

ESTIMATES OF GENETIC VARIABILITY AND INBREEDING IN SELECTED POPULATIONS OF EUROPEAN SEA BASS

JASMIEN HILLEN

& CARR A, HELLEMANS B, OGDEN R, TAGGART J,
VANDEPUTTE M, VERGNET A, VOLCKAERT FAM,
AQUATRACE CONSORTIUM, COSCIA I



KU LEUVEN



INBREEDING AND LOSS OF GENETIC DIVERSITY IN AQUACULTURE

Artificial selection



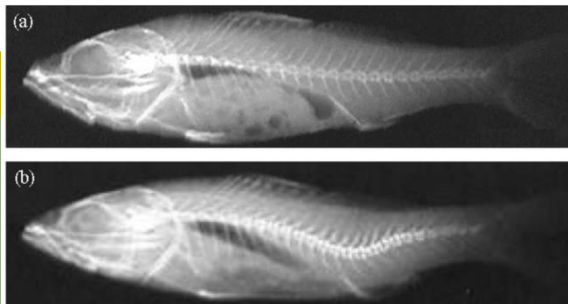
Growth,
Morphology,
Disease resistance



Reduces genetic variability

Inbreeding

Physical & developmental abnormalities, metabolic deficiencies ...



Kayim et al. 2010

RESEARCH QUESTIONS

- Does inbreeding increase over a few generations of selective breeding?
- Does genetic diversity within lines decrease over a few generations of selective breeding?

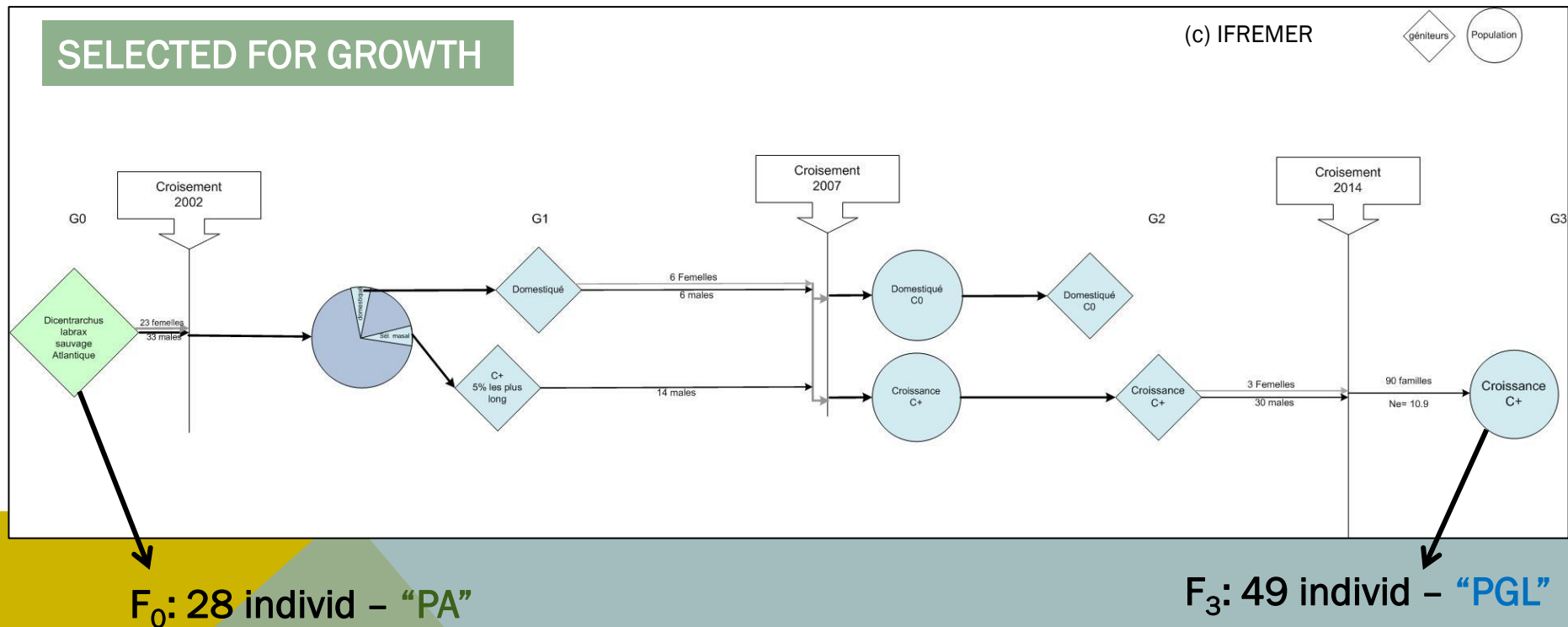
SAMPLING

- European sea bass (*Dicentrarchus labrax*)
- IFREMER experimental farm (Palavas-les-Flots, France)
- 2 lines : one selected for growth and one selected for resistance to starvation



SAMPLING

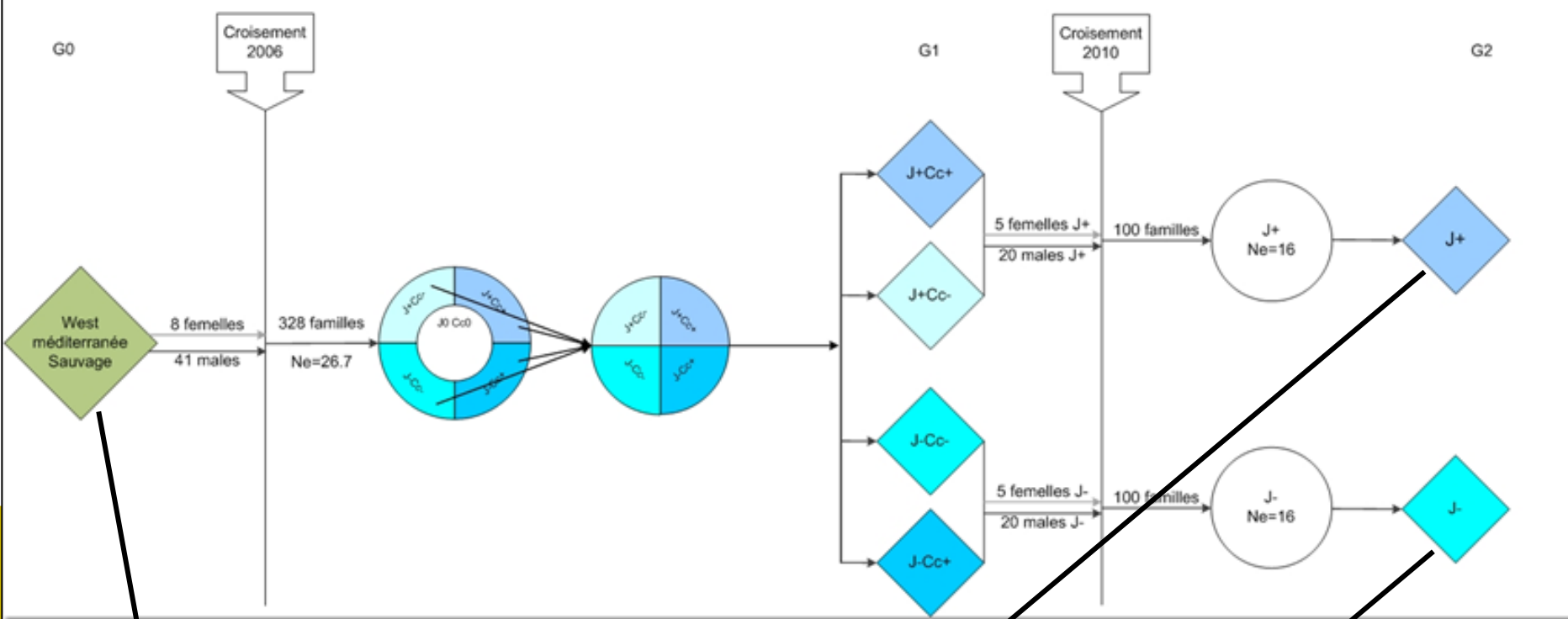
- IFREMER experimental farm (Palavas-les-Flots, France)
- 2 lines : one selected for growth and one selected for resistance to starvation



SAMPLING

- IFREMER experimental farm (Palavas-les-Flots, France)
- 2 lines : one selected for growth and one selected for resistance to

SELECTED FOR RESISTANCE TO STARVATION

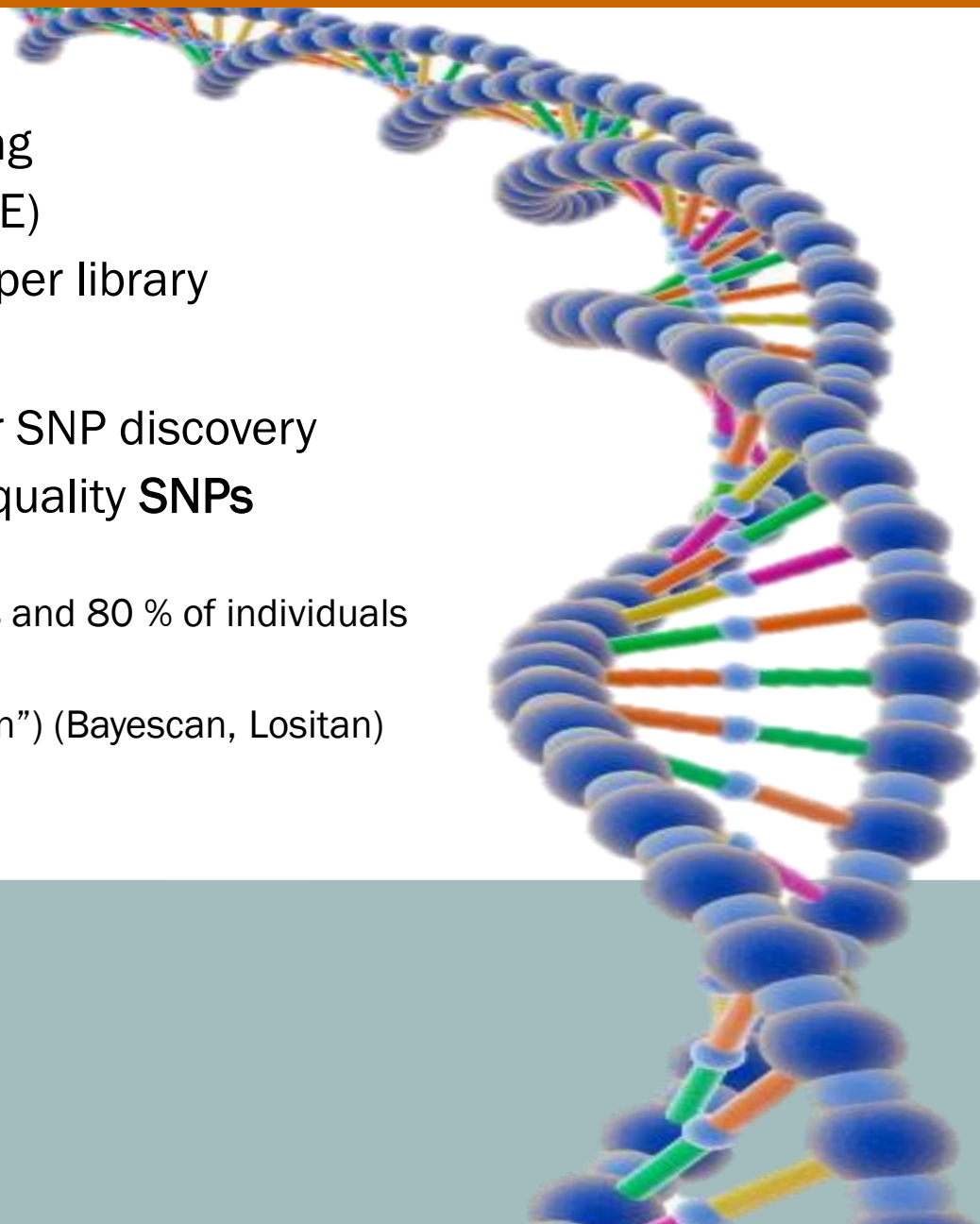


F_0 : 19 individ - "PM"

F_2 : 28 individ - "PSP"

F_2 : 35 individ - "PSN"

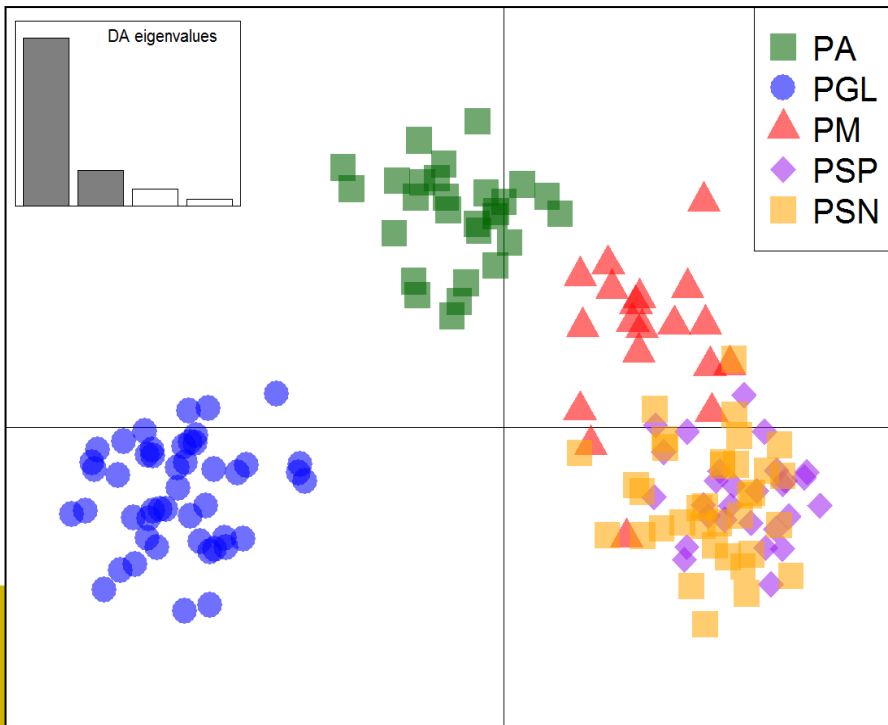
- Next generation sequencing
 - **ddRAD** sequencing (2 RE)
 - pooled 144 individuals per library
- Bioinformatics: STACKS for SNP discovery
 - after filtering **200** high quality **SNPs**
 - 1 SNP per tag
 - SNPs present in all pops and 80 % of individuals
 - maf 2.5 %
 - outliers (“under selection”) (Bayescan, Lositan)



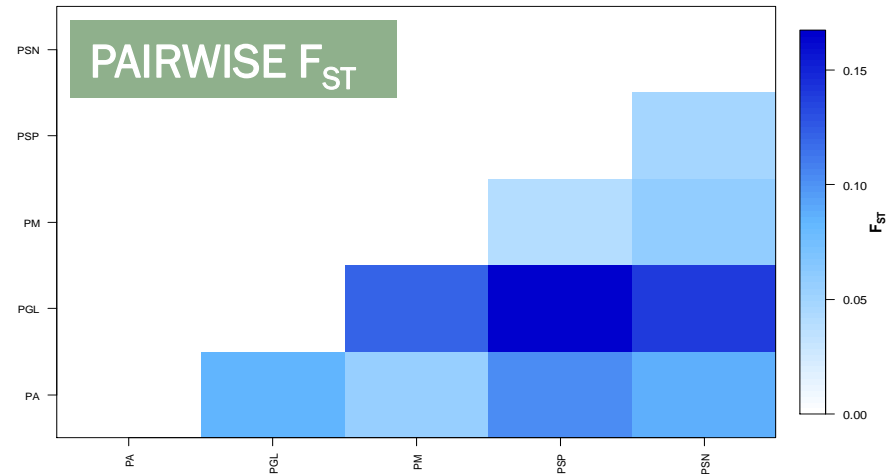
GENETIC DIFFERENTIATION

- All pairwise F_{st} estimates are significant ($p=0.0000$)
- ATL (growth line) and MED (starvation line) are most differentiated

DAPC



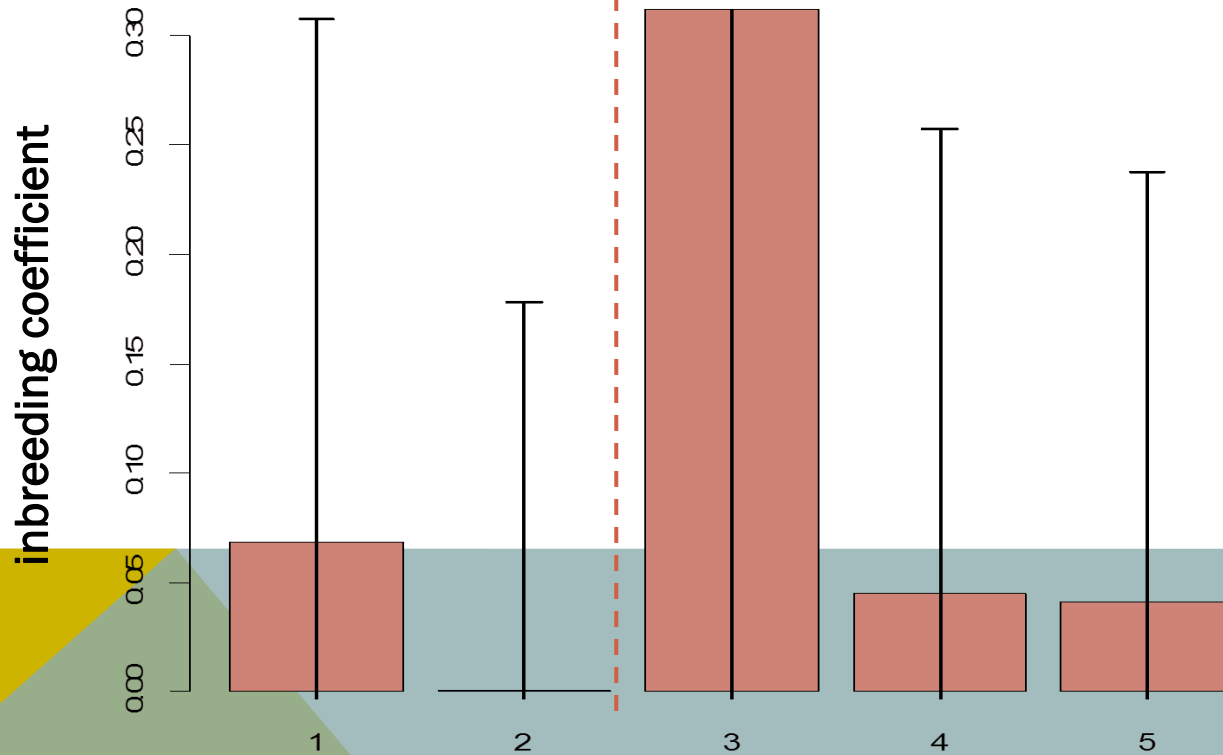
Matrix of pairwise F_{ST}



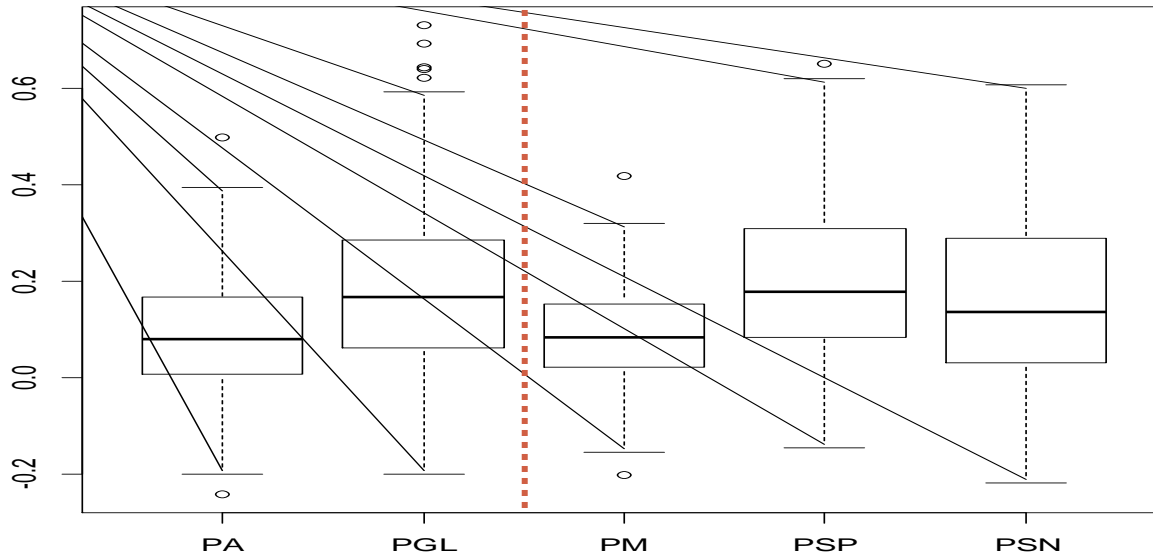
PSP					0.047
PM				0.042	0.060
PGL			0.122	0.167	0.141
PA	0	0.084	0.057	0.104	0.089
	PA	PGL	PM	PSP	PSN
	F0	F3	F0	F2	F2
	Growth line		Starvation line		

INBREEDING

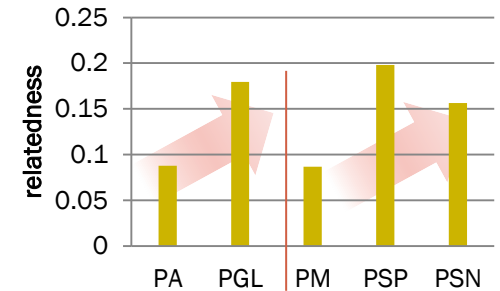
INBREEDING ESTIMATES (Fis)				
GROWTH LINE		STARVATION LINE		
F ₀	F ₃	F ₀	F ₂ (+)	F ₂ (-)
PA (1)	PGL (2)	PM (3)	PSP (4)	PSN (5)
0.0682	0.0009	0.3119	0.0447	0.0412



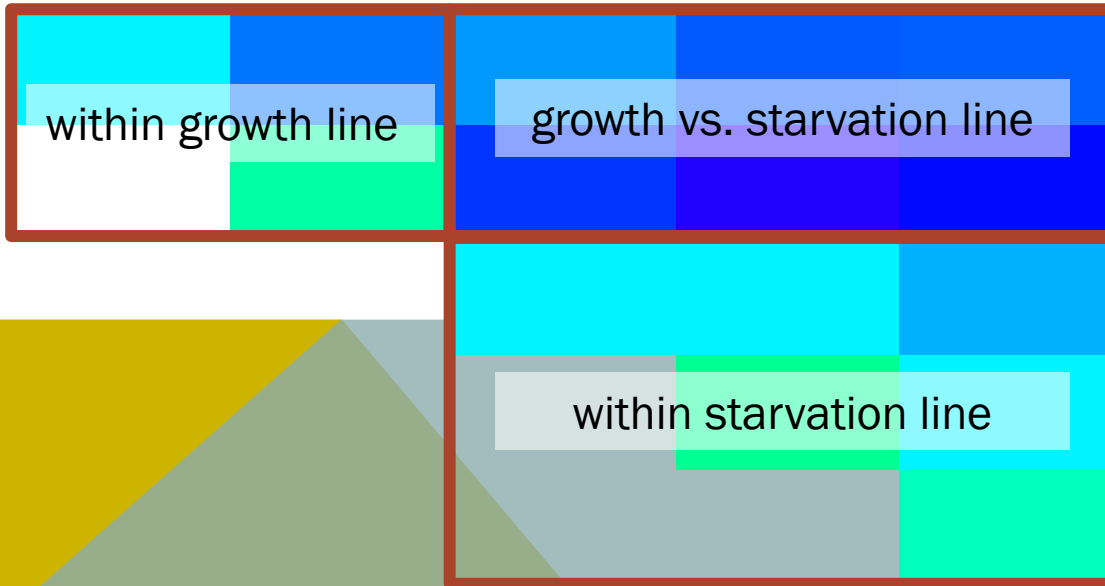
RELATEDNESS



- Average of pairwise relatedness coefficients (r) (Queller & Goodnight 1989)
- Increase average r over generations

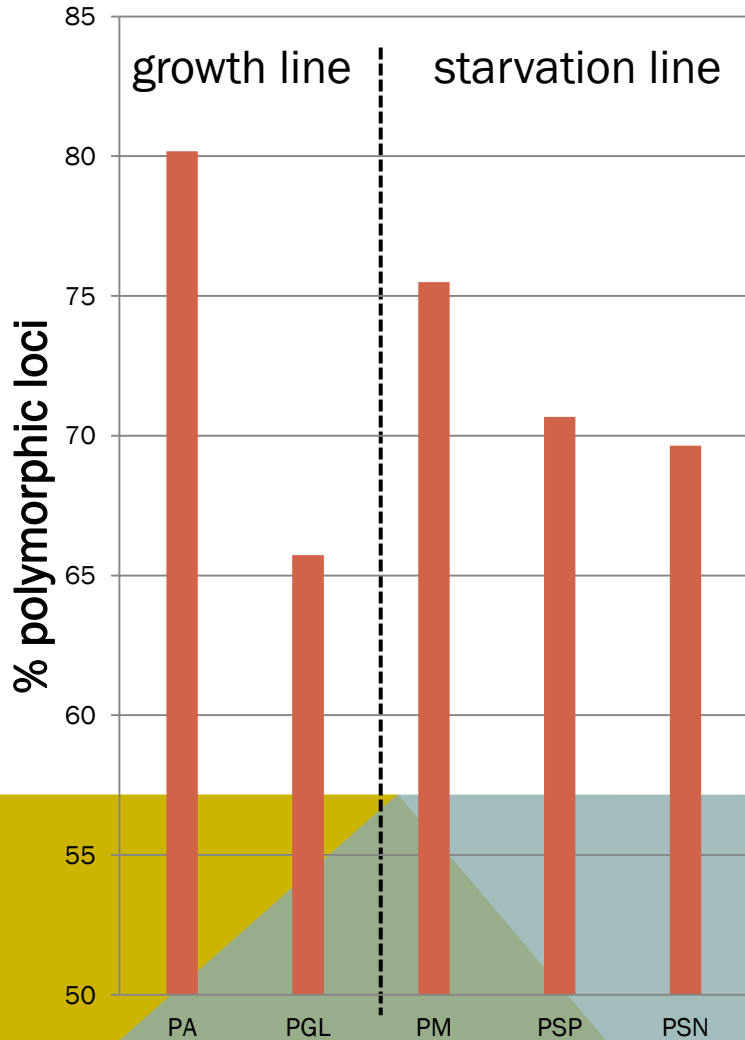


- Significant differences between F_0 and F_2 or F_3

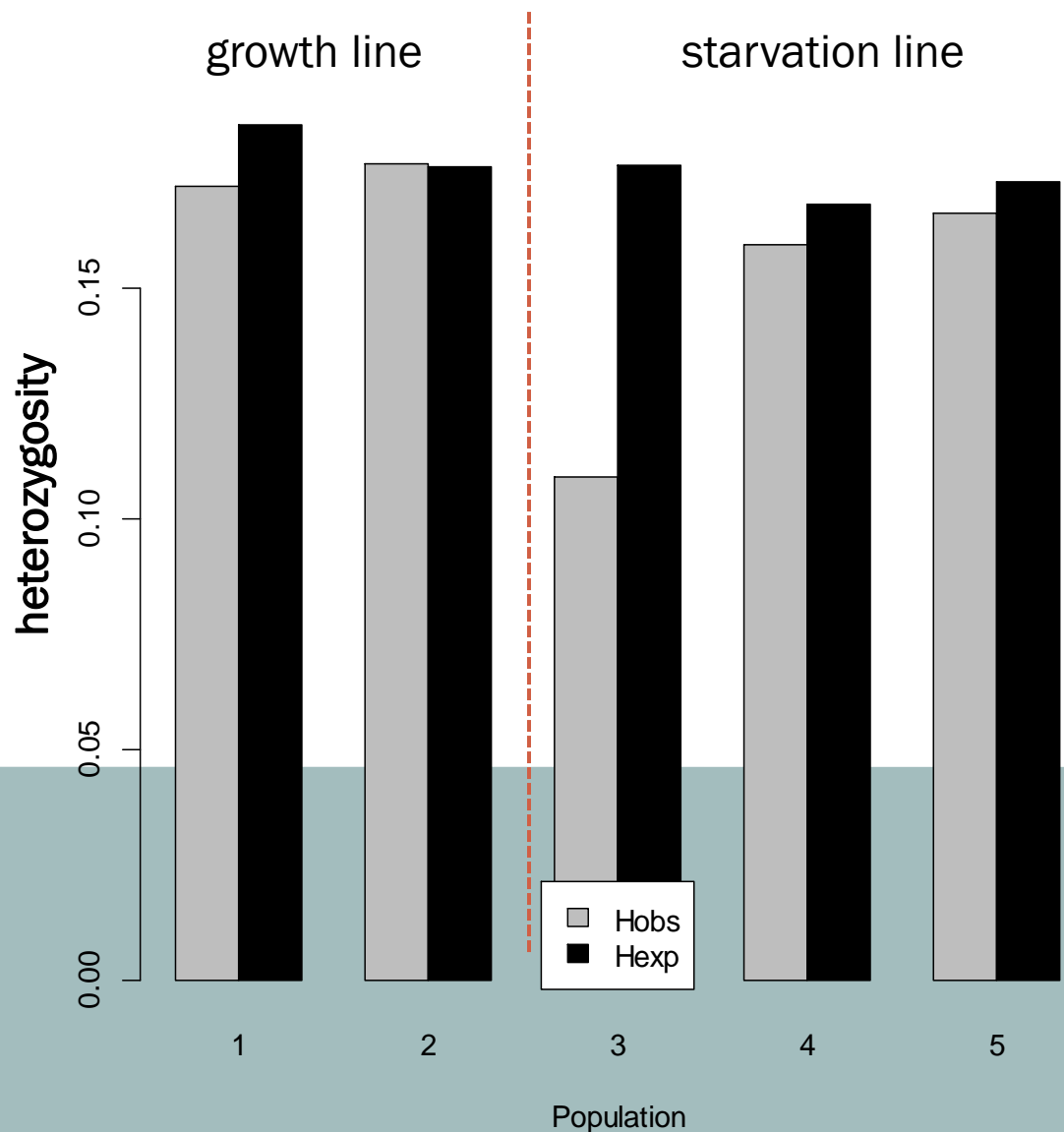


GENETIC DIVERSITY

% polymorphic loci

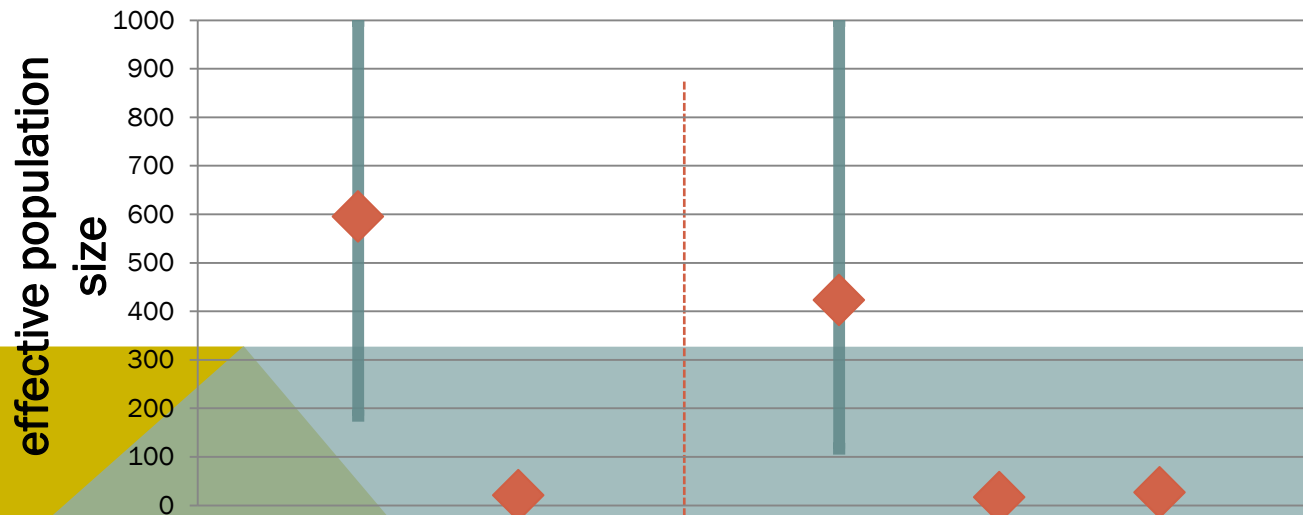


expected and observed heterozygosities



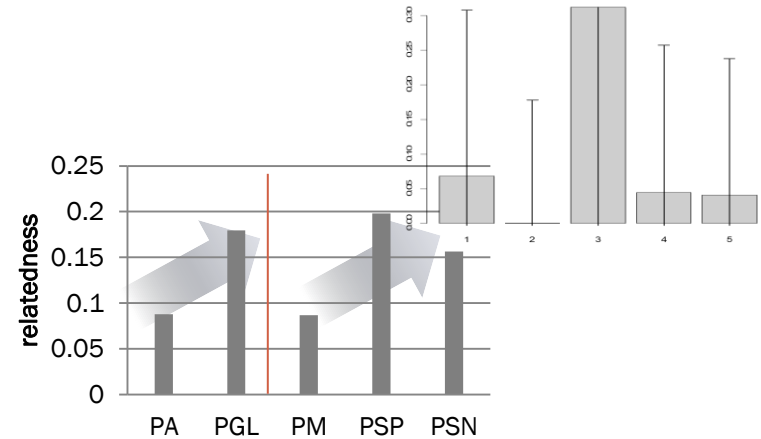
EFFECTIVE POPULATION SIZE

EFFECTIVE POPULATION SIZE (N_e)				
LINE 1 (ATL – GROWTH)		LINE 2 (MED – STARVATION)		
F_0	F_3	F_0	$F_2(+)$	$F_2(-)$
PA	PGL	PM	PSP	PSN
594	21	423	16	26
(185-∞)	(19-23)	(117-∞)	(15-18)	(23-30)



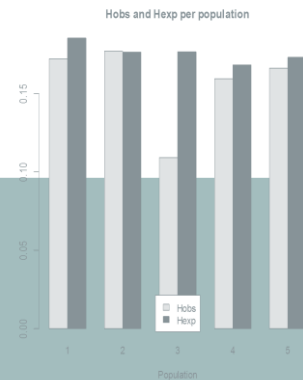
○ Does inbreeding increase over a few generations of selective breeding?

- NO increase in inbreeding coefficient found
- preliminary results
- Increase in the relatedness & decrease in N_e



○ Does genetic diversity within lines decrease over a few generations of selective breeding?

- NO decrease in heterozygosity
- Decrease in % polymorphic loci in the growth line



THANKS!

JASMIEN HILLEN

iWT

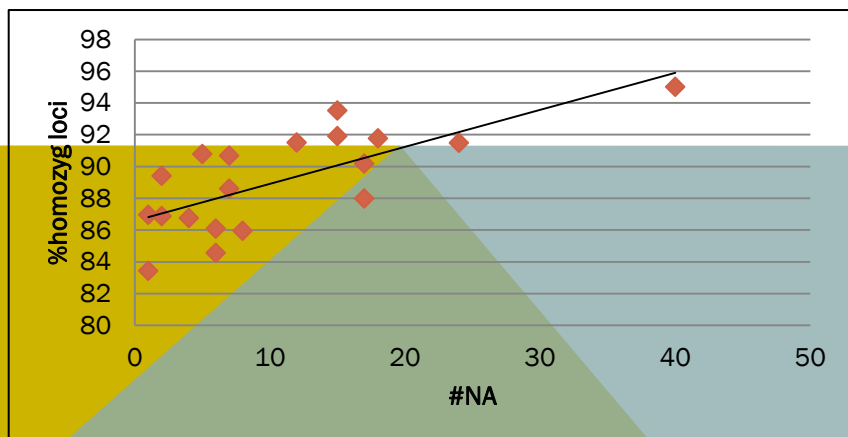
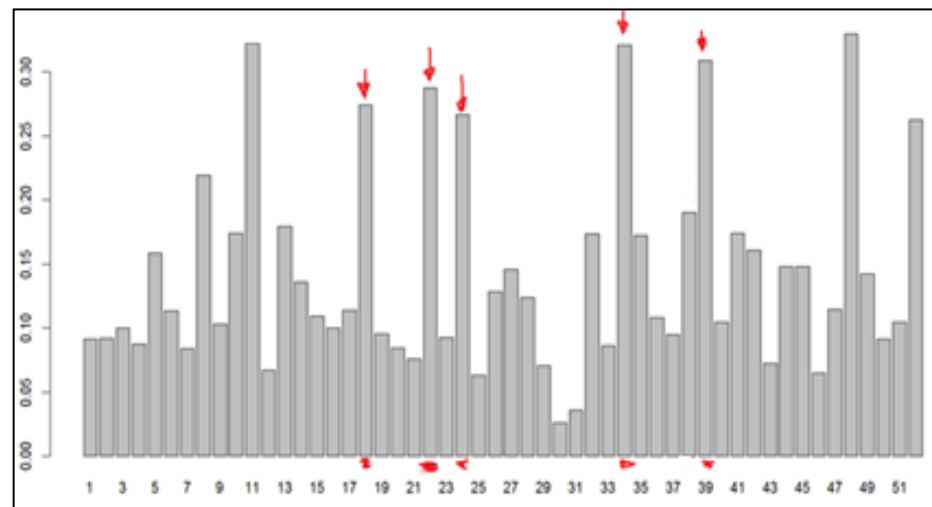
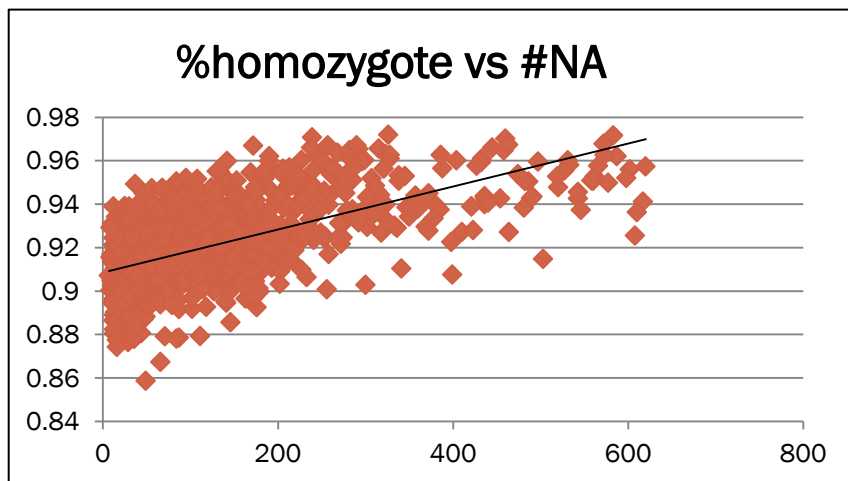
KU LEUVEN

 aquatrace

INTERLIBRARY VARIABILITY

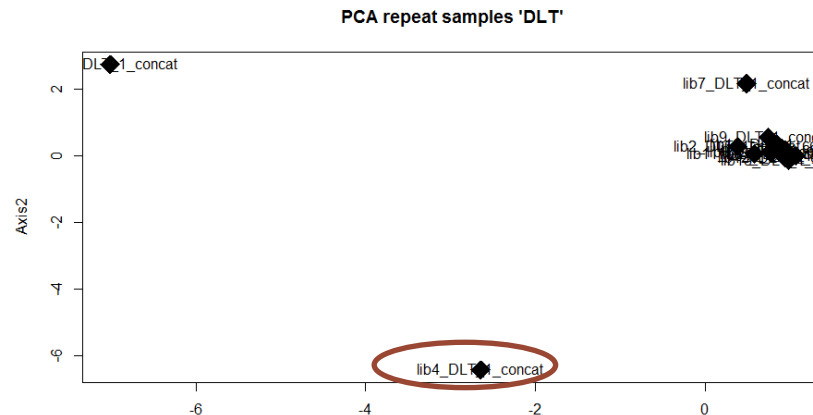
High inbreeding values in the broodstock population of line 2 are difficult to explain

- groups (populations) were sequenced in different libraries
- something odd about this library
- no substructure



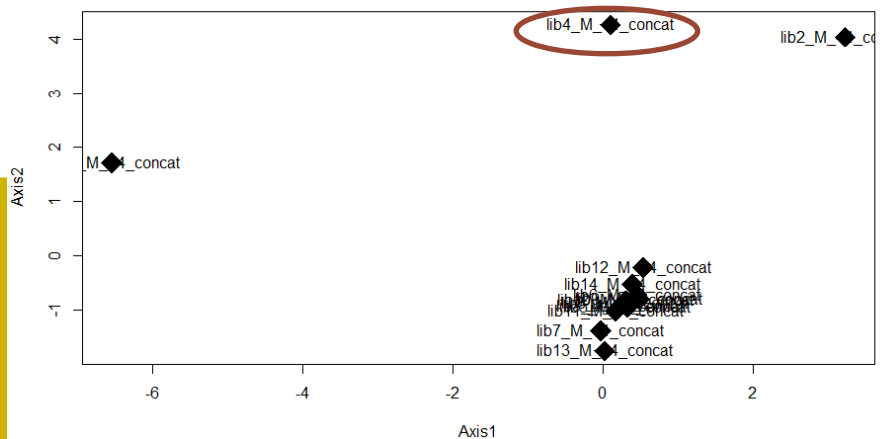
INTERLIBRARY VARIABILITY

- 3 identical samples were included in all libraries
- PCA: library 4 is an outlier

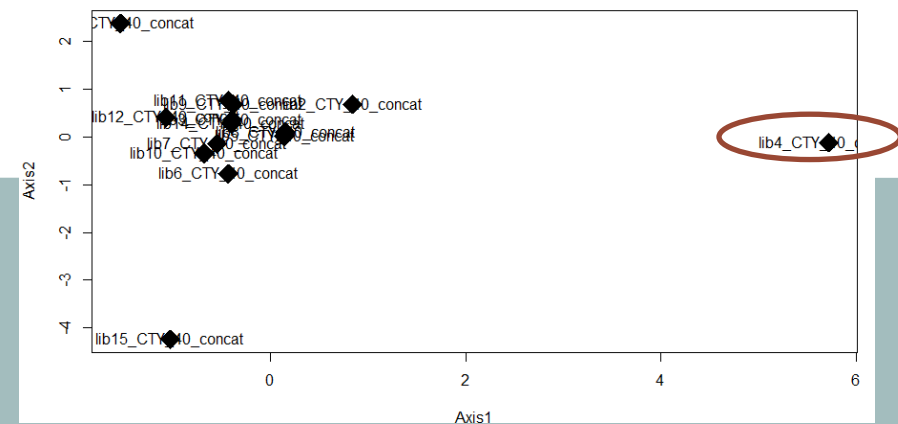


Observed levels of homozygosity are library specific and thus an ARTEFACT

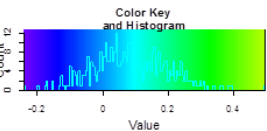
PCA repeat samples 'M'



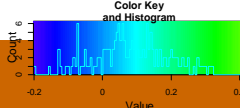
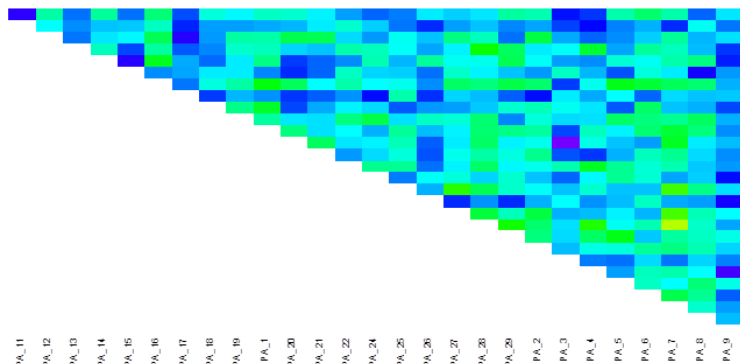
PCA repeat samples 'CTY'



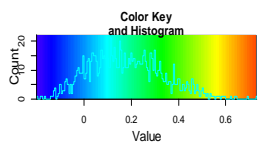
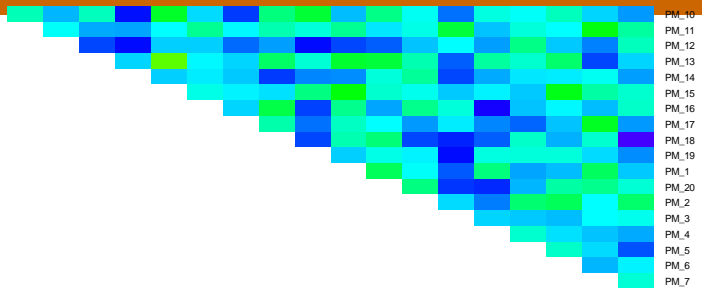
RELATEDNESS



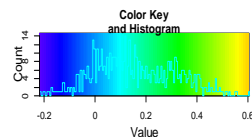
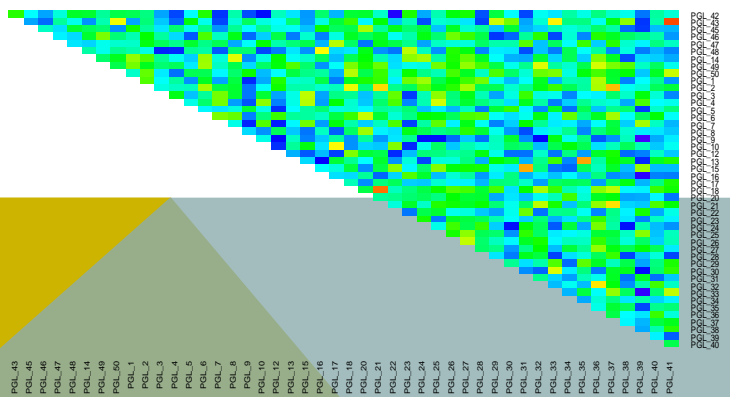
PA



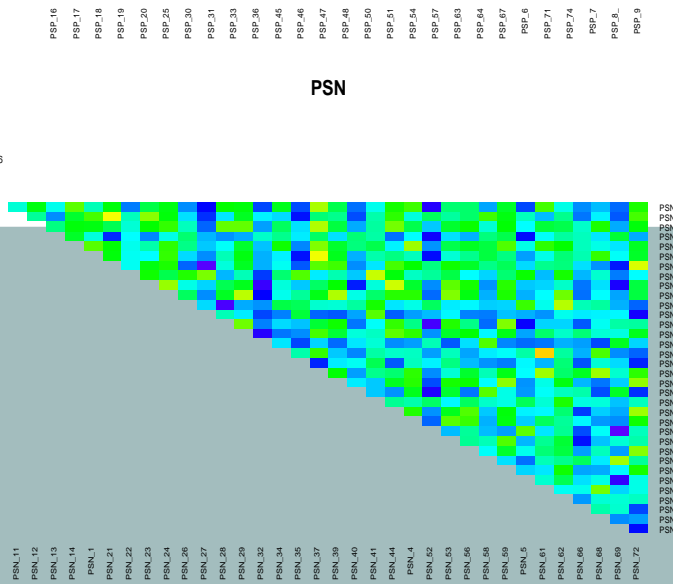
PM



PGL



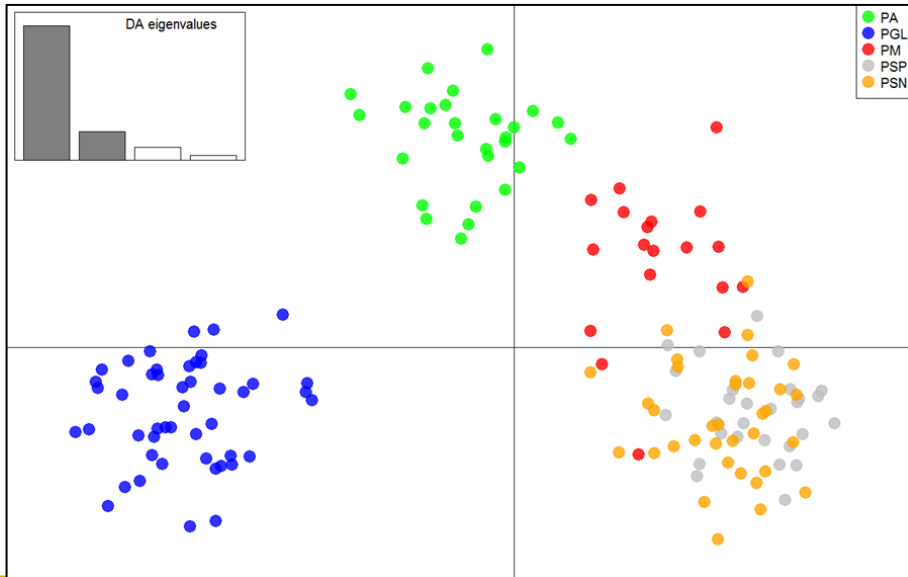
PSN



GENETIC DIFFERENTIATION

- All pairwise F_{st} estimates are significant ($p=0.0000$)
- ATL (line 1) and MED (line 2) are most differentiated

DAPC



Roger's Euclidean genetic distance

			PA	PGL	PM	PSP	PSN
line 1	F ₀	PA	0				
	F ₃	PGL	0.09563048				
line 2	F ₀	PM	0.09377498	0.12770844			
	F ₂	PSP	0.11530849	0.1453126	0.07295516		
	F ₂	PSN	0.10711473	0.1422888	0.08756016	0.077067	0

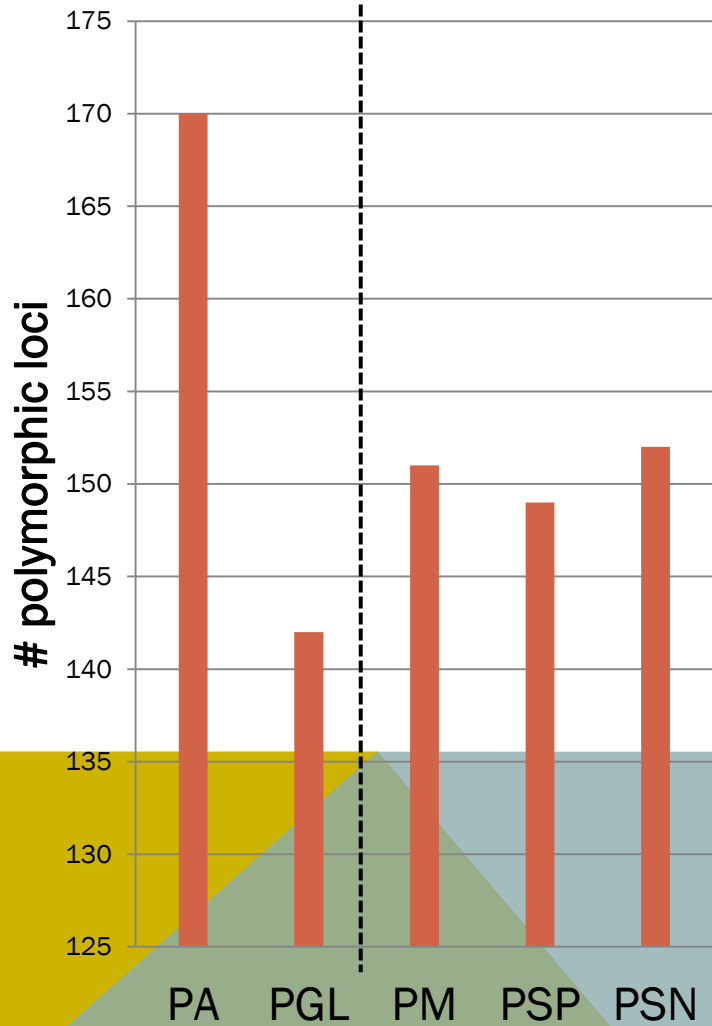
SUMMARY & TAKE HOME

- question 2

- with increasing number of selective breeding programs, it is important to assess inbreeding, genetic diversity and effective population size
- Be careful when considering results of next gen sequencing → library effects! → here clear effect on homozygosity → (or heterozygosity) measures lay at the basis of nearly all population genetic measures ...

GENETIC DIVERSITY

polymorphic loci



INTRO - M&M - RESULTS - DISCUSSION

expected and observed heterozygosities

