

Conservation Genetics of *M. margaritifera* in Brittany and Normandy - preliminary results



Jürgen Geist

Bernhard Gum

Ralph Kuehn



geist@wzw.tum.de

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Genetics of FPM populations in Brittany and Normandie

❖ **Methods**

Haemolymph sampling, DNA extraction, microsatellite genotyping, statistical analysis



❖ **Preliminary results**

Genetic diversity (H_e , H_o , allelic richness, private alleles)

Genetic differentiation and population structure

❖ **Summary**

Conservation prioritisation – priority populations for recovery

Management strategies for captive breeding



6 populations, 135 individuals

Sampling 2011

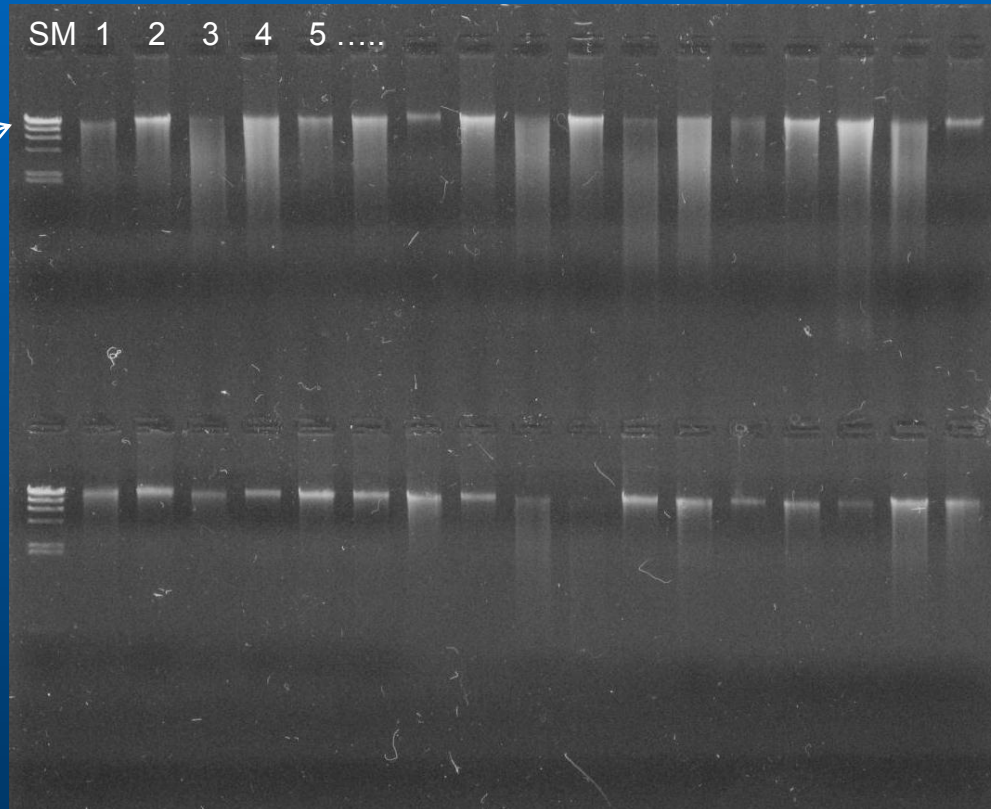
POP	Code	N	GPS	
			N	W
ELEZ	EL	25	N 48 ° 20.305	W 03 ° 49.096
LOC'H	LO	25	N 48 ° 21.982	W 03 ° 15.980
BONNE CHERE BC		25	N 48 ° 03.790	W 03 ° 07.540
AIROU	AI	18	N 48 ° 53.871	W 01 ° 23.236
ROUVRE	RV	16	N 48 ° 49.024	W 00° 23.509
SARTHON	SO	26	N 48 ° 28.991	W 00 ° 02.783`



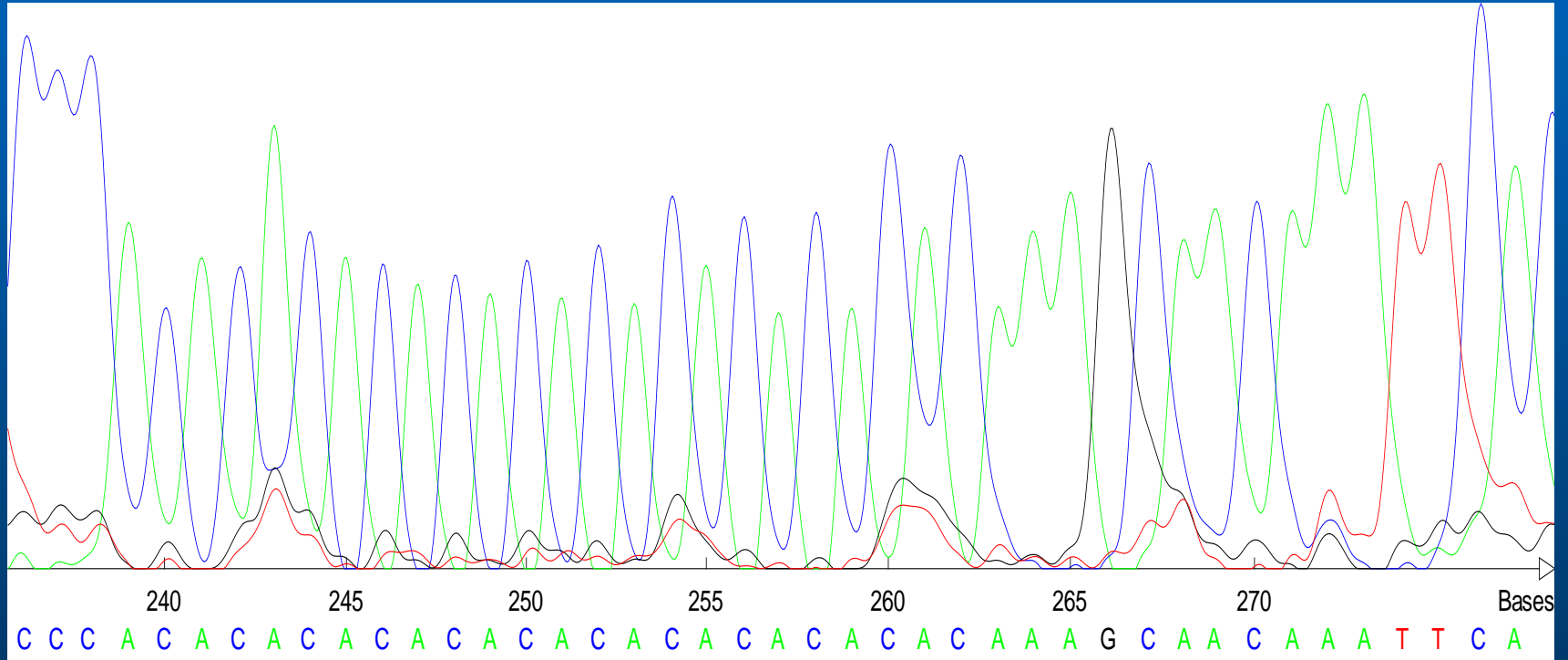
DNA-preparation of 34 haemolymph samples from populations Loc`h / Airou (0.8 % Agarose-Gel)

SM = Size Marker

20 kb



Methodology: Microsatellites (SSR, STR)



Genotyping of Microsatellites (SSR, STR)

1. PCR with specific primers
2. Genotyping on automated sequencer



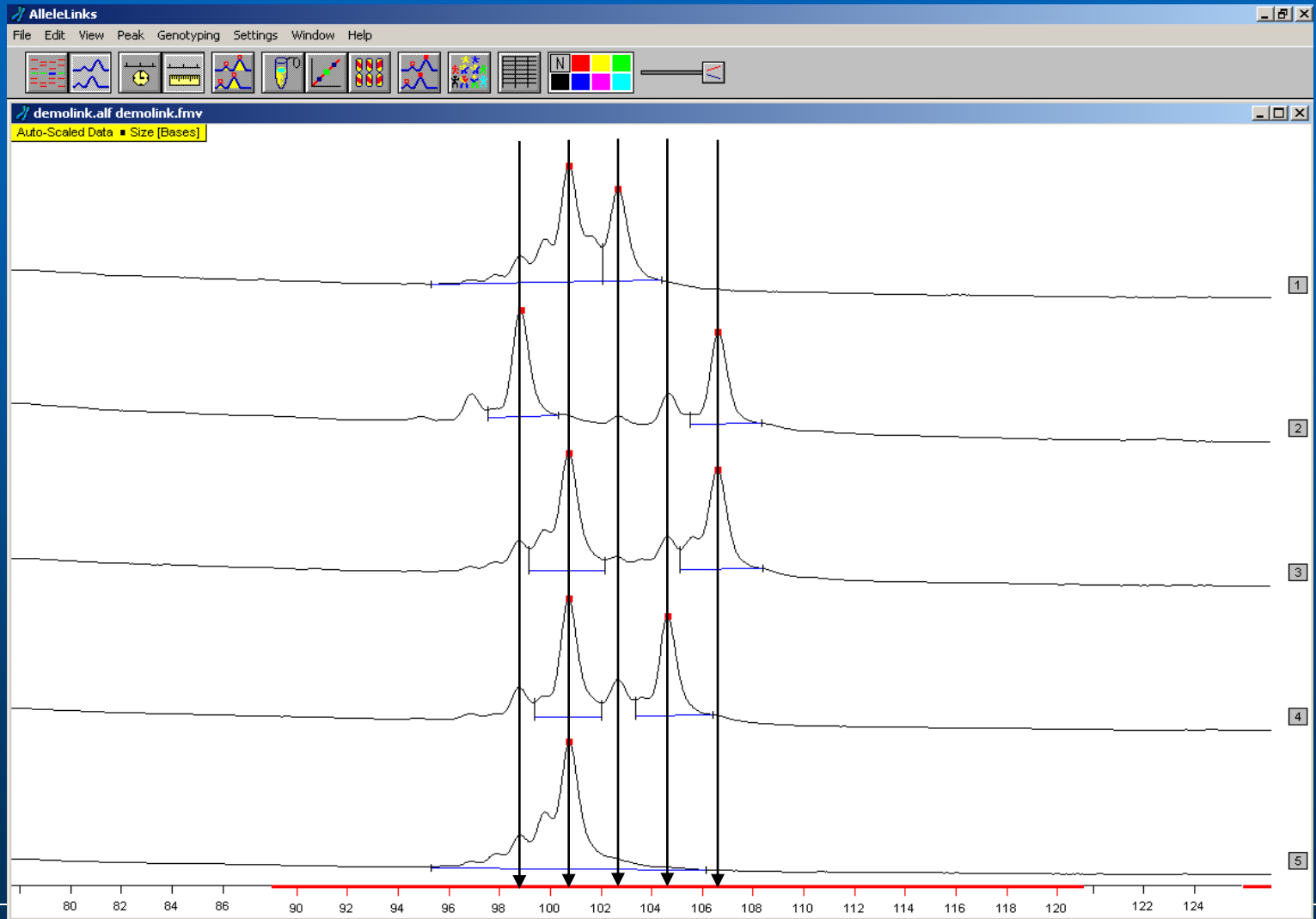
Animal 1, homozygous:

...ACTGCTGATCGATG CACACACACACACACACACACACAGTGTGTCGCTAGC....
 ...ACTGCTGATCGATG CACACACACACACACACACACACAGTGTGTCGCTAGC....

Animal 2, heterozygous:

...ACTGCTGATCGATG CACACACACACACACACACACACAGTGTGTCGCTAGC....
 ...ACTGCTGATCGATG CACACACACACACACACAGTGTGTCGCTAGC....





Parameters of genetic diversity

Expected & observed heterozygosity (H_e , H_o), allelic richness (AR), private alleles

Population	Sample size	Loci typed	H_e	H_o	Average No alleles	AR	Private alleles (% frequency)
Elez	25	9	0,018	0,009	1,33	1,24	2 (2,0; 4,0)
Loc'h	25	9	0,164	0,049	1,78	1,70	2 (2,0; 4,0)
Bonne Chere	25	9	0,095	0,063	1,56	1,54	2 (28,0; 96,0)
Sarthon	26	9	0,073	0,017	1,56	1,45	1 (88,5)
Airou	18	9	0,174	0,049	2,00	1,96	1 (2,8)
Rouvre	16	9	0,123	0,035	1,89	1,89	2 (87,5; 3,1)
Elez (2004)	29	9	0,004	0,004	1,11	1,06	
Loc'h (2004)	23	9	0,199	0,092	1,67	1,63	1 (6,5)

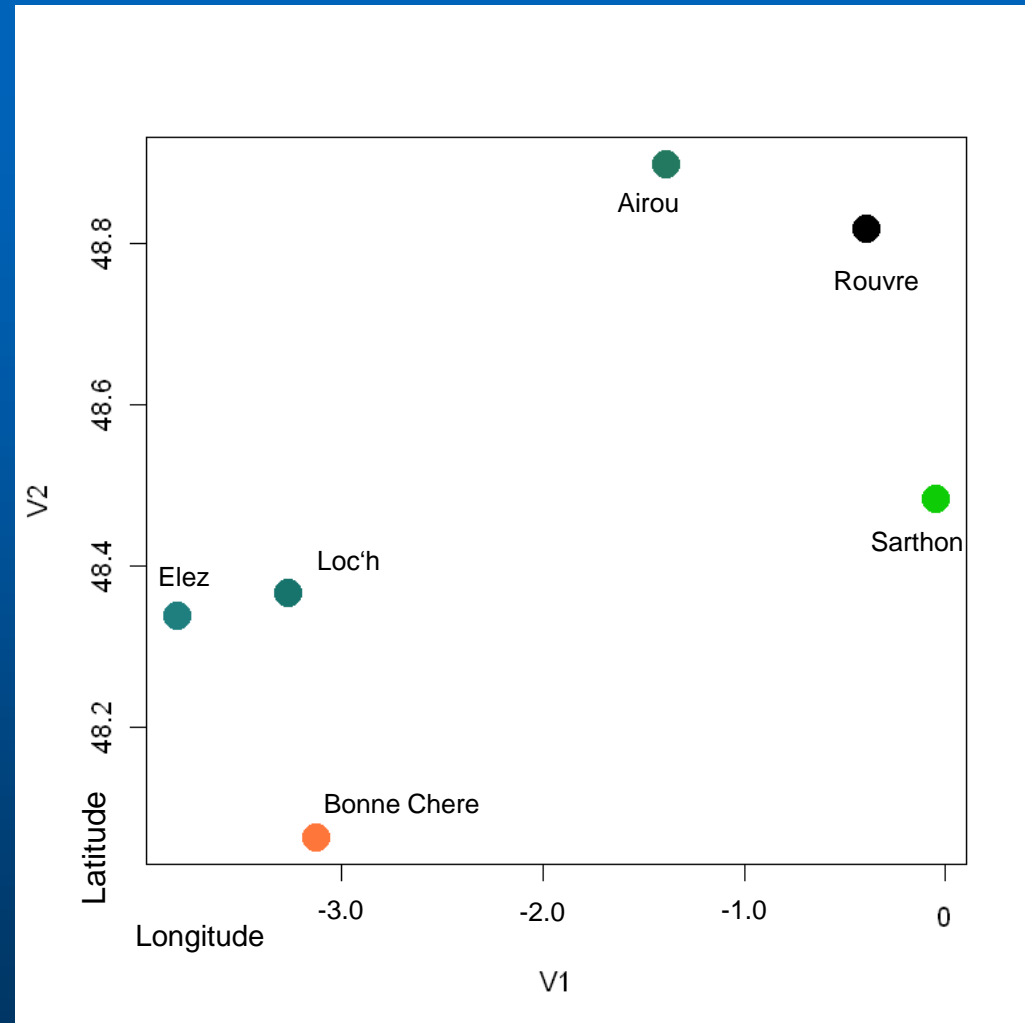
Discriminant analysis of the principle components (DAPC)

on the basis of genotypes for populations and individuals

→ Detection of gene flow/differentiation

= **basis for management strategies**

- population recovery
- captive breeding



Transition between colours
represents degree of relatedness

Genetic differentiation between and within populations

Discriminant analysis of the principle components (DAPC) using genotypes for:

→ detection of gene flow/differentiation

between populations

= *basis for management strategies*

- conservation priorities
- population recovery

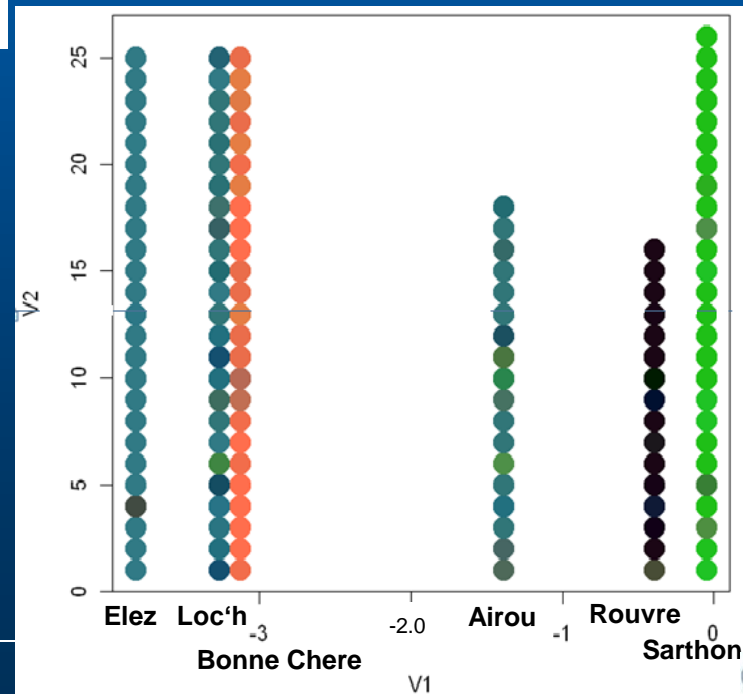
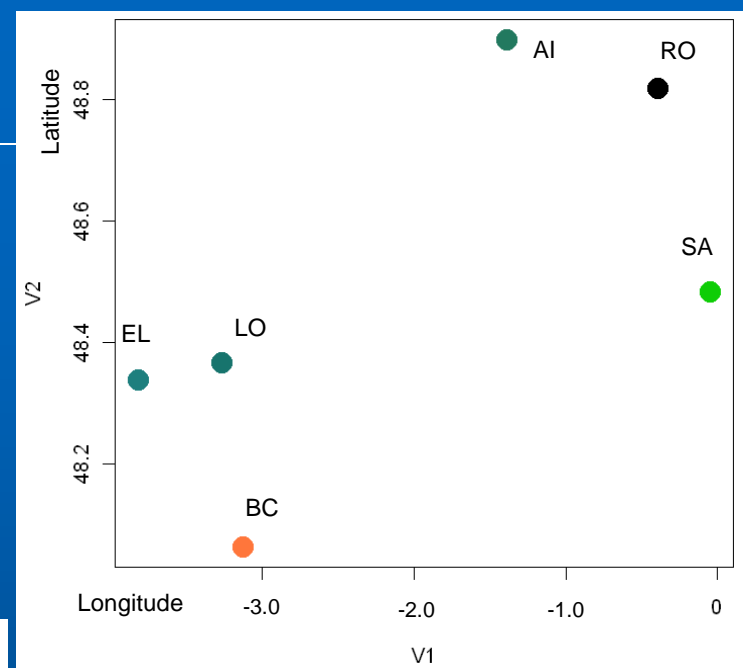
Transition between colours represents degree of relatedness

→ detection of individual genetic composition

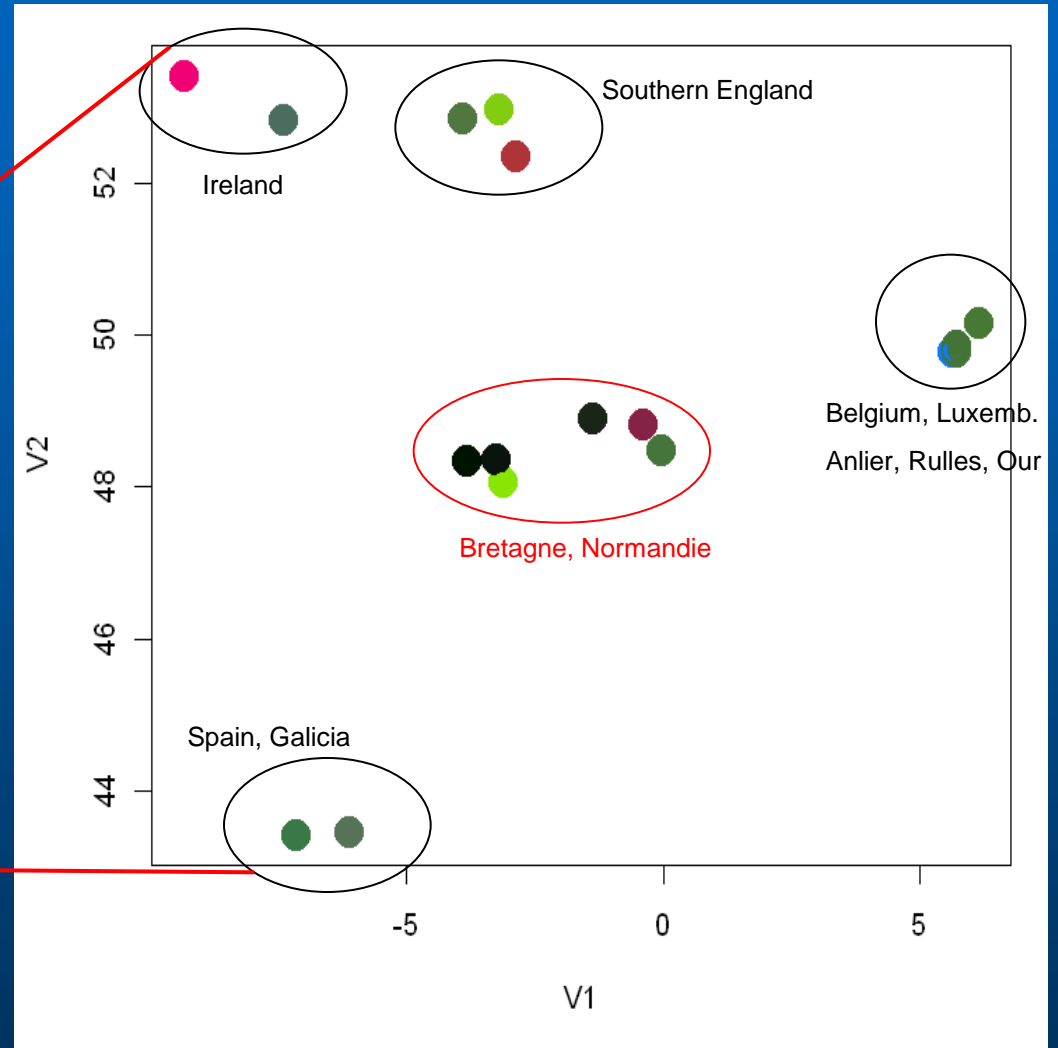
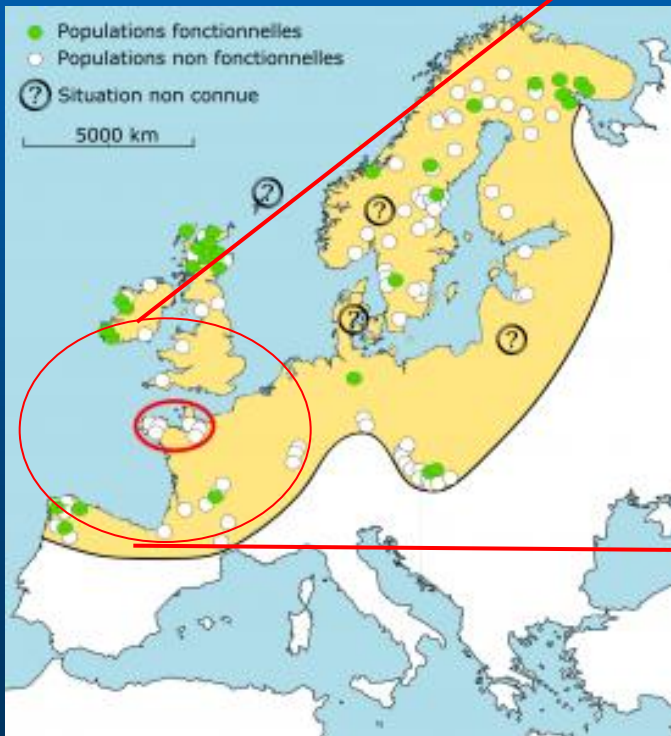
within populations / individuals

= *basis for management strategies*

- breeding strategies



Relatedness of gene pools in the west European distribution area of FPM populations (9 loci)



- Moderate to low level of genetic diversity (H_e , allelic richness)
- Degree of genetic differentiation does not strictly fit to drainage - or connected rivers systems („discrete gene pools“)
- Relative close relatedness of Elez, Loc'h and Airou
- High frequency of private alleles (> 80 %) in 3 populations:
Bonne Chere, Rouvre, Sarthon
- High level of genetic drift / highly restricted gene flow between subpopulations probably as a result of population breakdown, extremely low census population sizes, hermaphroditism, ...

Conservation genetics is needed for establishment of sound and sustainable management strategies and decision making

- identification of priority populations, population recovery, development of captive breeding strategies



Thank you for your attention

