

Range expansion of the Bluetongue vector, *Culicoides imicola*, in continental France likely due to rare wind-transport events

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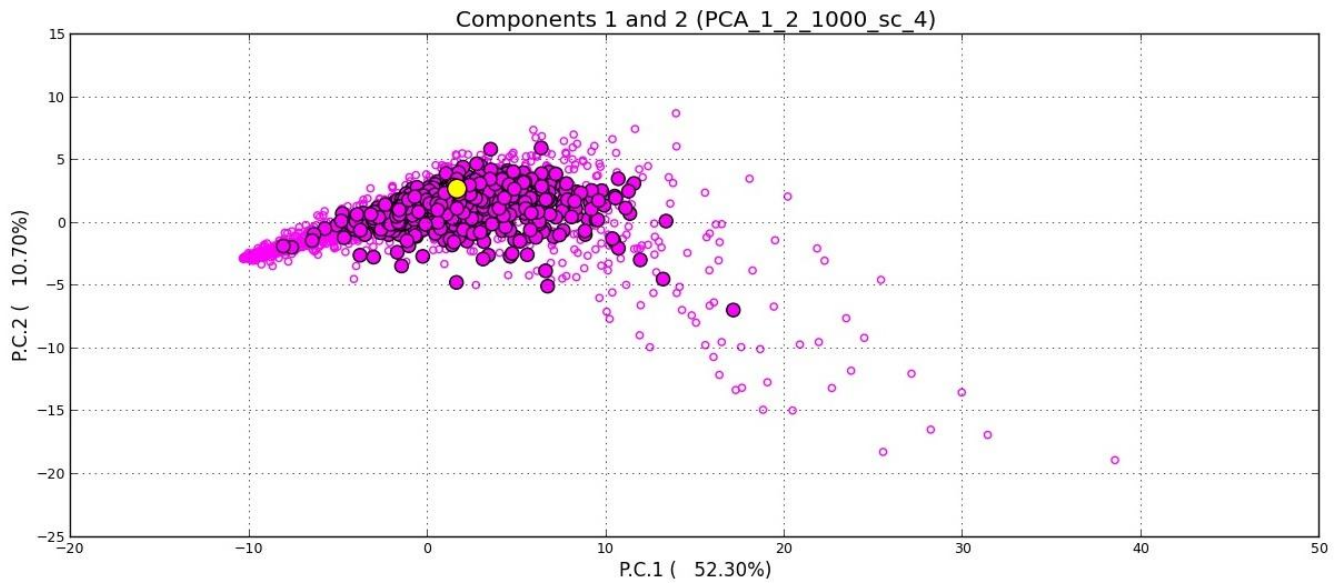
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Supplementary Information



Supplementary Figure 1 | Principal component analysis (PCA) in the space of summary statistics performed under the most probable scenario (Scenario 4). The observations are the simulated datasets and the variables are the summary statistics. Small pink circles correspond to simulated statistics with parameters drawn from the prior distributions, the large pink dots correspond to the simulated datasets drawn from the posteriors distributions and the yellow dot represents the real *C. imicola* data set.

Supplementary Video clip 1 | NAME simulations of individual trajectories. Full 36-hour back-trajectories for all particles together are presented for each day during the full observation period. Maps were generated using ArcGIS software v10.2.2 (ESRI, Redlands, CA).

22	Vilanova Muga	52	6,486	27/03/2008	1	13	52	7,887	-	0	-															
France																										
9	St Jean Pla de Corts	20	144	07/10/2008	3	20																				
2	Vebre						25	8,972	-	0	-	26	23,788	0	25	2,305	0	27	1,155	0						
1	Clermont						23	740	-	0	-	26	446	0	26	5,306	0	27	3,069	0						
5	Argeles Sur Mer						23	3,080	-	0	-															
4	Argeles Sur Mer											25	92	0	24	81	0	21	62	0						
3	Toreilles	21	229	-	0	-																				
Sentinel sites																										
France																										
6	Vives						1	7	19/10/2009	0	7															
10	Ceret						1	16	19/10/2009	0	16															
18	Reynes						1	1	19/10/2009	0	1	1	408	11/10/2010	0	408	1	105	18/10/2011	0	105	1	466	25/09/2012	8	466
15	Ceret											1	186	11/10/2010	0	186	1	194	18/10/2011	0	194	1	2	26/09/2012	3	2
17	Amélie Les Bains						1	1	19/10/2009	0	1															
	Palalda																									
7	Taillet						1	1	19/10/2009	0	1															
21	Maureillas Las Illas											1	0	11/10/2010	0	0	1	109	18/10/2011	0	109	1	10	25/09/2012	11	10
20	Maureillas Las Illas											1	6	11/10/2010	0	6	1	0	18/10/2011	0	0	1	20	25/09/2012	0	20
14	Albere											1	6	11/10/2010	1	6	1	3	18/10/2011	0	3	1	1	26/09/2012	2	1

19	Cerbere			1	0	21/10/2009	0	0	1	5	14/10/2010	0	5	1	3	19/10/2011	0	3	1	9	24/09/2012	3	9
16	Banyuls			1	0	19/10/2009	0	0	1	2	14/10/2010	0	2	1	2	19/10/2011	0	2	1	0	24/09/2012	0	0
13	Montesquieu			1	0	20/10/2009	0	0	1	9	13/10/2010	0	9	1	0	18/10/2011	0	0	1	0	26/09/2012	0	0
	Des Alberes																						
11	Laroque								1	1	13/10/2010	0	1	1	37	17/10/2011	0	37	1	7	24/09/2012	0	7
	Des Alberes																						
12	Collioure								1	1	14/10/2010	0	1	1	14	19/10/2011	0	14	1	103	25/09/2012	1	103
8	Sorede								1	41	13/10/2010	0	41	1	1	19/10/2011	0	1	1	53	24/09/2012	0	53

For *C. imicola* collections, we reported only the data for the maximum abundance collection date. Nb = number. Locations and collection dates in bold are positive sites for *C. imicola* in the Pyrénées-Orientales department.

Supplementary Table 2 | COI and Cytb concatenated genetic diversity and haplotype composition within sample site.

Site	N	H	Hd ± SD	π ± SD	Haplotype composition																															
					H1	H2	H3	H4	H5	H6	H7	H8	H9	H10	H11	H12	H13	H14	H15	H16	H17	H18	H19	H20	H21	H22	H23	H24	H25	H26	H27	H28	H29	H30	H31	
Algeria	17	7	0.86 ± 0.05	0.0015 ± 0.0002	5	3	1	3	1	2	2																									
Morocco	14	11	0.95 ± 0.04	0.0020 ± 0.0002		1						3	1	1				2						1	1	1	1	1	1							
Portugal	15	7	0.81 ± 0.09	0.0013 ± 0.0003						2	7		1	2																		1	1	1		
Continental Spain	22	11	0.83 ± 0.07	0.0013 ± 0.0002		2					9		1	1	1	1	1	3	1	1	1															
Balearic Islands, Spain	8	3	0.67 ± 0.12	0.0007 ± 0.0001	4						3	1																								
Pyénées- Orientales, France	17	6	0.75 ± 0.09	0.0010 ± 0.0002	2	3				1	8									2		1														
Var, France	16	3	0.54 ± 0.09	0.0056 ± 0.0001		10					5													1												
Corsica, France	16	6	0.85 ± 0.02	0.0013 ± 0.0001	1	5		3			5										1	1														
Sardinia, Italy	8	3	0.68 ± 0.12	0.0007 ± 0.0002				3		1	4																									

For each site, the number of samples (N), the number of haplotypes (H), haplotype (Hd) and nucleotide (π) diversity and their standard deviations (SD) are indicated.

1 **Supplementary Table 3 | P-values inferred by the Wilcoxon test of bottleneck, F_{IS} values within samples and effective population sizes**

Country	Sites	code	IAM	TPM	SMM	F_{IS}
Algeria	Skikda	J	0.0185*	0.5000	0.9355	0.107
	Wilaya de Jijel	I	0.0136*	0.3671	0.8984	0.050
Morocco	Khemisset	H	0.4101	0.9179	0.9951	0.030
	Sidi Yahia El Gharb	G	0.5898	0.9179	0.9970	0.140
Portugal	Castelo Branco	B	0.1250	0.5898	0.9179	0.096
	Beja	A	0.0644	0.5898	0.8984	0.122
Balearic Islands, Spain	Majorca	F	0.1015	0.5898	0.9814	0.097
Continental Spain	Girona	E	0.0644	0.5898	0.1503	0.080
	Toledo	D	0.0097**	0.4101	0.8984	0.010
	Huelva	C	0.0019**	0.0644	0.5449	0.025
Continental France	Pyrénées-Orientales	M	0.0068**	0.1503	0.3671	-0.015
	Roquebrune-sur-Argens	K	0.0019**	0.0097**	0.3261	-0.038
	Bormes-les-Mimosas	L	0.0097**	0.1503	0.4550	0.024
Corsica, France	Figari	N	0.0097**	0.2480	0.8496	0.036
	Pietracorbara	O	0.0019**	0.0644	0.8750	0.112
Sardinia, Italy	San Giovanni Suergiu	P	0.0185*	0.2481	0.7871	0.052

2 For the bottleneck analysis, p-values correspond to the Wilcoxon unilateral test under each mutation model (Infinite Allele Mutation: IAM, Two-phase model: TPM and
3 Stepwise Mutation Model: SMM). Statistical significance is tested over 10000 replicates (**P < 0.01, *P < 0.05). P-values obtained for the Hardy-Weinberg test were adjusted
4 for multiple comparisons at the nominal level (5%) of 0.00037.

Supplementary Table 4 | Mitochondrial pairwise F_{ST} values between *C. imicola* populations.

	Algeria	Sardinia, Italy	Corsica, France	Pyrénées- Orientales, France	Var, France	Morocco	Portugal	Balearics Island, Spain
Sardinia, Italy	0.03188							
Corsica, France	0.04440	0.00444						
Pyrénées- Orientales, France	0.04421	0.19543	0.04354					
Var, France	0.15972	0.34694	0.10000	0.03702				
Morocco	0.07275	0.11014	0.04071	0.00905	0.03303			
Portugal	0.06163	0.07438	0.07590	0.02891	0.07054	0.02240		
Balearics Island, Spain	0.02336	0.28571	0.24953	0.19914	0.47986	0.12475	0.19556	
Continental Spain	0.12118	0.12695	0.07619	0.05231	0.05430	0.01229	0.03447	0.20952

Significant values are highlighted in bold.

Supplementary Table 5 | Approximate Bayesian computation (ABC) results.

Description of tested scenarios	Posterior probability	95% credibility interval	Type I error	Type II error
Independent introductions from North Africa into Spain, Sardinia, Corsica and Pyrénées-Orientales	0.07	[0.01-0.13]	0.16	0.06
Introduction from North Africa into Spain, then colonization of Pyrénées-Orientales out from Spain	0.01	[0.00-0.06]	0.18	0.06
Introduction from North Africa into Sardinia, then colonization of Pyrénées-Orientales out from Sardinia	0.29	[0.26-0.32]	0.21	0.09
Introduction from North Africa into Sardinia, then introduction in Corsica out from Sardinia, and then colonization of Pyrénées-Orientales out from Corsica	0.62	[0.60-0.64]	0.28	0.06

Type 1 error is the probability of selecting another scenario when the chosen scenario is true. Type 2 error is the mean probability of selecting the chosen scenario when it is false. The selected (most probable) scenario is highlighted in bold (see also Fig. S7).

Supplementary Table 6 | ABC model checking of the most probable scenario (Scenario 4).

summary statistics	observed value	proportion (simulated<observed)	summary statistics	observed value	proportion (simulated<observed)	summary statistics	observed value	proportion (simulated<observed)
NAL_1_1	5.0000	0.6330	V2P_1_1&4	1.3863	0.3315	DAS_1_2&3	0.3945	0.3635
NAL_1_2	4.3333	0.5850	V2P_1_1&5	1.3480	0.3255	DAS_1_2&4	0.3845	0.3985
NAL_1_3	4.6667	0.5440	V2P_1_2&3	1.3258	0.3310	DAS_1_2&5	0.4048	0.3855
NAL_1_4	5.0000	0.5915	V2P_1_2&4	1.3718	0.3355	DAS_1_3&4	0.3984	0.4425
NAL_1_5	4.4444	0.5445	V2P_1_2&5	1.3245	0.3420	DAS_1_3&5	0.4049	0.4220
HET_1_1	0.6101	0.6745	V2P_1_3&4	1.3911	0.3290	DAS_1_4&5	0.3989	0.4565
HET_1_2	0.6113	0.7160	V2P_1_3&5	1.3621	0.3420	DM2_1_1&2	0.0504	0.0805
HET_1_3	0.5909	0.6200	V2P_1_4&5	1.4067	0.3375	DM2_1_1&3	0.0468	0.1135
HET_1_4	0.6074	0.6310	FST_1_1&2	0.0332	0.2965	DM2_1_1&4	0.0354	0.0825
HET_1_5	0.5939	0.6340	FST_1_1&3	0.0352	0.4550	DM2_1_1&5	0.0605	0.1440
VAR_1_1	1.3344	0.3385	FST_1_1&4	0.0261	0.4365	DM2_1_2&3	0.0616	0.2345
VAR_1_2	1.2770	0.3340	FST_1_1&5	0.0320	0.3400	DM2_1_2&4	0.0450	0.0860
VAR_1_3	1.3534	0.3460	FST_1_2&3	0.0146	0.3340	DM2_1_2&5	0.0639	0.3585
VAR_1_4	1.4478	0.3500	FST_1_2&4	0.0159	0.1545	DM2_1_3&4	0.0173	0.0165 (*)
VAR_1_5	1.3576	0.3595	FST_1_2&5	-0.0004	0.2160	DM2_1_3&5	0.0776	0.3590
MGW_1_1	0.9854	0.8330	FST_1_3&4	0.0042	0.0420 (*)	DM2_1_4&5	0.0579	0.1545
MGW_1_2	0.9000	0.6515	FST_1_3&5	0.0119	0.3580			
MGW_1_3	1.0286	0.9160	FST_1_4&5	0.0049	0.0590			
MGW_1_4	0.9712	0.7930	LIK_1_1&2	1.0667	0.5670			
MGW_1_5	0.9677	0.8430	LIK_1_1&3	1.0523	0.6180			
N2P_1_1&2	5.7778	0.6655	LIK_1_1&4	0.9948	0.6055			
N2P_1_1&3	5.7778	0.6080	LIK_1_1&5	1.0554	0.5920			
N2P_1_1&4	5.7778	0.5920	LIK_1_2&1	0.9423	0.4770			
N2P_1_1&5	5.6667	0.6085	LIK_1_2&3	0.8331	0.4720			
N2P_1_2&3	5.0000	0.5110	LIK_1_2&4	0.8503	0.3980			
N2P_1_2&4	5.3333	0.5390	LIK_1_2&5	0.8065	0.5155			
N2P_1_2&5	4.7778	0.5125	LIK_1_3&1	1.0029	0.5390			
N2P_1_3&4	5.5556	0.5470	LIK_1_3&2	0.9266	0.5165			

N2P_1_3&5	5.0000	0.4750	LIK_1_3&4	0.9104	0.4740
N2P_1_4&5	5.4444	0.5520	LIK_1_3&5	0.9307	0.5560
H2P_1_1&2	0.6210	0.6675	LIK_1_4&1	0.9566	0.5355
H2P_1_1&3	0.6120	0.6430	LIK_1_4&2	0.9286	0.4315
H2P_1_1&4	0.6183	0.6590	LIK_1_4&3	0.8742	0.4170
H2P_1_1&5	0.6134	0.6520	LIK_1_4&5	0.9132	0.4460
H2P_1_2&3	0.6038	0.6490	LIK_1_5&1	0.8989	0.4915
H2P_1_2&4	0.6145	0.6485	LIK_1_5&2	0.7852	0.5140
H2P_1_2&5	0.6022	0.6685	LIK_1_5&3	0.8042	0.4940
H2P_1_3&4	0.6010	0.5915	LIK_1_5&4	0.8158	0.4165
H2P_1_3&5	0.5966	0.6160	DAS_1_1&2	0.3730	0.3740
H2P_1_4&5	0.6033	0.5920	DAS_1_1&3	0.3790	0.3770
V2P_1_1&2	1.3115	0.3100	DAS_1_1&4	0.3770	0.3605
V2P_1_1&3	1.3455	0.3230	DAS_1_1&5	0.3826	0.4000

All the summary statistics (used and unused for model selection) were used. For each statistic, the observed value and probability (simulated < observed) are given. For a detail description of the summary statistics, see the DIYABC v.2.0.4 manual. Significant probabilities are represented with an asterisk.

Supplementary Table 7 | Primers characteristics.

Loci	Motif	Forward	Reverse	Allele size range	T (°C)
68	(GT) _n	CTTTTCCGTTTCTTTTTATTTCTTT	GTTTCTTTCTGGTCGCGTTGGTTGCTG	99-105	60
12b	(CT) _n	TTATGTGTGTATGTTAGCAAGGTCA	GTTTCTTCTTCGGATCAAAGAAATTTTGCC	129-139	50
3b	(AC) _n	ATGCGGATGTTTGAAGTG	GTTTCTTTTTTGTGTCTTATTGCC	154-175	50
31	(CAA) _n	TTCTGTTCGGCTGTTGCGTT	GTTTCTTCTTTTTACGTGGTGGTCATT	152-168	60
41b	(CT) _n	GAGGAGGAGGTAGAA	GTTTCTTCTATTAGTCAATGGTG	155-166	50
35t	(AC) _n	TTTGTA AAAAGCCAGTTCAACCG	GTTTCTTATCGAACGAAGGAAATAACCAC	171-194	60
88b	(AC) _n	TTTGTTTCGATTTGTAGTG	GTTTCTTCCTCTCTTTTCATTTCGC	243-256	50
16	(TG) _n	TTGCCTTTGCTTGTTGAGGATG	GTTTCTTTCCTCTTTAAAATCACTGACGTG	292-299	60
88	(CAT) _n	GTTGGTGCTTTGTTGTGTTGT	GTTTCTTTTTCTTTTTCTCCTTTTTGTTTCTTTC	344-348	50

Supplementary Table 8 | Prior distributions of demographic, historical and mutation parameters used for ABC inferences.

Parameter description	Parameter	Prior distribution
Stable effective population size	N	Loguniform [1000; 200000]
Time of colonization events in Pyrénées-Orientales	t_p	Uniform [40; 10000]
Time of colonization events in Sardinia, Corsica and Spain	t_s, t_c, t_e	Uniform [140; 10000]
Duration of bottleneck	D_B	Uniform [0; 50]
Founding effective population sizes	N_s	Loguniform [2; 100]
Mean mutation rate	$\mu_{\text{microsatellites}}$	Loguniform [1E-6; 1E-4]
Mean parameter of the geometric distribution of length	P	Uniform [1E-1; 3E-1]
Mean mutation rate for nucleotide instability	SNI	Uniform [1E-8; 1E-4]

Effective population sizes (N) are expressed in number of diploid individuals and times of events (t) in number of generations going back to the past. Conditions among the parameters used during the simulations were $t_s \geq t_p$, $t_e \geq t_p$, $t_c \geq t_p$.