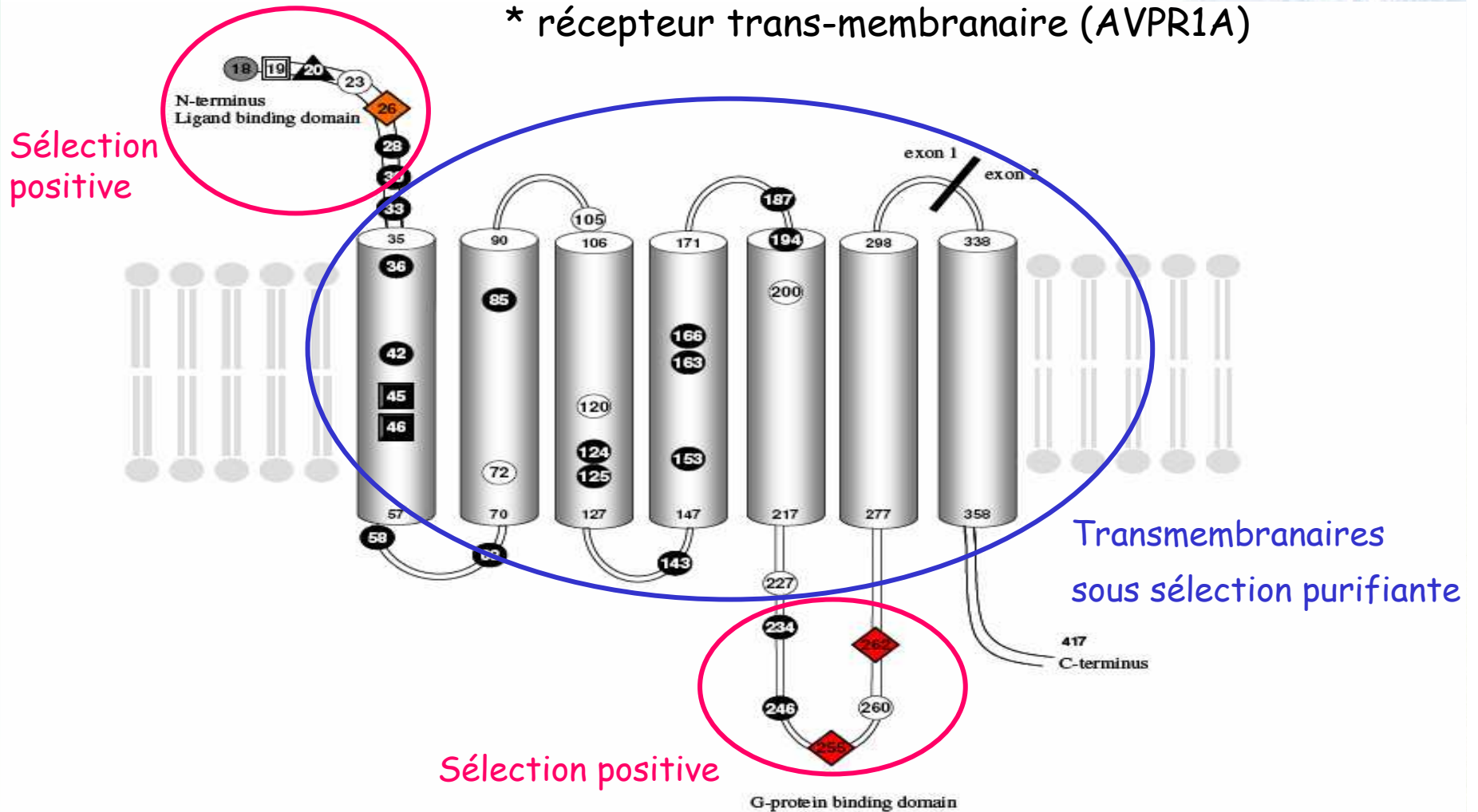
J. Bryja · M. Galan · N. Charbonnel · J. F. Cosson

Duplication, balancing selection and trans-species evolution explain the high levels of polymorphism of the *DQA* MHC class II gene in voles (*Arvicolinae*)

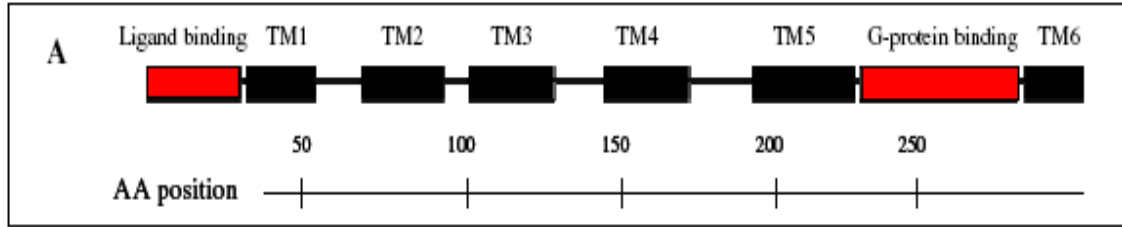


Mix de sélection positive et purifiante sur un même gène:

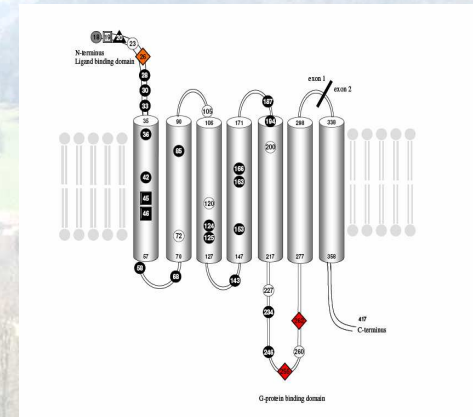
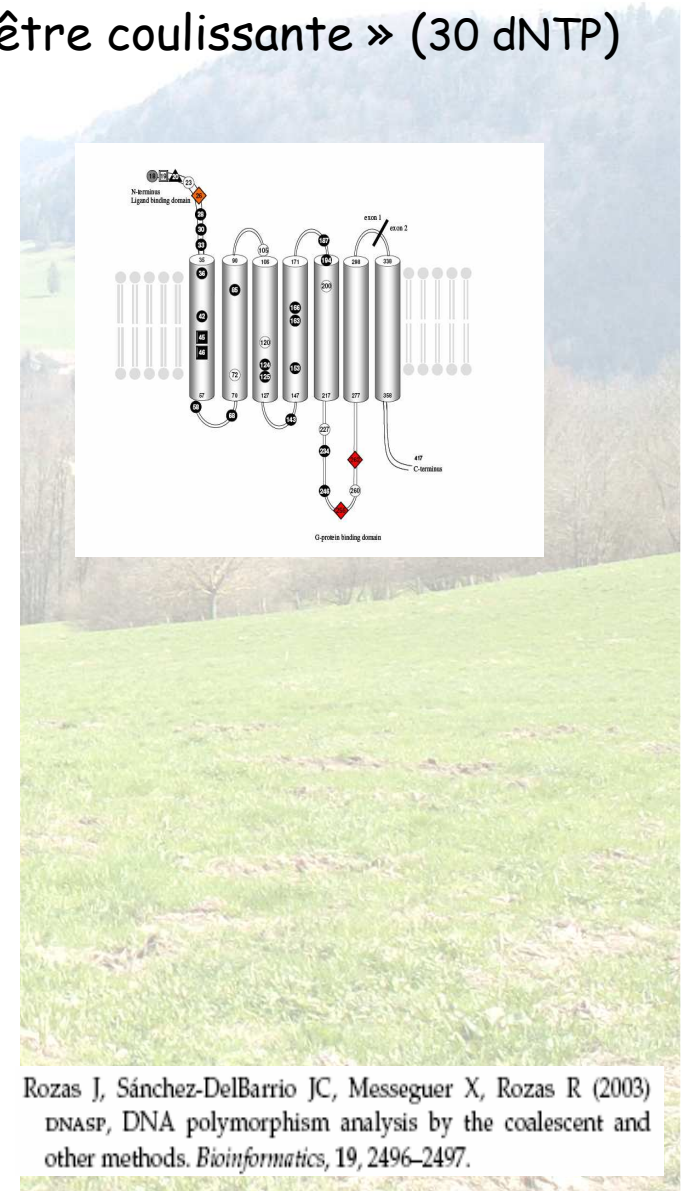
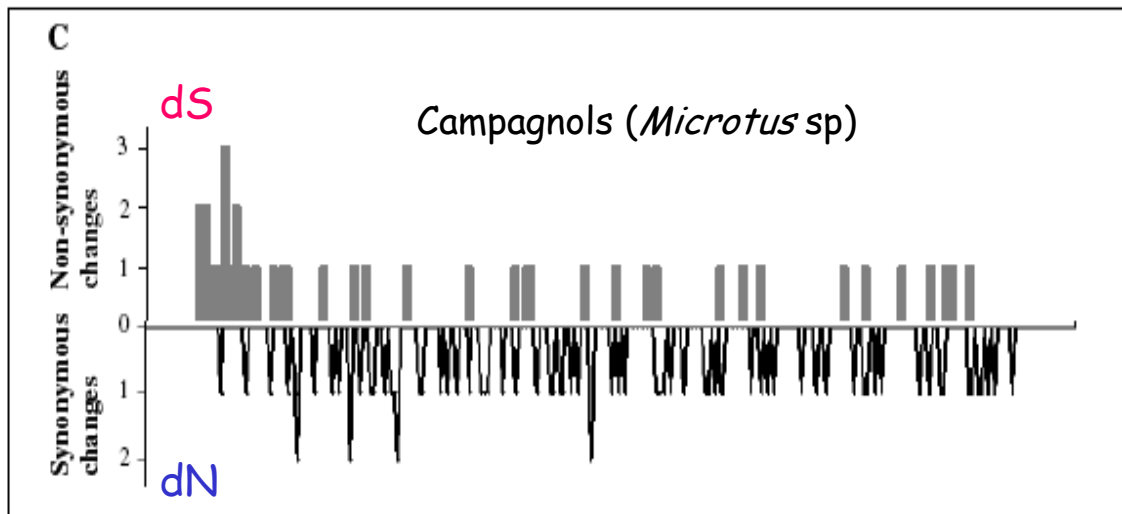
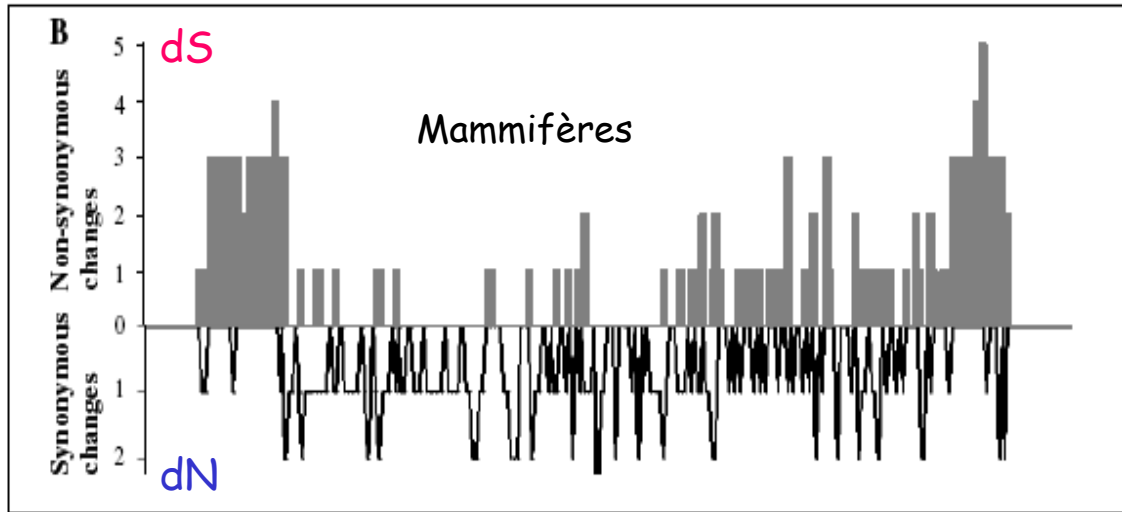
* récepteur trans-membranaire (AVPR1A)



Mise en évidence de la sélection aux gènes du MHC

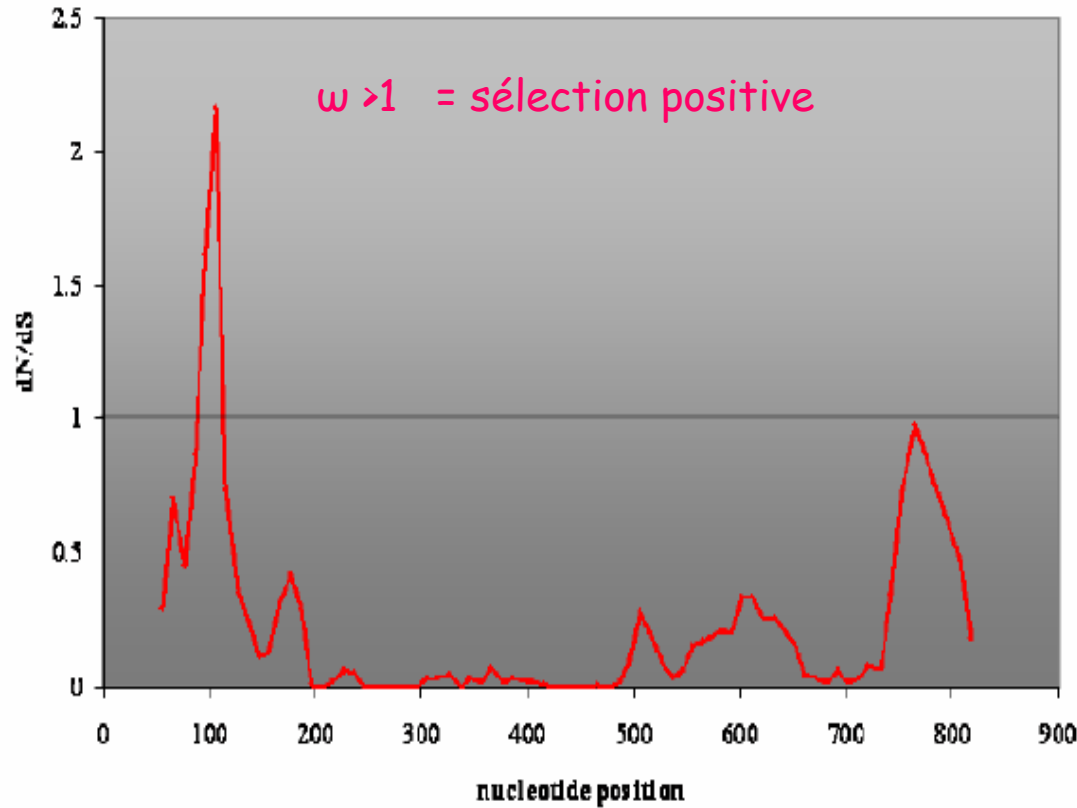
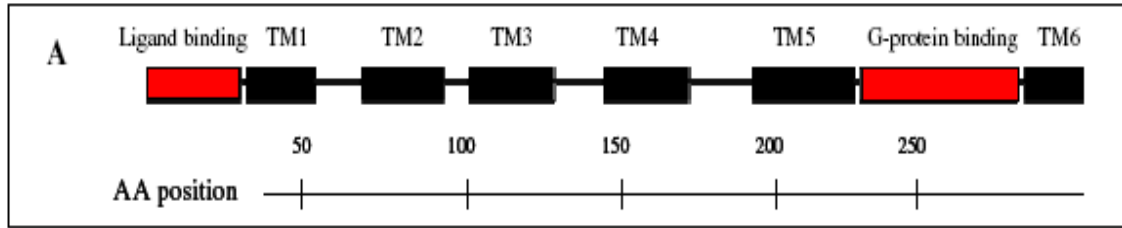


Analyse sur « fenêtre coulissante » (30 dNTP)



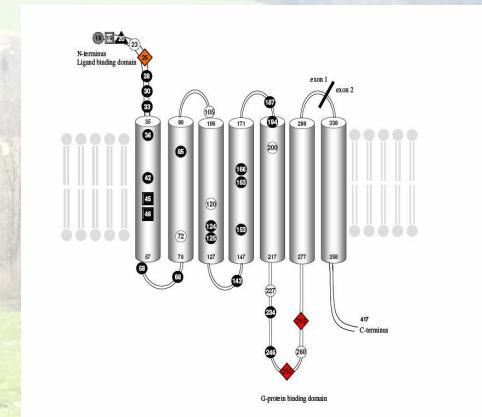
Rozas J, Sánchez-DelBarrio JC, Messeguer X, Rozas R (2003) DNASP, DNA polymorphism analysis by the coalescent and other methods. *Bioinformatics*, 19, 2496-2497.

Mise en évidence de la sélection aux gènes du MHC



$\omega < 1$ = sélection purifiante

Détection des sites sous sélection positive / négative (approche Bayésienne, PALM)



Yang Z: PAML: a program package for phylogenetic analysis by maximum likelihood. CABIOS 1997, 13:555-556.

Mise en évidence de la sélection aux gènes du MHC

Pour en savoir plus

BMC Evolutionary Biology

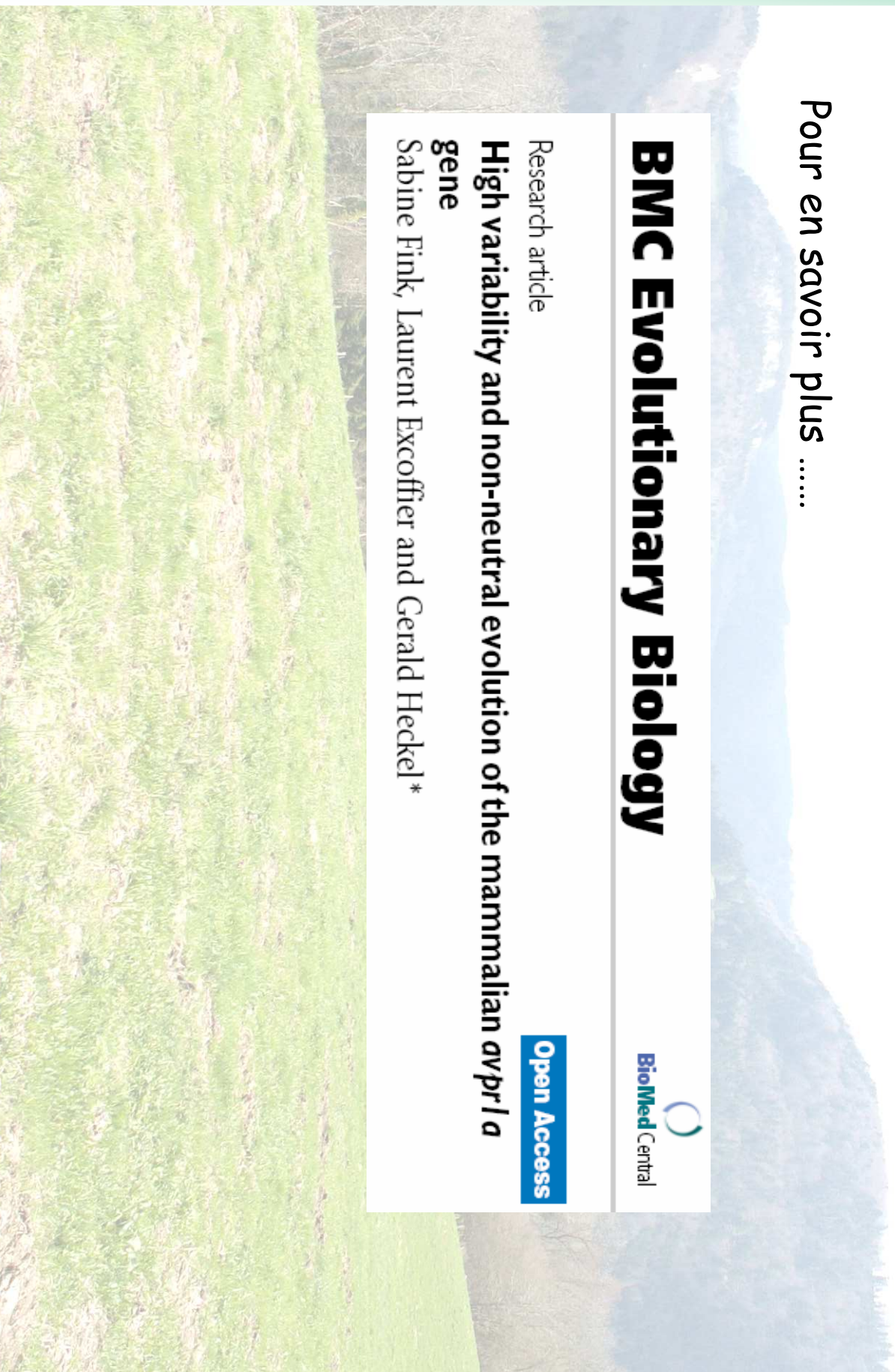


Research article

High variability and non-neutral evolution of the mammalian *avpr1a* gene

Sabine Fink, Laurent Excoffier and Gerald Heckel *

Open Access



Sélection contemporaine:

- * signature par l'analyse de génétique des populations
- * approche comparative locus neutres / sélectionné
- * locus neutre = référence neutre

- * diversité : sélectionné vs. neutre
 - déficit en allèles rares = freq. dépendance
- * structuration spatiale
 - sélectionné > neutre = adaptation locale
 - sélectionné < neutre = sélection balancée

Système biologique:

- * fluctuation démographiques du campagnol terrestre
- * variation densité => cortège parasitaire
- * parasites = régulation démographie

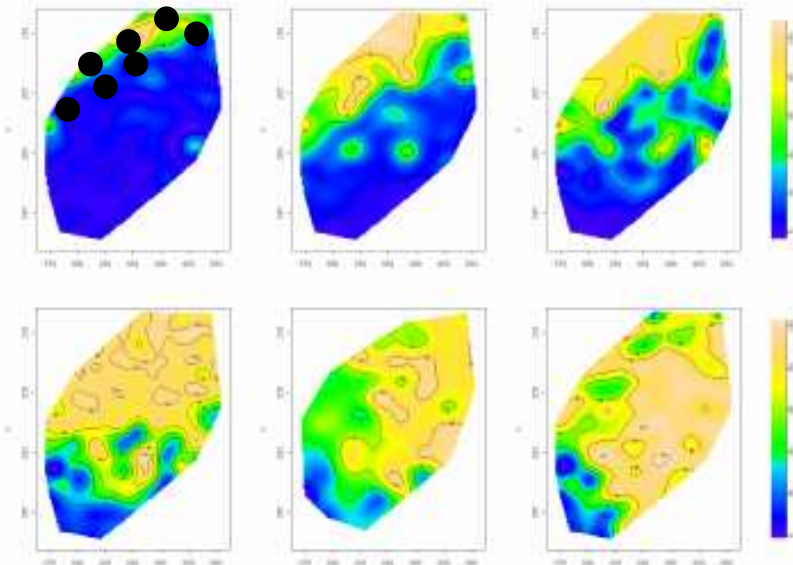
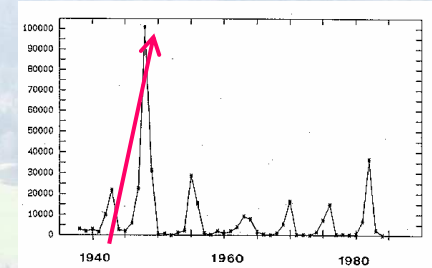


Figure 5. Dynamique d'invasion du campagnol terrestre entre Avril 2002 et Octobre 2004 (de gauche à droite, puis de haut en bas) sur le canton de Nozeroy (10x15 kms). Les zones en jaunes sont en forte densité, en bleu faible densité.

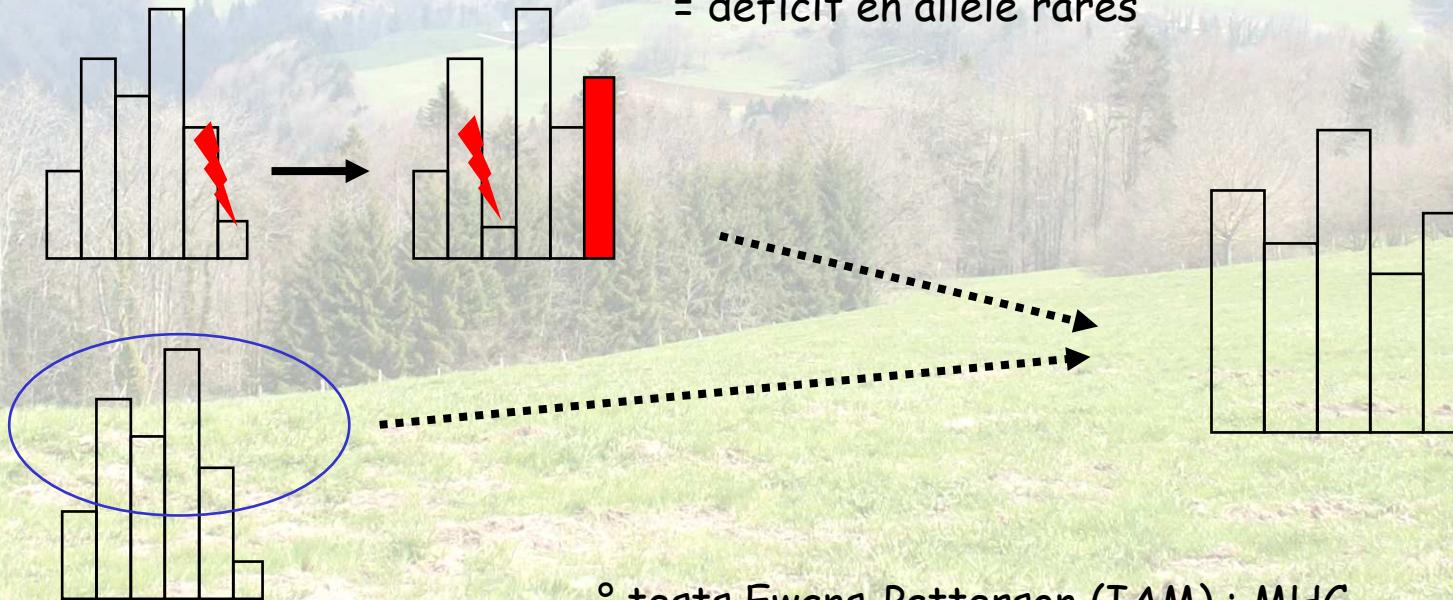
Sept populations échantillonnées pendant trois ans au cours de la phase d'expansion démographique

Diversité : sélectionné vs. neutre

° déficit en allèles rares = freq. dépendance

* facteur confondant

° bottleneck : même signature que sélection balancée
= déficit en allèle rares



- ° tests Ewans-Patterson (IAM) : MHC
- ° tests Bottleneck (IAM) : MHC
- ° tests Bottleneck (GSM) : microsats

Mise en évidence de la sélection aux gènes du MHC

Table 2. Estimates of F_S and the probabilities associated with rejection of the mutation-drift equilibrium hypothesis (Wilcoxon test) in bottleneck for DQA1, DRB, and 14 microsatellite loci (14MS). F_S estimates significantly different from zero (1000 permutations) are shown in bold. Probability values for the Wilcoxon test — $P < 0.05$ (in bold) — for DQA1, DRB, and 14 microsatellites suggest excess heterozygosity due to a demographic bottleneck or balancing selection

Year	Population	N	F_S			Mutation-drift equilibrium			14MS	Significant microsatellite loci
			DQA1	DRB	MS	DQA1	DRB			
2001	01	27	-0.033	-0.012	0.011	0.129	0.033	0.548	AV3 ($P = 0.042$); AVM12 ($P = 0.011$)	
	02	28	-0.013	-0.070	0.034	0.271	0.000	0.714	AT19 ($P = 0.005$)	
	03	22	-0.008	0.295	0.057	0.024	0.019	0.042	AT9 ($P = 0.021$); AV11 ($P = 0.017$); AVM9 ($P = 0.046$)	
	04	15	-0.268	-0.022	-0.059	0.353	0.144	0.024	AT2 ($P = 0.019$); AT3 ($P = 0.020$); AT9 ($P = 0.048$); AT19 ($P = 0.020$); AT9 ($P = 0.048$);	
	05	27	-0.068	0.250	-0.010	0.020	0.265	0.749	AT2 ($P = 0.019$); AT3 ($P = 0.020$); AT9 ($P = 0.048$); AT19 ($P = 0.020$); AT9 ($P = 0.048$);	
	06	33	-0.023	0.104	-0.009	0.103	0.427	0.583	AVM8 ($P = 0.001$); AT2 ($P = 0.016$)	
	07	35	0.024	0.231	0.044	0.048	0.418	0.541	AT19 ($P = 0.039$); AV10 ($P = 0.041$)	
	01	28	-0.022	0.172	0.067	0.015	0.003	0.295	AV15 ($P = 0.013$)	
	02	26	0.133	0.161	-0.001	0.002	0.291	0.670	AV3 ($P = 0.010$); AT13 ($P = 0.020$); AT9 ($P = 0.048$);	
03	27	0.149	0.063	0.000	0.066	0.185	0.685	AT9 ($P = 0.048$);		
2002	04	22	-0.109	0.062	0.016	0.101	0.190	0.903	AT19 ($P = 0.041$); AT25 ($P = 0.048$); AVM10 ($P = 0.018$); AVM8 ($P = 0.009$)	
	05	23	0.119	0.303	0.007	0.077	0.027	0.173	AT19 ($P = 0.041$); AT25 ($P = 0.048$); AVM10 ($P = 0.018$); AVM8 ($P = 0.009$)	
	06	27	0.085	0.248	-0.018	0.001	0.465	0.042	AT13 ($P = 0.022$)	
	07	30	0.121	0.277	0.007	0.023	0.279	0.626	AV11 ($P = 0.036$)	
	01	34	0.061	0.132	0.017	0.006	0.063	0.626	AT15 ($P = 0.030$)	
2003	02	30	-0.065	0.161	-0.004	0.079	0.116	0.267	AV15 ($P = 0.046$)	
	03	37	-0.077	-0.106	0.049	0.010	0.347	0.808	AV11 ($P = 0.046$); AVM9 ($P = 0.035$)	
	04	28	-0.156	0.040	0.019	0.011	0.247	0.626	AV11 ($P = 0.046$); AVM9 ($P = 0.035$)	
	05	30	-0.146	-0.011	0.006	0.020	0.000	0.217	AV11 ($P = 0.046$); AVM9 ($P = 0.035$)	
	06	25	0.212	0.049	0.008	0.004	0.090	0.058	AV3 ($P = 0.040$)	
	07	27	0.176	0.021	0.009	0.001	0.456	1.000	AT25 ($P = 0.029$); AVM9 ($P = 0.001$)	

Déficit en allèles rares

* facteur confondant

° bottleneck vs sélection balancée ?

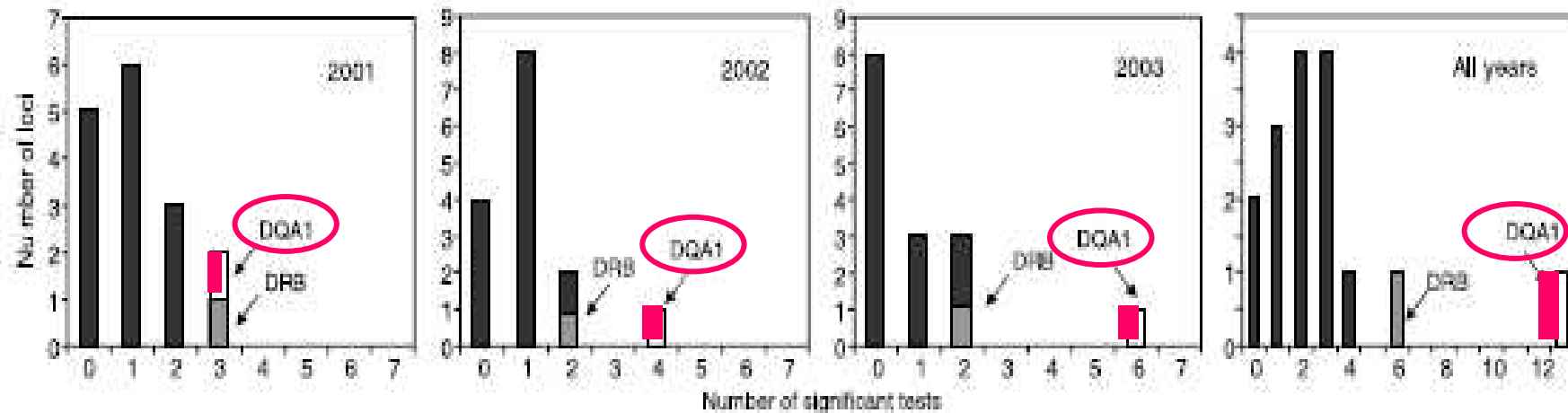


Fig. 3 Number of statistical tests at individual loci indicating departure from the mutation-drift equilibrium (excess heterozygosity, $P < 0.05$) in different years and for all years together.

° tests Bottleneck (IAM) : MHC

° tests Bottleneck (GSM) : microsats

Structuration spatiale :

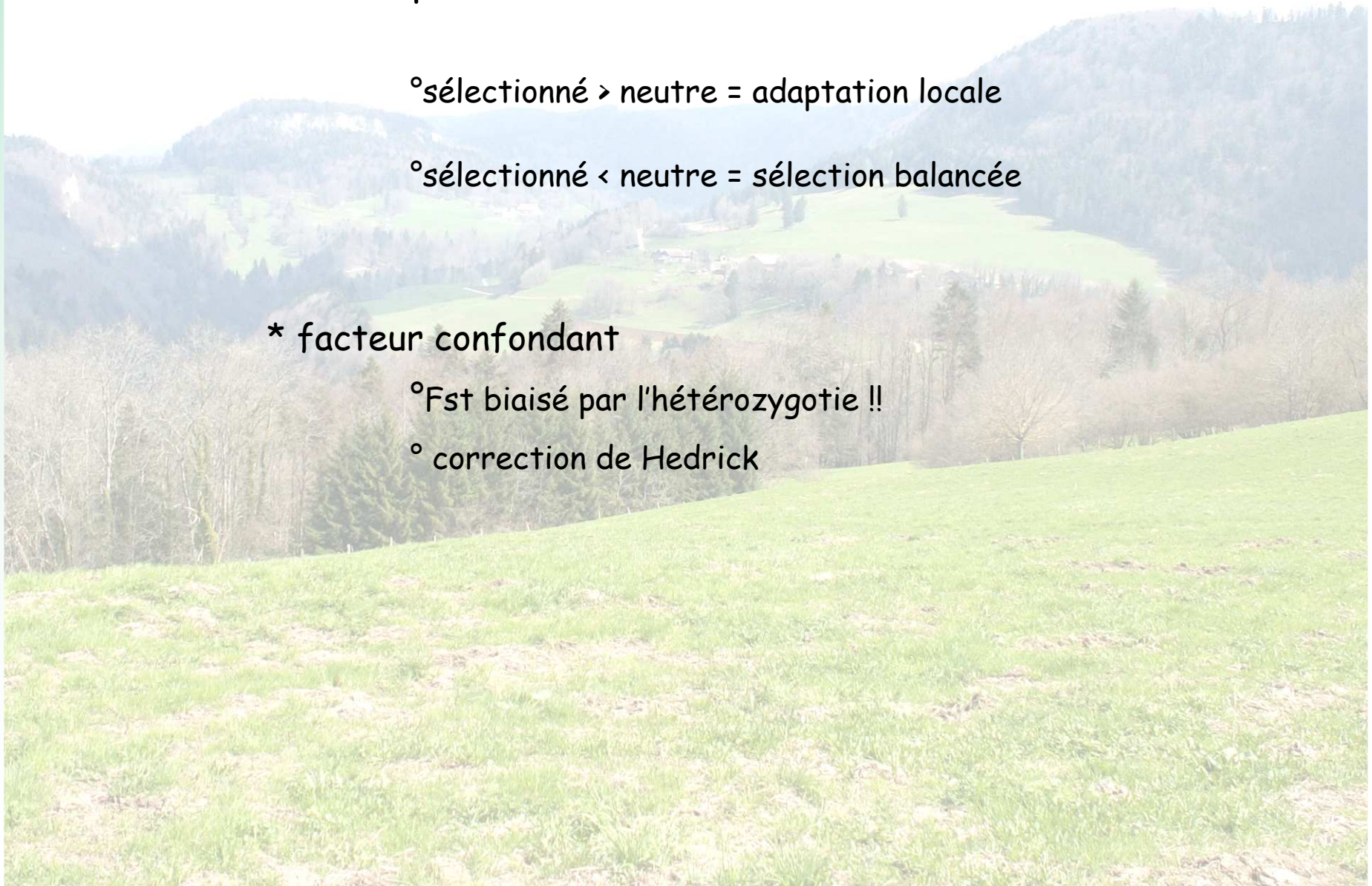
° sélectionné > neutre = adaptation locale

° sélectionné < neutre = sélection balancée

* facteur confondant

° F_{st} biaisé par l'hétérozygotie !!

° correction de Hedrick



Mise en évidence de la sélection aux gènes du MHC

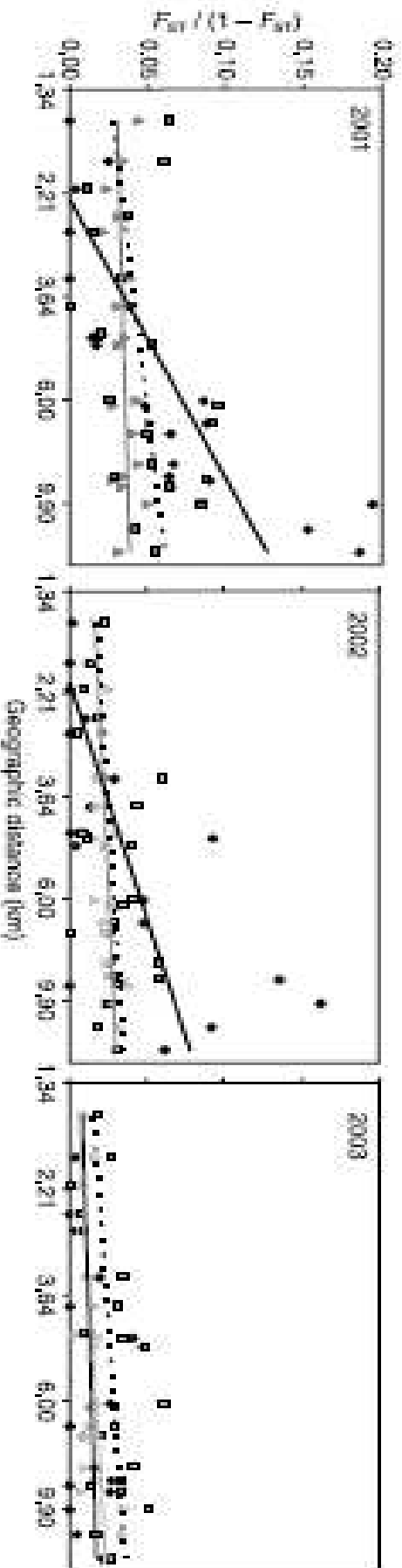
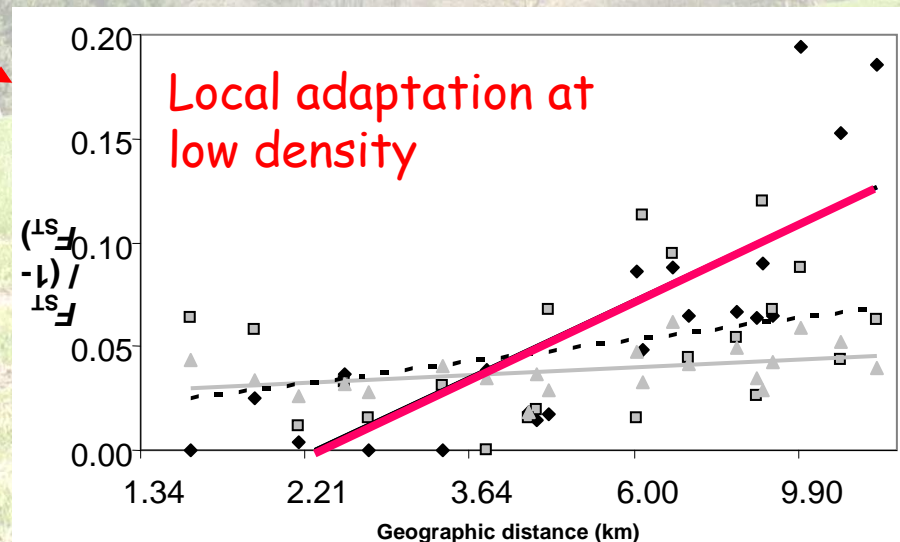
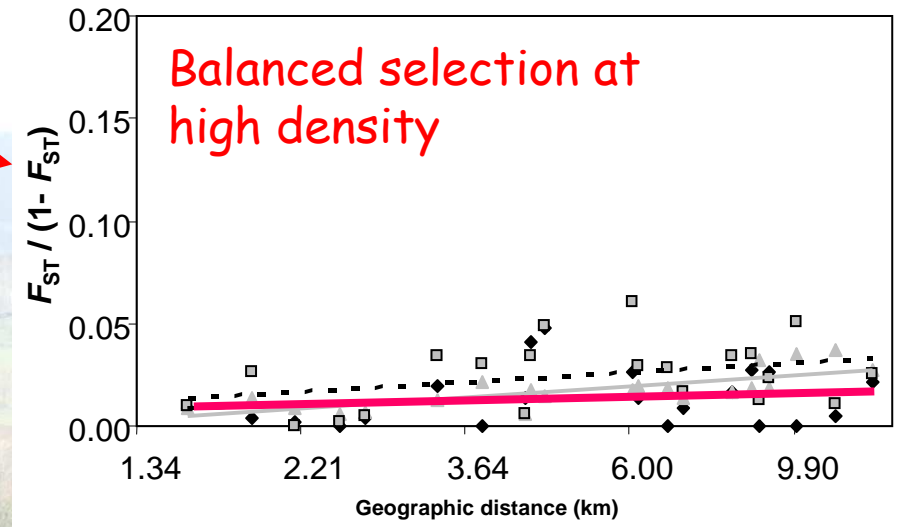
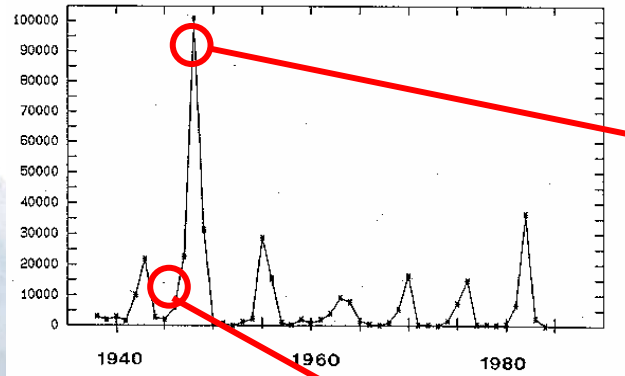


Fig. 4 Correlation between genetic $F_{ST}/(1 - F_{ST})$ and geographical distance (log scale) for three samplings of MHC and neutral markers: DQA1 (diamond and solid black line), DRB (square and dashed black line), 14 microsatellites (triangle and solid grey line).

Table 3 Overall F_{ST} estimates and isolation by distance characteristics — probability (IBD P), correlation coefficient (R), intercept and slope — calculated for each marker type in 3 years. 95% confidence intervals (CI) for overall F_{ST} and the slope of the IBD were obtained by bootstrapping over 14 microsatellite (14MS) loci

Date	Genes	Overall F_{ST} (95% CI)	IBD P	R	Intercept	Slope [95% CI]
October 2001	14MS	0.034 [0.029; 0.039]	0.1039	0.274	0.004	0.0031 [-0.0024; 0.0114]
	DQA1	0.064	0.0022	0.807	-0.597	0.0768
	DRB	0.045	0.0458	0.378	-0.132	0.0212
October 2002	14MS	0.024 [0.017; 0.030]	0.0011	0.617	-0.031	0.0065 [0.0032; 0.0104]
	DQA1	0.036	0.0086	0.593	-0.246	0.0449
	DRB	0.027	0.0536	0.355	-0.080	0.0125
October 2003	14MS	0.015 [0.011; 0.020]	0.0221	0.564	-0.054	0.0062 [0.0045; 0.0130]
	DQA1	0.009	0.2270	0.123	-0.016	0.0032
	DRB	0.023	0.0918	0.378	-0.065	0.0104

Effets de la sélection : modèle d'isolement pas la distance



Effets de la sélection : modèle de coalescence (deux à deux)

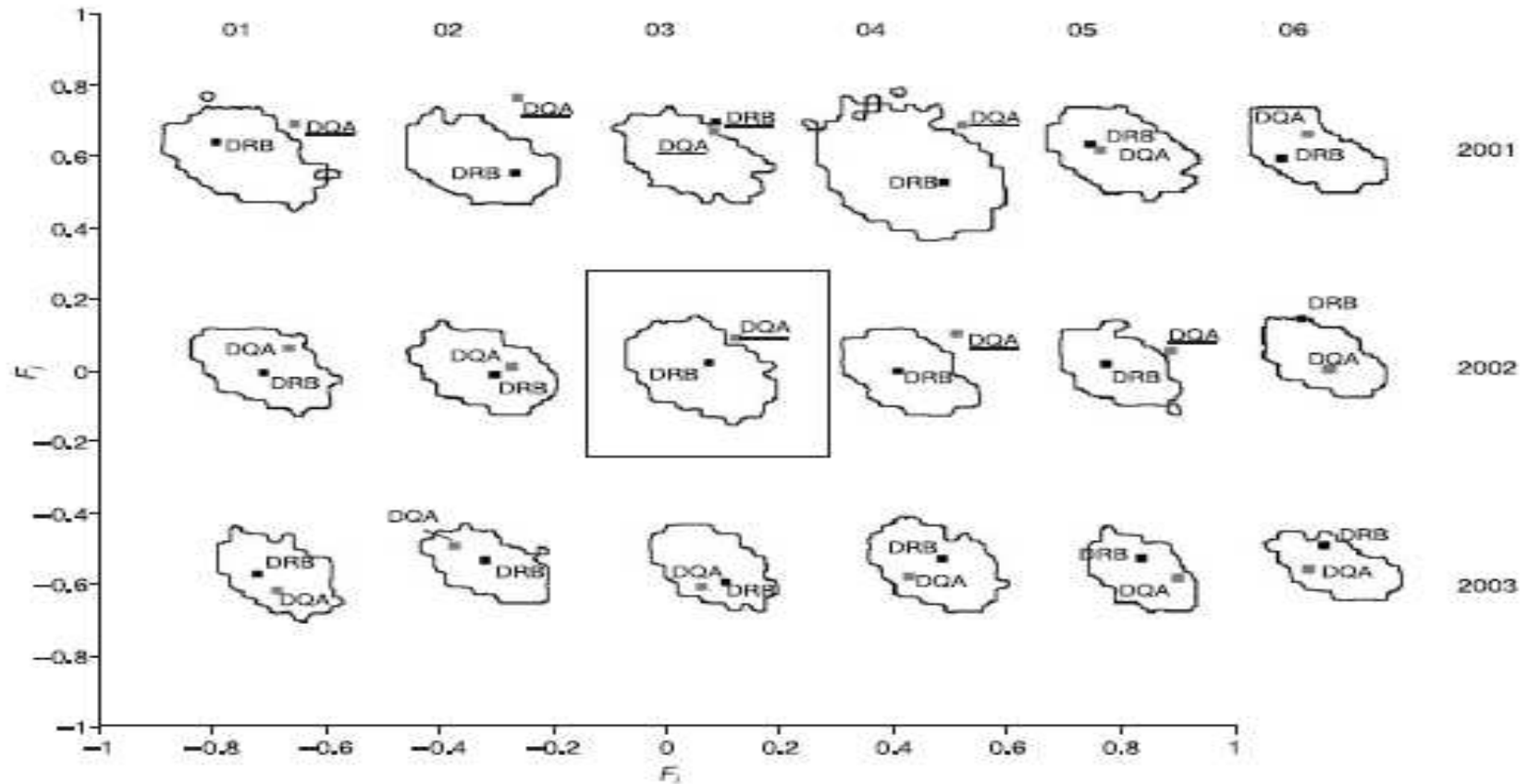


Fig. 5 Expected distribution of pairs of F_1 and F_2 values estimated from 14 microsatellites and two MHC loci for pairwise comparisons of population 07 with all other populations (01–06) in the years 2001, 2002, and 2003. Axes correspond to the comparison of populations 03 and 07 in 2002 (in the frame) but all the other graphs are on the same scale. Solid lines enclose a region in which 95% of the simulated data points (10 000 permutations in DERSSEL) are expected to lie. Only the positions of the DQA1 and DRB loci are shown. Significant outliers are underlined.

Vitalis R, Dawson K, Boursot P, Belkhir K (2002) DERSSEL 1.0: a computer program to detect markers responding to selection. *Journal of Heredity*, 94, 429–431.

Effets de la sélection : modèle de coalescence (global)

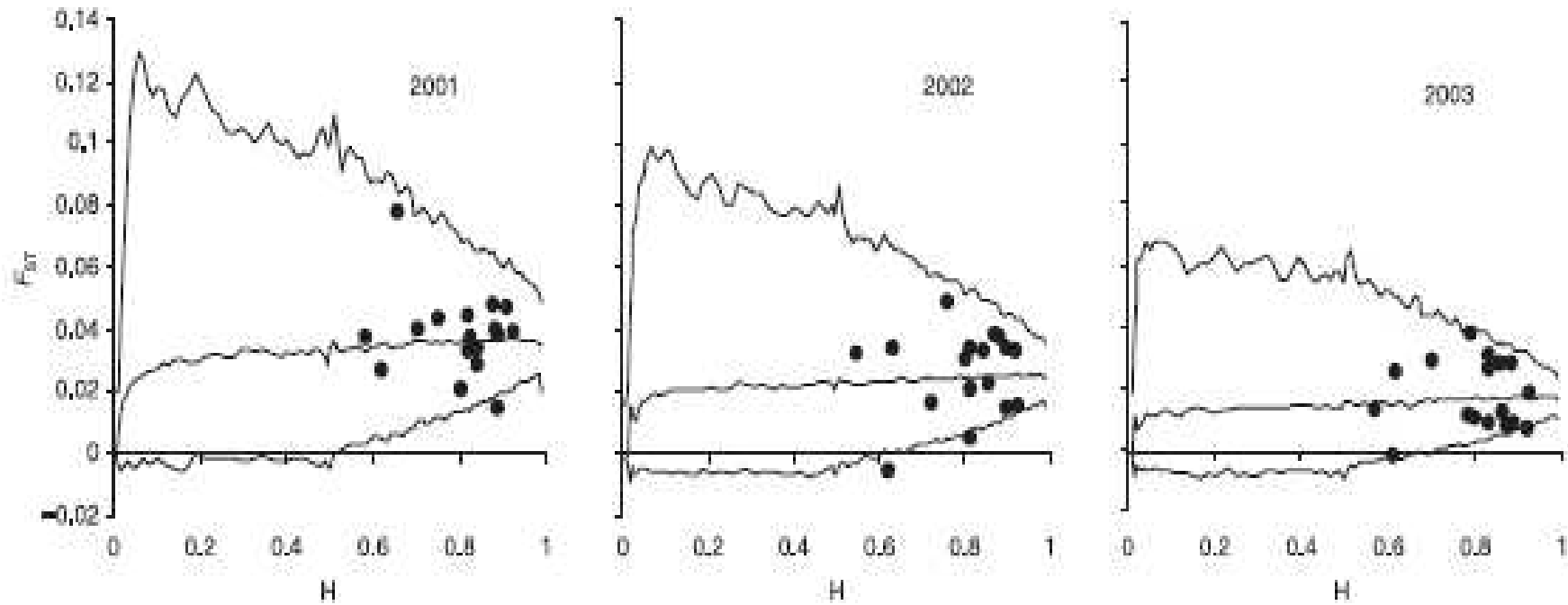


Fig. 1 F_{ST} values estimated from 17 microsatellites (black circles) plotted against heterozygosity. Lines denote the 0.975, 0.500 and 0.025 quantiles of the distribution of F_{ST} against heterozygosity estimated from 50 000 simulations in FDIST2.



Beaumont MA, Nichols RA (1996) Evaluating loci for use in the genetic analysis of population structure. *Proceedings of the Royal Society B: Biological Sciences*, 263, 1619-1626.

Pour en savoir plus

Molecular Ecology (2007) 16, 5084–5097

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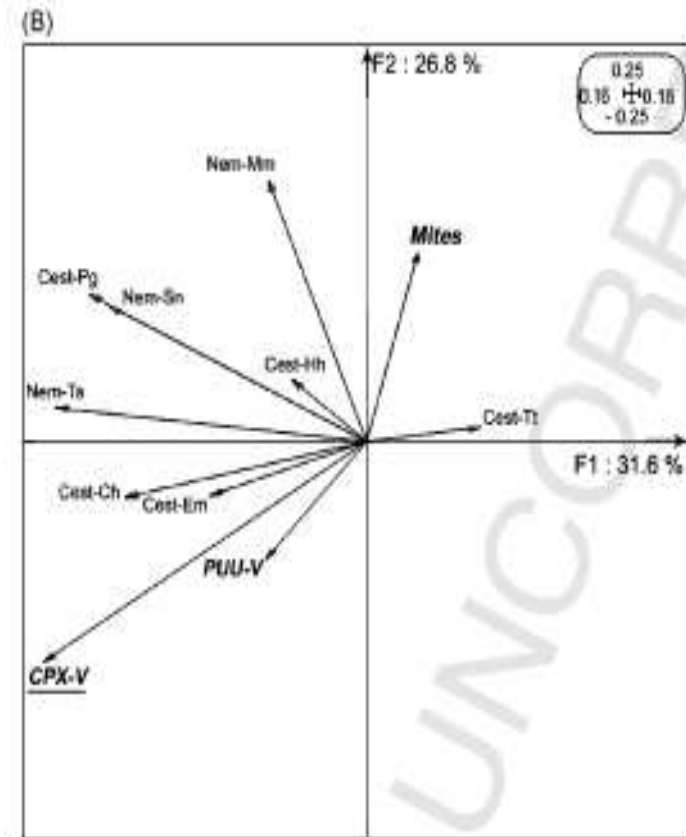
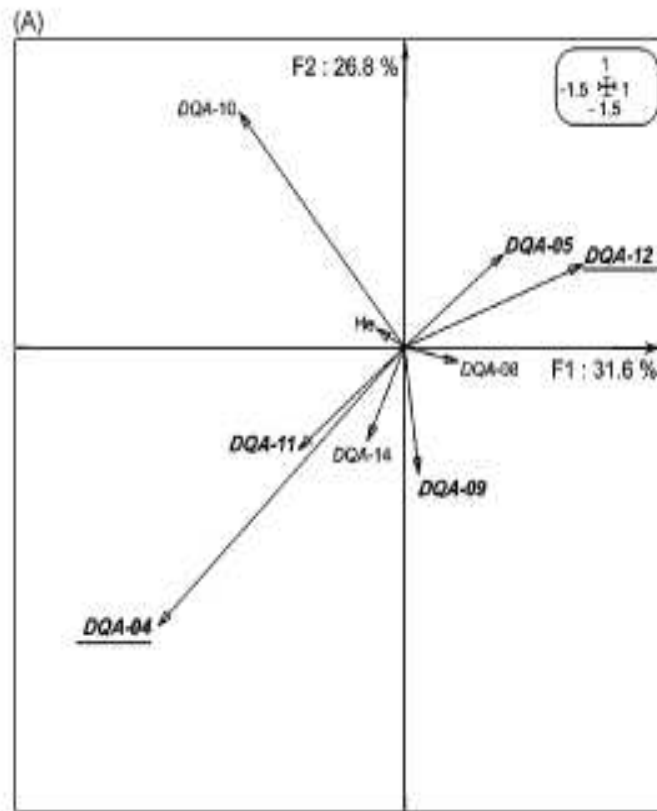
Density-related changes in selection pattern for major histocompatibility complex genes in fluctuating populations of voles

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Mise en évidence de la pression sélective

Approche corrélative: analyses de co-intertie



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Thioulouse, J., Simier, M., Chessel, D., 2004. Simultaneous analysis of a sequence of paired ecological tables. *Ecology* 85, 272–283.

Mise en évidence de la sélection aux gènes du MHC

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Association between the DQA MHC class II gene and Puumala virus infection in *Myodes glareolus*, the bank vole

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Antti Vaheri^d, Alexis Ribas Salvador^e, Serge Morand^f,
Jean-François Cosson^a, Nathalie Charbonnel^a