

# Supplementary materials

## S1. Details of sampled populations

Table S1: details of sampled populations: region, population number (ID; see map main manuscript), given population name (Population name), X- and Y-coordinates (X, Y) in coordinate system Belgian Lambert 72 (epsg:31370), sample year(s) (Year) and number of samples (n).

Region	ID	Population name	X	Y	Year	n
Coastal France	1	Mt St Frieux	-45055.836	147290.022	2018	19
	2	Slack	-42871.872	169089.634	2018	20
	3	Sangatte	-30478.698	186092.799	2018	20
Coastal Flanders	4	Westhoek Zuid	23274.352	197883.930	2018 2020	12 9
	5	Cabour	24000.043	196525.259	2018	10
	6	Veurne	31418.656	196887.771	2018	20
	7	Tropiflora	24109.489	198094.010	2018 2020	20 9
	8	Westhoek vissersdorp	23467.294	199618.259	2018 2020	20 3
	9	Westhoek NO	24120.869	199559.082	2018 2020	22 8
	10	Westhoek Oost	24446.785	199084.816	2018 2020	10 8
	11	Oosthoekduinen	26503.156	199039.926	2018 2020	19 10
	12	Belvedere	27469.461	199611.067	2018 2020	10 8
	13	HB-Noord	29615.521	201772.772	2018 2020	7 9
	14	HB-Doornpanne	29652.166	202069.447	2018 2020	10 7
	15	HB-Oost	29672.837	201505.012	2018 2020	10 6
	16	HB-Pylyserlaan	29915.987	201394.673	2018 2020	10 8
	17	Schipgatduinen	29945.549	202880.064	2018 2020	12 4
	18	Witte Burg	30561.564	202010.765	2018 2020	12 7
	19	Astridlaan	31560.066	203551.845	2018 2020	17 7
	20	Plaatsduinen	32343.888	203286.675	2018 2020	18 9
	21	Oostvoordduinen	33104.253	202483.973	2018 2020	20 10
	22	Ter Yde West	32486.049	203868.703	2018 2020	10 3
	23	Ter Yde IWVA	33151.347	203994.353	2018 2020	10 9
	24	Karthuizerduinen	33449.436	204338.378	2018 2020	9 9
	25	Simliduinen	33814.709	204776.506	2018 2020	20 7

	26	Sint-Laureins1	37336.964	207156.451	2020	9
	27	Sint-Laureins2	38042.734	207317.394	2020	7
	28	Warandeduinen Middelkerke	39485.855	208330.732	2020	7
	29	Raversijde1	41944.728	210035.728	2020	8
	30	Raversijde2	42218.098	210273.838	2020	10
	31	Raversijde3	42839.355	210691.179	2020	5
	32	Raversijde4	43074.002	210795.354	2020	5
	33	Fort Napoleon	50050.322	215428.560	2020	9
	34	Spanjaardduinen Oostende	51403.973	216230.489	2020	8
	35	Bredene	53808.105	217367.810	2020	10
	36	Duinbossen DeHaan	59600.497	221053.034	2020	12
	37	Zwinbosjes-grazed	77921.134	228387.482	2020	9
	38	Zwinbosjes	78243.444	228544.867	2018 2020	20 15
	39	Vloethemveld-Noord	60996.017	205437.804	2020	9
	40	Vloethemveld-Zuid	61176.550	204480.049	2020	11
Inland Flanders	41	Wetteren	117432.840	188634.139	2018 2020	8 20
	42	Kortenhoeff-NL	149108.508	234460.777	2020	10
	43	Kalmthout	154547.132	232375.786	2020	12
	44	Averbode	194424.342	192633.330	2020	9
	45	Arendschot	196699.590	190406.561	2020	9
	46	Geel-Bel	199027.845	205395.375	2018 2020	20 11
	47	Kopberg	201751.857	204674.642	2020	21
	48	Keiheuvel	210274.429	208479.656	2020	10
	49	Hamont-Achel2	230347.333	220397.920	2020	8
	50	Hamont-Achel3	230584.834	220105.267	2020	9
	51	Hamont-Achel1	230612.992	220822.730	2020	10
Inland	52	Harchies	100876.462	127411.662	2021	19
Wallonia	53	Lagland	249207.562	38937.742	2021	20

## S2. DNA-extraction and PCR protocol

### DNA-extraction protocol for wing tips *Bembix rostrata*

Eppendorfs with samples dried to the air were put in liquid nitrogen for a few minutes and homogenized with a crusher. 50 µL Chelex and 10 µL proteinase K were added and the samples were incubated (56°C) overnight. The boiling and centrifuge steps were performed the next morning.

#### Day 1

- Put a wing tip in a 1.5mL ep, let it dry for several minutes in the open air (to let the ethanol evaporate)
- Put the ep for 5' in liquid nitrogen
- Crush the wing tip firmly with a crusher
- Pipet 50 µL 6% Chelex InstaGene Matrix solution (Biorad) (while it is on the magnetiser) into the ep, while rinsing off the crusher
- Add 10 µL proteinase K (N600mAU/ml, Qiagen)
- Incubate overnight at 56°C (+ soft shaking)

#### Day 2

- Vortex (+ minicentrifuge) to get the drops of the lid
- 15' 99°C
- Vortex (+ minicentrifuge) to get the drops of the lid
- Centrifuge 3' at 14 000 rpm and store in the fridge awaiting PCR-amplification

### PCR protocol

For the primer mix, a ratio of '3 : 1 : 3' 'Forward primer : Reverse primer (tailed) : oligonucleotides dye (FAM, VIC, NED, PET)' is used (1µM concentration). Table S2 gives the partition of primers into 3 pairs of multiplexes: for each series/plate of samples, 6 PCRs were run (6 multiplexes: 1.1, 1.2, 2.1, 2.2, 3.1, 3.2). These PCR products were diluted and pairwise combined (1.1+1.2, 2.1+2.2, 3.1+3.2) before sending the PCR products to the ABI analyzer.

We worked with a total volume in each well of a PCR-plate of 5 µl:

- 2 µl Qiagen MultiPlex (Qiagen® Multiplex PCR kit cat. No. 206143)
- 2 µl microsatellite primer mix
- 1 µl of DNA

If the tissue material for the DNA extraction was very small, the 2 µl of DNA was air dried by putting it on a block heater (37°C) for at least 5 hours. This way, the concentration of DNA was increased in the PCR-volume.

#### PCR conditions:

- 95°C for 15 min
- 35 cycles of
  - 94°C for 30 sec
  - 57°C for 90 sec
  - 72°C for 60 sec
- 60°C for 30 min
- 4°C for ∞

Table S2: Partitioning of primers into 3 pairs multiplexes: 6 PCRs are run for each sample, but 3 PCRs products are used for the ABI analyzer.

1.1							2.1						3.1				
3 µL	F110	F16	F486	F9	F227	F57	3 µL	F76	F144	F234	F32	F35	6 µL	F12	F138	F161	
1 µL	R110	R16	R486	R9	R227	R57	1 µL	R76	R144	R234	R32	R35	2 µL	R12	R138	R161	
9 µL	6-FAM M13-21			VIC M13-21			9 µL	6-FAM M13-21					3 µL	F329	F111		
Dilution post PCR: 2x							6 µL	VIC M13-21					1 µL	R329	R111		
							Dilution post PCR: 4x						12 µL	6-FAM	VIC M13-21		
													Dilution post PCR: 4x				

1.2			
6 µL	F403	F299	
2 µL	R403	R299	
3 µL	F116	F375	F467
1 µL	R116	R375	R467
12 µL	NED M13 Moda		
9 µL	PET T7		
Dilution post PCR: 4x			

2.2						3.2					
6 µL	F20					6 µL	F337				
2 µL	R20					2 µL	R337				
3 µL	F437	F487	F298	F266	F153	3 µL	F196	F419	F480	F218	F307
1 µL	R437	R487	R298	R266	R153	1 µL	R196	R419	R480	R218	R307
9 µL	NED M13 Moda					6 µL	NED M13 Moda				
12 µL	PET T7					15 µL	PET T7				
Dilution post PCR: 2x						Dilution post PCR: 3x					

### S3. List of primers

Table S3: Characteristics of the 33 microsatellites used in our study for *Bembix rostrata*. A full list of the newly developed (by AllGenetics®, A Coruña, Spain) remaining non-tested (and tested but discarded) microsatellite loci can be obtained from the contacting author. Annealing temperature used for all primers is 57°C. Five loci had a lot of stutter in the amplification profiles and were discarded from the analysis (AGBro486, -329, -196, -437, -298). Following abbreviations are used: the multiplex mix in which the marker was included (Primer Mix) and fluorescent label used (Label), the observed fragment length range (Size range), the number of alleles observed (No. alleles), observed and expected heterozygosity (Ho and He), if they are used in the genetic analyses after assumption testing (Used) and both primer sequences (F = forward, R = reverse).

Locus	Repeat motif	No repeats	Primer Mix	Label	Size range (bp)	No. of alleles	Ho	He	Used	Primer sequences (5'-3')
AGBro110	AAG	7	1.1	FAM	95-124	7	0.58	0.6189	y	F: GCCATCACGTTTACAGCCAC R: AGAGGTGGTAGTGCTGGAGA
AGBro16	AGGC	7	1.1	FAM	188-208	5	0.1437	0.1573	n	F: CTCGCGTACTATTTCGCT R: TAACAGCGTGGTTCCGGAA
AGBro486	AG	11	1.1	FAM	366-414	/	/	/	n	F: ACAAACGTTTCACGGTACTTGT R: GGCAGGAGGACATCGTTGAT
AGBro9	AG	14	1.1	VIC	90-130	14	0.7089	0.8144	y	F: GAGTGAGAGGGAGGCAGAGA R: TACGTGCCTGAGGAAACGAC
AGBro227	AACG	6	1.1	VIC	144-180	8	0.3978	0.4198	y	F: CAAGCATGGCCAGTCTGTTT R: TGGCTACTGTGGGCTCACTA
AGBro57	AG	7	1.1	VIC	225-235	2	0.114	0.2806	n	F: GCACCGGGACACTGTCTTAT R: GGGTCACTCGATCGACGTTT
AGBro403	AACG	10	1.2	NED	122-180	12	0.6876	0.7435	y	F: TTATCCCGATCGCTTGGCAT R: GCTCGACGCTTCATCGATTAAC
AGBro116	AG	8	1.2	NED	213-235	5	0.4787	0.5597	y	F: CTCCTCTCCATACGACGCAC R: TTGGCAGTAGAACGAGGACC
AGBro375	ACAG	8	1.2	NED	267-279	3	0.3719	0.4279	y	F: CGAAGTTCCGCATTACCTTGC R: CCTGACAGGTGCTCACGTATT
AGBro299	AC	8	1.2	PET	100-123	5	0.4092	0.4418	y	F: GACGTAAGGGCGAAGAACGT R: GCATTCCGTGCGAGTGAATA
AGBro467	AAG	7	1.2	PET	158-202	11	0.6525	0.7317	y	F: GTCCAGAGAAGGTATGAGAGGG R: CGTGACGTAATATCCGGGCA
AGBro76	AAG	7	2.1	FAM	100-122	7	0.5356	0.5813	y	F: AATTGTGCCGAAACTTGCC R: TCGTTGCAAGTGTCGTGACA
AGBro144	ACGG	7	2.1	FAM	152-192	8	0.6386	0.745	y	F: GCCGTTTATCCGTCCATCCA R: CCTCTCATATCGGTGCCTCC
AGBro234	AG	8	2.1	FAM	270-282	4	0.5425	0.605	y	F: CGTGCTCCACCGAAATTCT R: CAGCTGCAGTTCGATGATCG

AGBro32	AAGC	5	2.1	VIC	133-149	4	0.4853	0.4955	y	F: GCGGCTGGTATCTGATCCAA R: CTAGCTGTCTGCCTACCTGC
AGBro35	AAG	5	2.1	VIC	229-240	2	0.1405	0.3423	n	F: AAGTTCTCACGAAACCGCCT R: GGGCCACCAGATTCTTACCC
AGBro437	AG	7	2.2	NED	104-110	/	/	/	n	F: CGATAGCAAGCACGCGAGG R: GAGGGTAAACCACGAGGAGC
AGBro487	ACG	12	2.2	NED	146-176	6	0.5191	0.6037	y	F: GGGAGAGTTCGCGAAGGTAC R: CCTTCAGAAATGCTTGTCGTTGT
AGBro298	AG	10	2.2	NED	230-306	/	/	/	n	F: AGCTTGTTGGACGCGTAAGA R: GGC GATCGACATTT CAGTCA
AGBro20	AAT	6	2.2	PET	309-320	3	0.0759	0.1001	n	F: TCTGATTGGACCGTTCGTCG R: ACGTGTCTGATCGTGCTTGT
AGBro266	AT	6	2.2	PET	112-122	4	0.3306	0.4099	y	F: CGCGAACATTAAGCACCGAA R: ATACCGTCACGACAGAGCCA
AGBro153	AG	7	2.2	PET	160-170	4	0.4447	0.5075	y	F: TAGCTCAGCCTCTACCGACC R: TGAACGAGAACGGCGTACAG
AGBro161	AAAG	6	3.1	FAM	248-263	4	0.4679	0.556	y	F: TCGCCGTAAGACCTTCGTAC R: GGTATGCGGTCTTCTCGGTG
AGBro329	ACC	6	3.1	FAM	85-133	/	/	/	n	F: TCCCTCTTCGTTCTCTCCT R: CTCGGCGAAAGATAGCACGG
AGBro111	AG	8	3.1	FAM	162-184	9	0.5723	0.6913	n	F: TGTACCAATCCGGCCTTTGT R: AACGTACGGTGGATTAGCCG
AGBro12	AG	8	3.1	VIC	198-220	10	0.5872	0.6902	y	F: GTGCCGTAATTCGACGAACG R: ATCTCGTAACGTTCTCTGCC
AGBro138	AAG	6	3.1	VIC	95-112	3	0.1869	0.3075	n	F: ACTGCCGTACCTGTAGCTTC R: CTTTCACGCTTCGCACATGT
AGBro196	AG	14	3.2	NED	126-158	/	/	/	n	F: ATGGCGAAGGAAACGGTCTT R: CTCCTCGCGTATTTCTCCT
AGBro419	AG	10	3.2	NED	248-264	6	0.398	0.5849	n	F: TGTGACCAGTGGTAACCCAT R: TGCACCCACTGTCCATATAGC
AGBro337	AGC	6	3.2	PET	113-130	5	0.3928	0.4102	y	F: CGACGGGACCCAATTCATCG R: ACCATCTCTTTCTACCGCC
AGBro480	AAAGC	7	3.2	PET	163-183	4	0.5074	0.5932	y	F: TCGTTTACTGTCGCAAATGACC R: TTGCTTCTCTTCGCTCCACT
AGBro218	AG	6	3.2	PET	299-315	4	0.4393	0.4919	y	F: CAATACCGTCAACTACCCGA R: CTGACACCTGACGGATAGCC
AGBro307	AAG	6	3.2	PET	220-236	4	0.3323	0.451	y	F: GTCGCAGCTGATAGCCAAGT R: ACGACTTATGTCCACGTGGA

## S4. Genetic differentiation measures

Figures S1-2 are similar to figure 2 in the main manuscript with Nei's standardized genetic distance ( $D_S$ ), but for the genetic differentiation measures  $F_{ST}$  (Weir and Cockerham 1984) and  $D$  (Jost 2008). Genetic differentiation measures were calculated with the R package *diversity* (Keenan et al. 2013). Unbiased confidence intervals of 95% were calculated from 1,000 bootstraps.

Tables S4-6 list the 10 populations with the highest genetic distances and differentiation values, which have the highest average differentiation from all other populations.

These two differentiation measures give similar results as the pairwise Nei's standardized genetic distance used in the main manuscript: differentiation values are overall high among inland sampling sites, and low among coastal sites. Values are medium to high between coastal and inland regions.

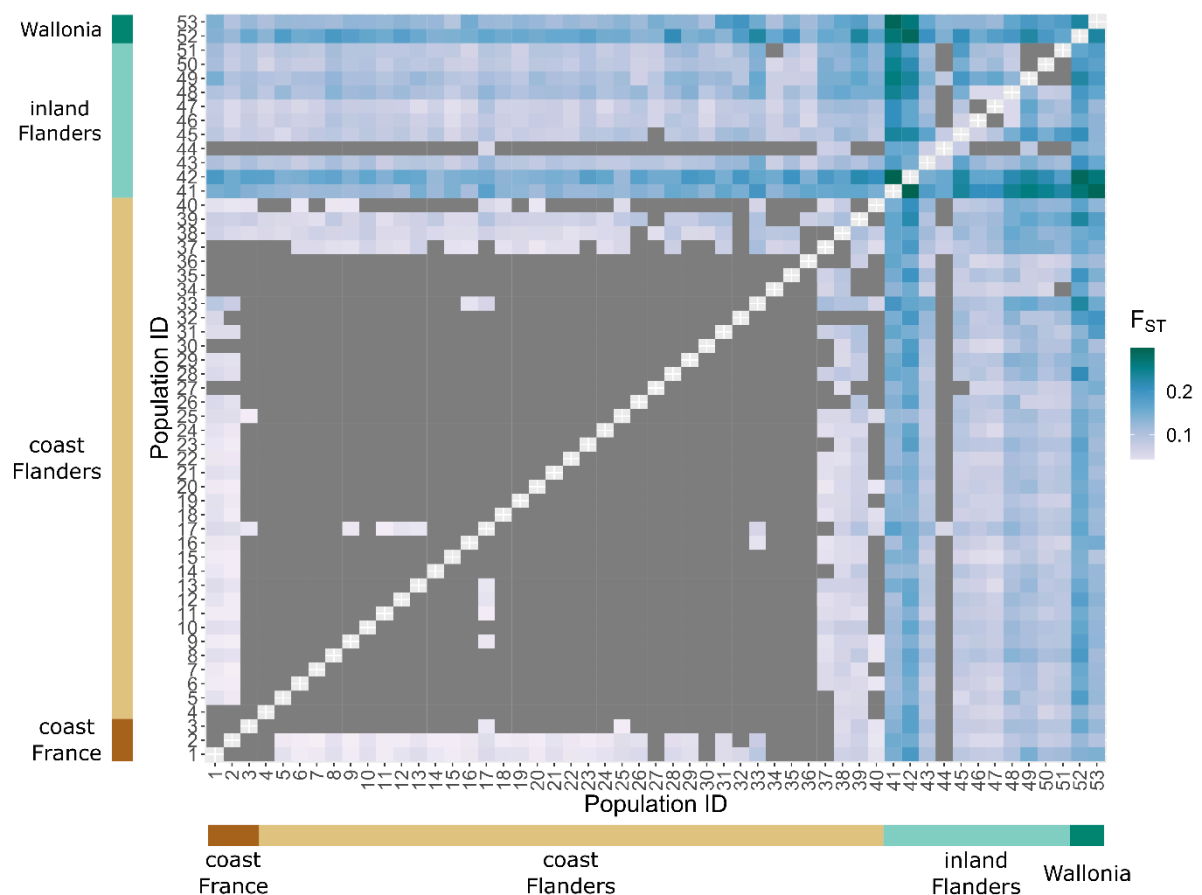


Figure S1: graphical matrix representation of pairwise genetic differentiation measure  $F_{ST}$ : light blue are low, dark blue are mid, and dark green are high pairwise genetic differentiation values between populations. Grey areas are non-significant pairwise genetic differentiation values (0 was included in the 95% confidence intervals of 95% were calculated from 1,000 bootstraps). The x- and y-axes represent the population ID, subdivided in the four different regions. Genetic distances are symmetrical and consequently the matrix is mirrored along the diagonal. There is overall high genetic differentiation within the inland regions (right upper corner) and low genetic differentiation within the coastal regions (left lower corner). The genetic distances between coastal and inland regions are medium to high.

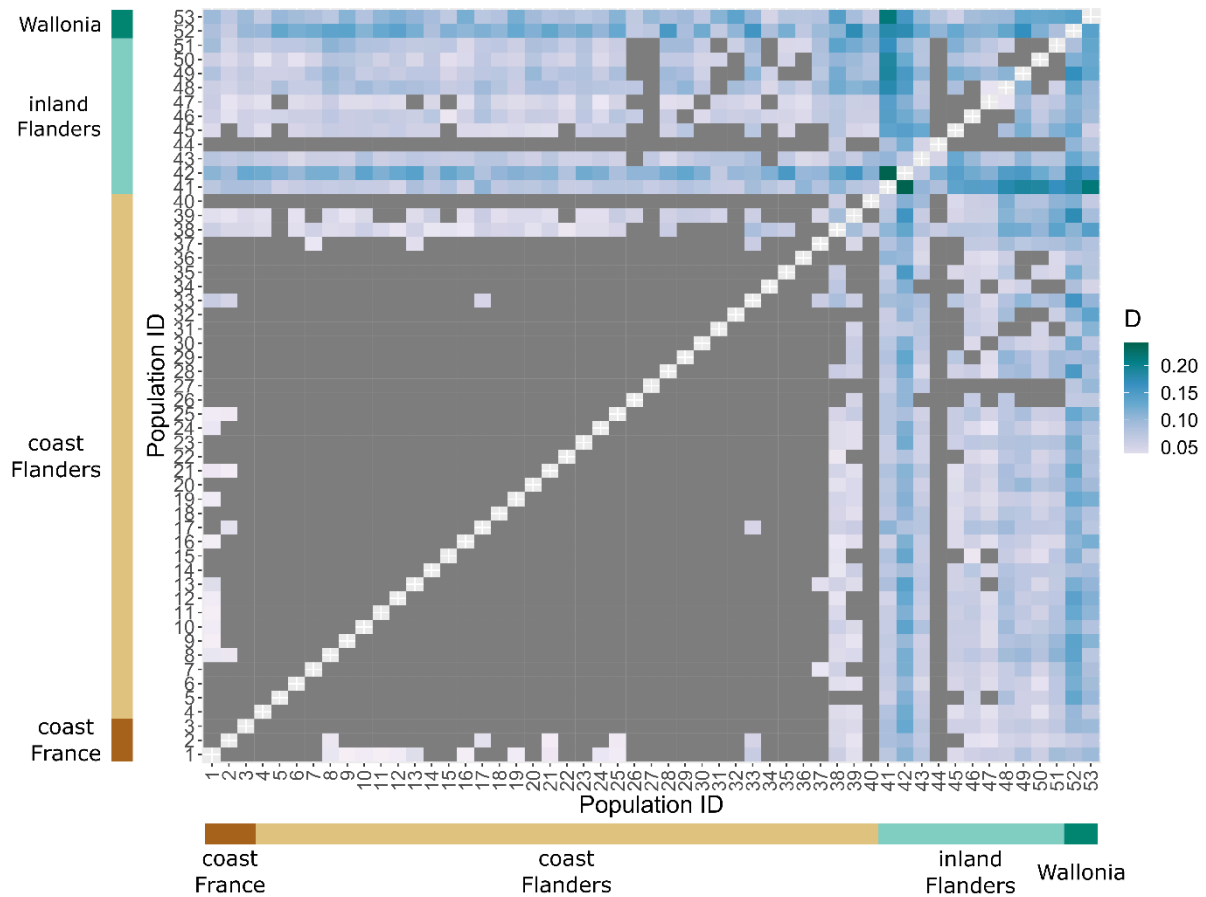


Figure S2: graphical matrix representation of pairwise genetic differentiation measure Jost's D: light blue are low, dark blue are mid, and dark green are high pairwise genetic differentiation values between populations. Grey areas are non-significant pairwise genetic differentiation values (0 was included in the 95% confidence intervals of 95% were calculated from 1,000 bootstraps). The x- and y-axes represent the population ID, subdivided in the four different regions. Genetic distances are symmetrical and consequently the matrix is mirrored along the diagonal. There is overall high genetic differentiation within the inland regions (right upper corner) and low genetic differentiation within the coastal regions (left lower corner). The genetic distances between coastal and inland regions are medium to high.



Table S4: the 10 populations with highest averaged Nei's distance values (Mean( $D_s$ )). ID is population ID from figure 1 and table S1, SD( $D_s$ ) is the standard deviation of mean( $D_s$ ).

Region	Population name	ID	Mean( $D_s$ )	SD( $D_s$ )
Flanders-inland	Kortenhoeff-NL	42	0.291	0.069
Flanders-inland	Hamont-Achel2	49	0.257	0.075
Wallonia	Harchies	52	0.256	0.063
Flanders-inland	Keiheuvel	48	0.230	0.065
Flanders-inland	Wetteren	41	0.229	0.082
Wallonia	Lagland	53	0.215	0.065
Flanders-inland	Arendschot	45	0.207	0.069
Flanders-inland	Kalmthout	43	0.201	0.048
Flanders-inland	Hamont-Achel1	51	0.200	0.061
Flanders-inland	Halomt-Achel3	52	0.197	0.061

Table S5: the 10 populations with highest averaged  $F_{ST}$  values (Mean( $F_{ST}$ )). ID is population ID from table S1, SD( $F_{ST}$ ) is the standard deviation of mean( $F_{ST}$ ).

Region	Population	ID	Mean( $F_{ST}$ )	SD( $F_{ST}$ )
Flanders-inland	Kortenhoeff-NL	42	0.173	0.039
Wallonia	Harchies	52	0.171	0.035
Flanders-inland	Wetteren	41	0.161	0.049
Wallonia	Lagland	53	0.142	0.039
Flanders-inland	Hamont-Achel2	49	0.119	0.047
Flanders-inland	Keiheuvel	48	0.116	0.039
Flanders-inland	Kalmthout	43	0.106	0.029
Flanders-inland	Arendschot	45	0.101	0.043
Flanders-inland	Hamont-Achel1	51	0.1	0.04
Flanders-inland	Hamont-Achel3	50	0.098	0.043

Table S6: the 10 populations with highest averaged Jost's D values (Mean(D)). ID is population ID from table S1, SD(D) is the standard deviation of mean(D).

Region	Population	ID	Mean(D)	SD(D)
Flanders-inland	Kortenhoeff-NL	42	0.119	0.028
Wallonia	Harchies	52	0.116	0.028
Wallonia	Lagland	53	0.097	0.029
Flanders-inland	Wetteren	41	0.094	0.045
Flanders-inland	Keiheuvel	48	0.079	0.030
Flanders-inland	Hamont-Achel2	49	0.077	0.036
Flanders-inland	Hamont-Achel1	51	0.073	0.032
Flanders-inland	Kalmthout	43	0.070	0.019
Flanders-inland	Hamont-Achel3	50	0.061	0.032
Flanders-inland	Geel-Bel	46	0.061	0.026

## S5. Population level statistics

Population level statistics for all sampled population are given in table S6.

Table S7: population level statistics for all sampled populations (table S1). Following abbreviations are used: Region, population number (ID; see map main manuscript), given population name (Population name), number of samples (n), number of private alleles (NP), rarefied allelic richness (AR), expected heterozygosity ( $H_e$ ), observed heterozygosity ( $H_o$ ) and inbreeding coefficient ( $F_{IS}$ ). Standard errors (SE) are given for AR,  $H_e$ ,  $H_o$  and  $F_{IS}$ .

Region	ID	Population name	n	NP	AR $\pm$ SE	$H_e \pm$ SE	$H_o \pm$ SE	$F_{IS} \pm$ SE
France-Picardie	1	Mt St Frieux	19	1	2.523 $\pm$ 0.153	0.547 $\pm$ 0.037	0.559 $\pm$ 0.041	-0.022 $\pm$ 0.026
	2	Slack	20	1	2.605 $\pm$ 0.141	0.587 $\pm$ 0.031	0.585 $\pm$ 0.038	0.003 $\pm$ 0.035
	3	Sangatte	20	0	2.630 $\pm$ 0.160	0.588 $\pm$ 0.029	0.555 $\pm$ 0.033	0.057 $\pm$ 0.027
Flanders-coast	4	Westhoek Zuid	21	0	2.623 $\pm$ 0.148	0.584 $\pm$ 0.032	0.520 $\pm$ 0.035	0.105 $\pm$ 0.042
	5	Cabour	10	0	2.769 $\pm$ 0.160	0.63 $\pm$ 0.028	0.619 $\pm$ 0.033	0.004 $\pm$ 0.046
	6	Veurne	20	0	2.570 $\pm$ 0.145	0.586 $\pm$ 0.03	0.498 $\pm$ 0.032	0.149 $\pm$ 0.028
	7	Tropiflora	29	1	2.628 $\pm$ 0.157	0.575 $\pm$ 0.036	0.535 $\pm$ 0.038	0.072 $\pm$ 0.032
	8	Westhoek vissersdorp	23	0	2.511 $\pm$ 0.138	0.563 $\pm$ 0.03	0.494 $\pm$ 0.036	0.126 $\pm$ 0.036
	9	Westhoek NO	30	1	2.657 $\pm$ 0.162	0.594 $\pm$ 0.032	0.547 $\pm$ 0.034	0.083 $\pm$ 0.021
	10	Westhoek Oost	18	0	2.647 $\pm$ 0.162	0.587 $\pm$ 0.034	0.558 $\pm$ 0.048	0.054 $\pm$ 0.057
	11	Oosthoekduinen	29	0	2.711 $\pm$ 0.154	0.613 $\pm$ 0.028	0.584 $\pm$ 0.034	0.047 $\pm$ 0.040
	12	Belvedere	18	0	2.670 $\pm$ 0.147	0.604 $\pm$ 0.029	0.515 $\pm$ 0.038	0.151 $\pm$ 0.042
	13	HB-Noord	16	0	2.686 $\pm$ 0.164	0.594 $\pm$ 0.039	0.545 $\pm$ 0.051	0.110 $\pm$ 0.054
	14	HB-Doornpanne	17	0	2.659 $\pm$ 0.154	0.589 $\pm$ 0.036	0.501 $\pm$ 0.033	0.137 $\pm$ 0.035
	15	HB-Oost	16	1	2.725 $\pm$ 0.156	0.617 $\pm$ 0.028	0.576 $\pm$ 0.030	0.057 $\pm$ 0.041
	16	HB-Pylyserlaan	18	0	2.661 $\pm$ 0.16	0.595 $\pm$ 0.033	0.551 $\pm$ 0.045	0.087 $\pm$ 0.049
	17	Schipgatduinen	16	0	2.478 $\pm$ 0.16	0.539 $\pm$ 0.037	0.490 $\pm$ 0.030	0.063 $\pm$ 0.040
	18	Witte Burg	19	0	2.629 $\pm$ 0.142	0.599 $\pm$ 0.028	0.577 $\pm$ 0.024	0.023 $\pm$ 0.036
	19	Astridlaan	24	0	2.688 $\pm$ 0.153	0.603 $\pm$ 0.030	0.555 $\pm$ 0.034	0.071 $\pm$ 0.046
	20	Plaatsduinen	27	0	2.630 $\pm$ 0.147	0.590 $\pm$ 0.030	0.513 $\pm$ 0.036	0.140 $\pm$ 0.035
	21	Oostvoordduinen	30	0	2.634 $\pm$ 0.136	0.594 $\pm$ 0.027	0.580 $\pm$ 0.033	0.021 $\pm$ 0.039
	22	Ter Yde West	13	0	2.614 $\pm$ 0.147	0.595 $\pm$ 0.029	0.582 $\pm$ 0.036	0.005 $\pm$ 0.058
	23	Ter Yde IWVA	19	0	2.581 $\pm$ 0.13	0.582 $\pm$ 0.027	0.576 $\pm$ 0.027	-0.009 $\pm$ 0.045
	24	Karthuizerduinen	18	0	2.614 $\pm$ 0.147	0.585 $\pm$ 0.031	0.503 $\pm$ 0.036	0.136 $\pm$ 0.052
	25	Simliduinen	27	0	2.621 $\pm$ 0.143	0.590 $\pm$ 0.030	0.560 $\pm$ 0.024	0.032 $\pm$ 0.030
	26	Sint-Laureins1	9	0	2.655 $\pm$ 0.163	0.602 $\pm$ 0.033	0.502 $\pm$ 0.036	0.141 $\pm$ 0.065
	27	Sint-Laureins2	7	0	2.842 $\pm$ 0.176	0.64 $\pm$ 0.036	0.528 $\pm$ 0.049	0.173 $\pm$ 0.060
	28	Warandeduinen Middelkerke	7	0	2.718 $\pm$ 0.148	0.612 $\pm$ 0.034	0.517 $\pm$ 0.042	0.125 $\pm$ 0.070
	29	Raversijde1	8	0	2.634 $\pm$ 0.162	0.597 $\pm$ 0.042	0.369 $\pm$ 0.045	0.361 $\pm$ 0.069
	30	Raversijde2	10	0	2.576 $\pm$ 0.136	0.597 $\pm$ 0.03	0.470 $\pm$ 0.038	0.211 $\pm$ 0.054
	31	Raversijde3	5	0	2.442 $\pm$ 0.18	0.529 $\pm$ 0.058	0.395 $\pm$ 0.05	0.201 $\pm$ 0.072
	32	Raversijde4	5	0	2.724 $\pm$ 0.188	0.616 $\pm$ 0.036	0.604 $\pm$ 0.059	0.018 $\pm$ 0.084
	33	Fort Napoleon	9	0	2.502 $\pm$ 0.139	0.556 $\pm$ 0.036	0.517 $\pm$ 0.041	0.053 $\pm$ 0.064
	34	Spanjaardduinen Oostende	8	0	2.696 $\pm$ 0.161	0.617 $\pm$ 0.035	0.451 $\pm$ 0.042	0.264 $\pm$ 0.055
	35	Bredene	10	1	2.513 $\pm$ 0.157	0.576 $\pm$ 0.034	0.364 $\pm$ 0.044	0.359 $\pm$ 0.069
	36	Duinbossen DeHaan	12	0	2.575 $\pm$ 0.134	0.603 $\pm$ 0.027	0.403 $\pm$ 0.034	0.333 $\pm$ 0.050

	37	Zwinbosjes-grazed	9	0	$2.448 \pm 0.151$	$0.544 \pm 0.045$	$0.481 \pm 0.048$	$0.098 \pm 0.054$
	38	Zwinbosjes	35	0	$2.551 \pm 0.152$	$0.567 \pm 0.035$	$0.504 \pm 0.034$	$0.108 \pm 0.022$
	39	Vloethemveld-Noord	9	0	$2.412 \pm 0.13$	$0.528 \pm 0.040$	$0.458 \pm 0.037$	$0.102 \pm 0.047$
	40	Vloethemveld-Zuid	11	0	$2.535 \pm 0.153$	$0.555 \pm 0.042$	$0.483 \pm 0.042$	$0.123 \pm 0.038$
Flanders-inland	41	Wetteren	28	0	$2.127 \pm 0.129$	$0.443 \pm 0.046$	$0.446 \pm 0.049$	$0.005 \pm 0.030$
	42	Kortenhoeff-NL	10	0	$2.178 \pm 0.14$	$0.446 \pm 0.046$	$0.392 \pm 0.044$	$0.091 \pm 0.048$
	43	Kalmthout	12	0	$2.387 \pm 0.151$	$0.518 \pm 0.042$	$0.432 \pm 0.042$	$0.171 \pm 0.054$
	44	Averbode	9	0	$2.607 \pm 0.177$	$0.579 \pm 0.044$	$0.466 \pm 0.049$	$0.182 \pm 0.065$
	45	Arendschot	9	0	$2.355 \pm 0.148$	$0.523 \pm 0.042$	$0.435 \pm 0.043$	$0.106 \pm 0.078$
	46	Geel-Bel	31	1	$2.525 \pm 0.143$	$0.547 \pm 0.036$	$0.510 \pm 0.039$	$0.071 \pm 0.040$
	47	Kopberg	21	0	$2.433 \pm 0.145$	$0.522 \pm 0.039$	$0.431 \pm 0.049$	$0.220 \pm 0.062$
	48	Keiheuvel	10	0	$2.433 \pm 0.148$	$0.528 \pm 0.038$	$0.479 \pm 0.045$	$0.079 \pm 0.064$
	49	Hamont-Achel2	8	0	$2.379 \pm 0.142$	$0.545 \pm 0.042$	$0.486 \pm 0.053$	$0.114 \pm 0.060$
	50	Hamont-Achel3	9	0	$2.306 \pm 0.112$	$0.523 \pm 0.033$	$0.521 \pm 0.038$	$-0.010 \pm 0.055$
	51	Hamont-Achel1	10	0	$2.35 \pm 0.123$	$0.532 \pm 0.032$	$0.540 \pm 0.042$	$-0.025 \pm 0.055$
Wallonia	52	Harchies	19	2	$2.114 \pm 0.134$	$0.433 \pm 0.049$	$0.336 \pm 0.040$	$0.217 \pm 0.051$
	53	Lagland	20	1	$2.154 \pm 0.124$	$0.450 \pm 0.037$	$0.330 \pm 0.041$	$0.269 \pm 0.057$

## S6. DAPC scatterplots

Coastal and inland regions separately

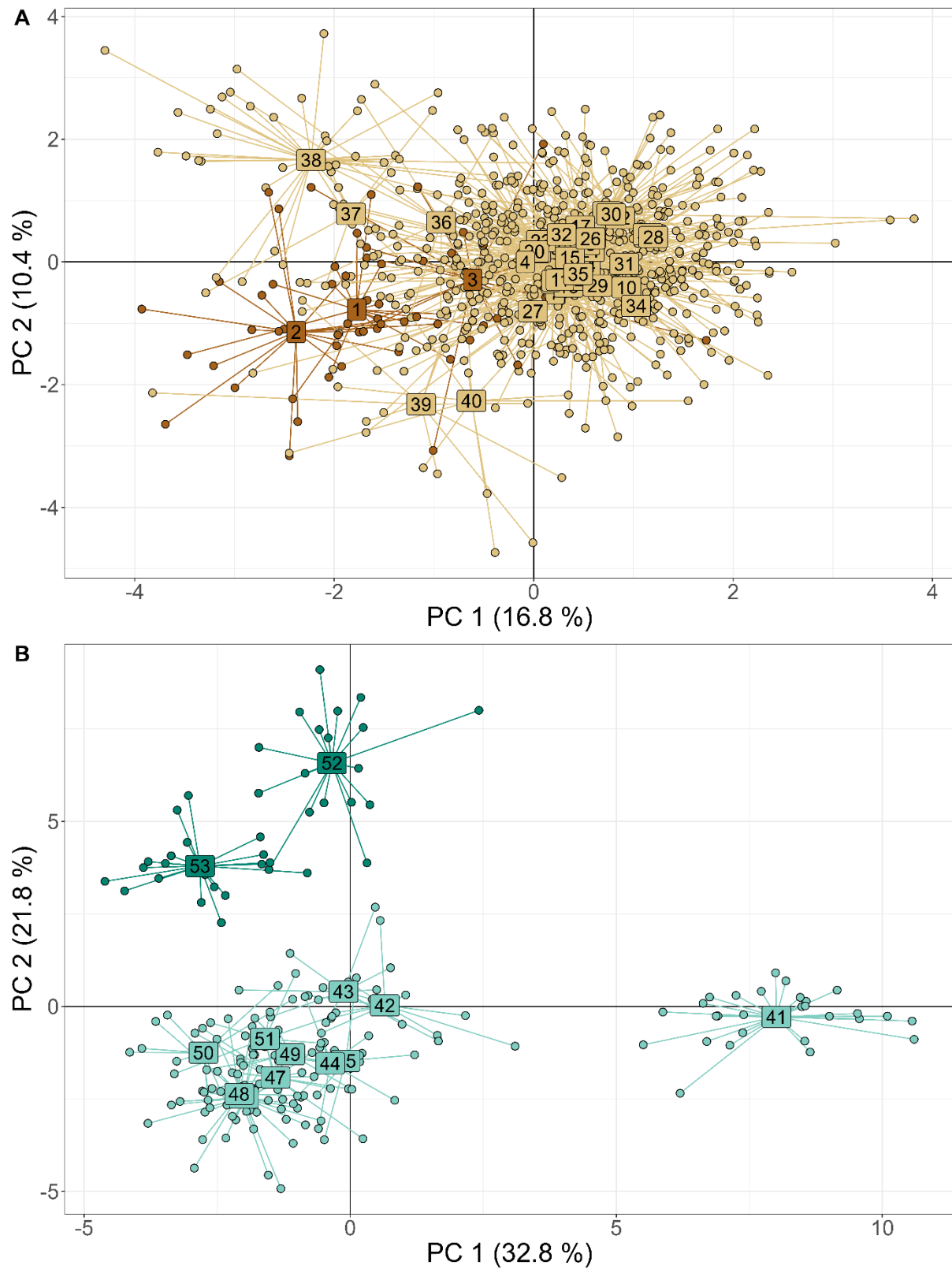


Figure S3: DAPC scatterplots for coastal (A) and inland (B) regions separately. Numbers are population IDs and are centered in the point cloud of each population.

## S7. Derived dispersal kernel

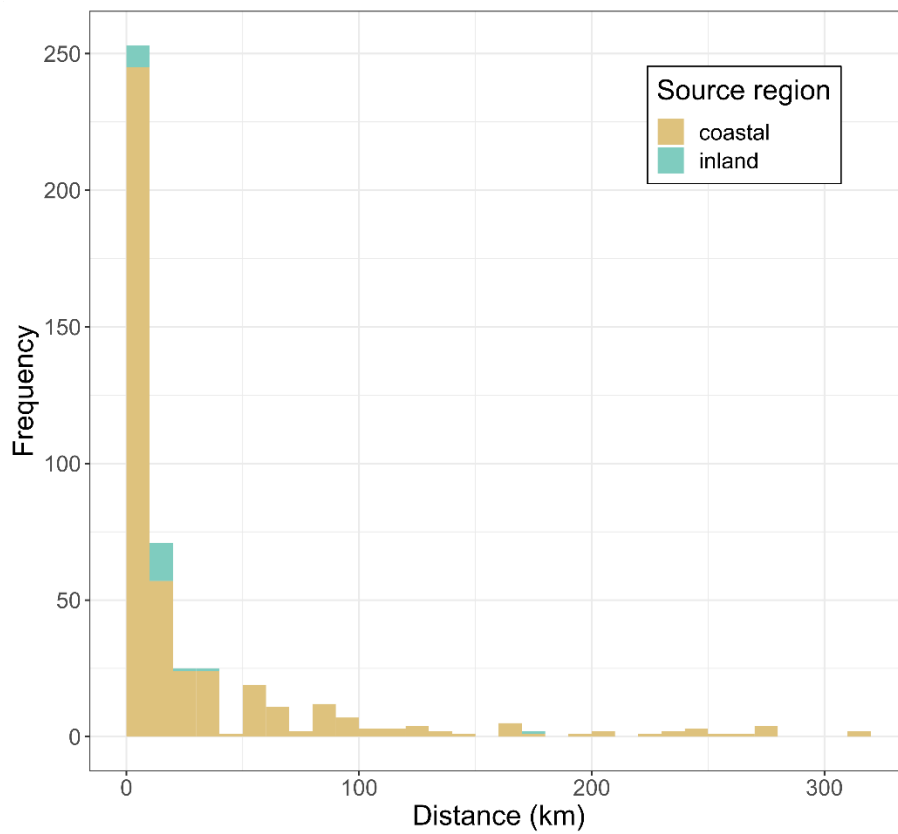


Figure S4: histogram of pairwise distances of genetic connections based on assignment tests, depicting an indirectly derived dispersal kernel. Colors depict source population with coastal Flanders and coastal France combined together in the coastal region.