

97th Annual Meeting of the National Shellfisheries Association

Microsatellite-based parentage
analysis of factorial crosses in
Pacific oyster (*Crassostrea gigas*)
larvae and spat

Nicolas Taris, Christopher Sauvage, Bruno Ernande, Pierre Boudry

Laboratoire IFREMER de Génétique et Pathologie, La Tremblade – France

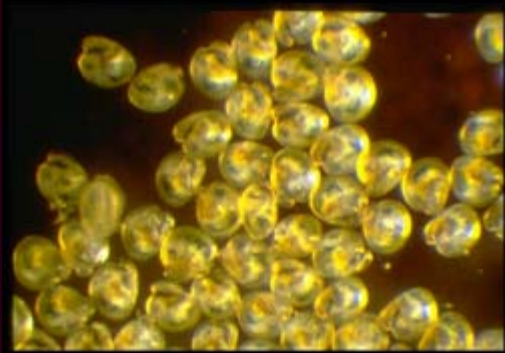


Two possible sources of oyster spat

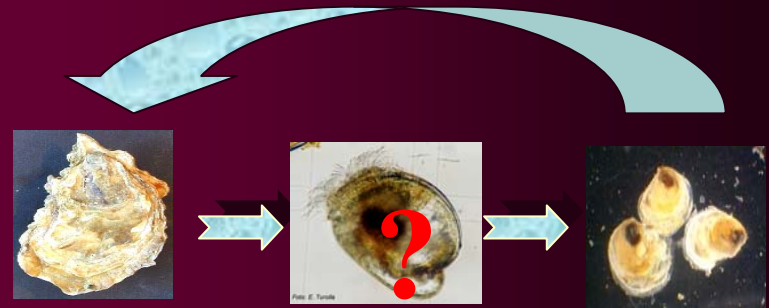
(1) natural settlement



(2) hatchery propagation



Is there selection (**domestication**) at early development stage in hatchery ?



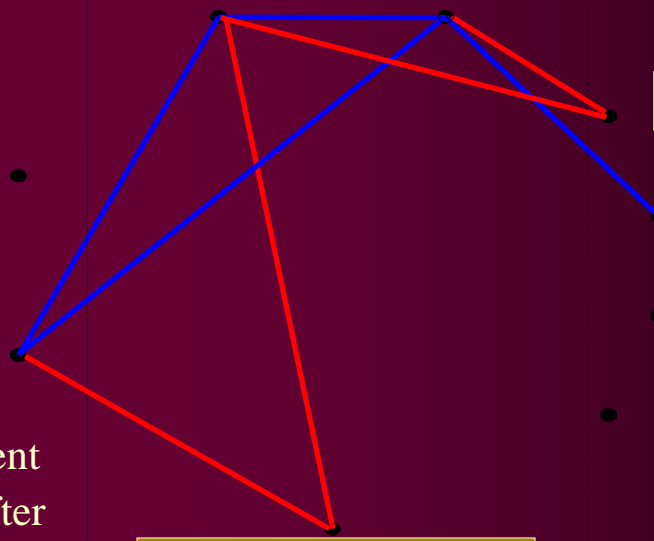
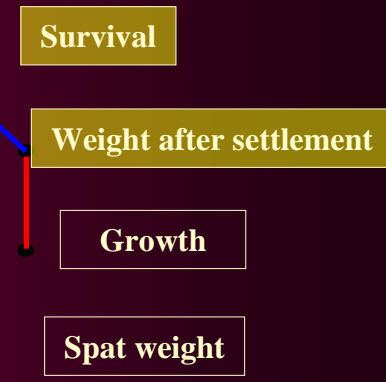
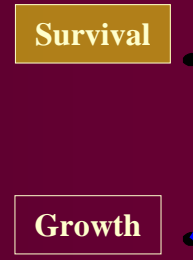
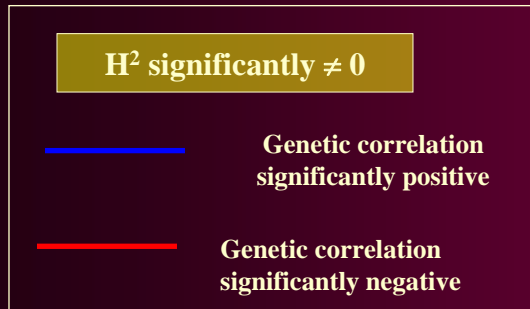
Genetic variability of early life traits

	1	2	3	4	5
1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
14					
15					

Larval traits

Metamorphic traits

Post-metamorphic traits

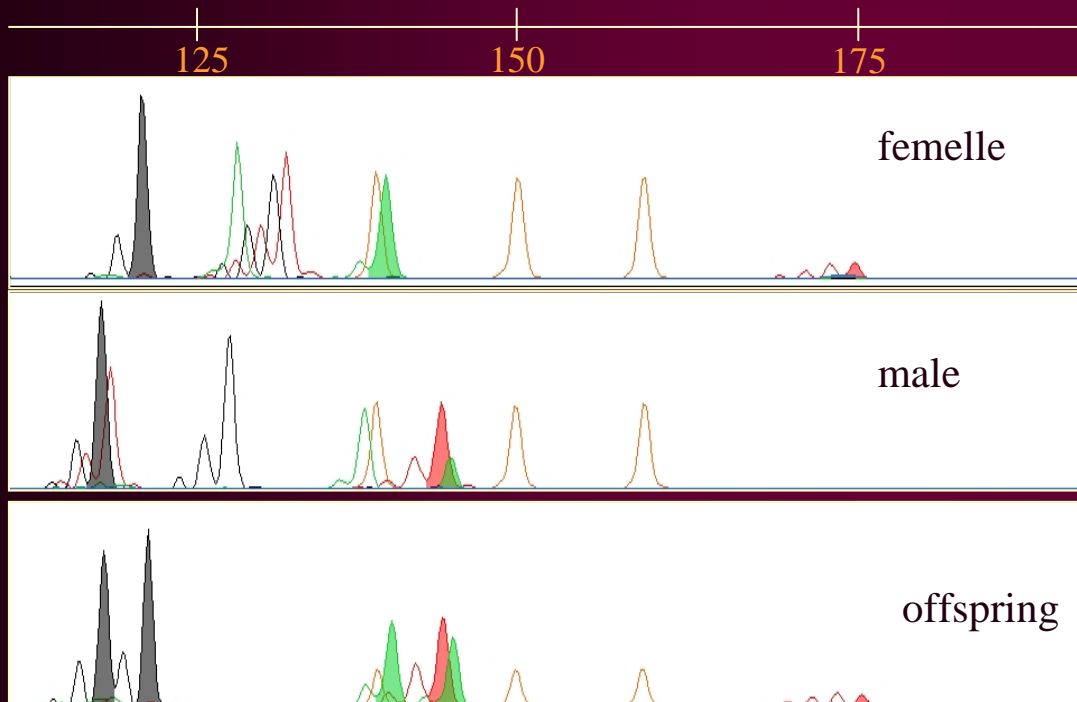


Two extreme «strategies» :

- High larval growth rate and larval size at settlement but low settlement success, growth and survival after settlement
- Lower larval growth rate and larval size at settlement but higher settlement success, growth and survival after settlement

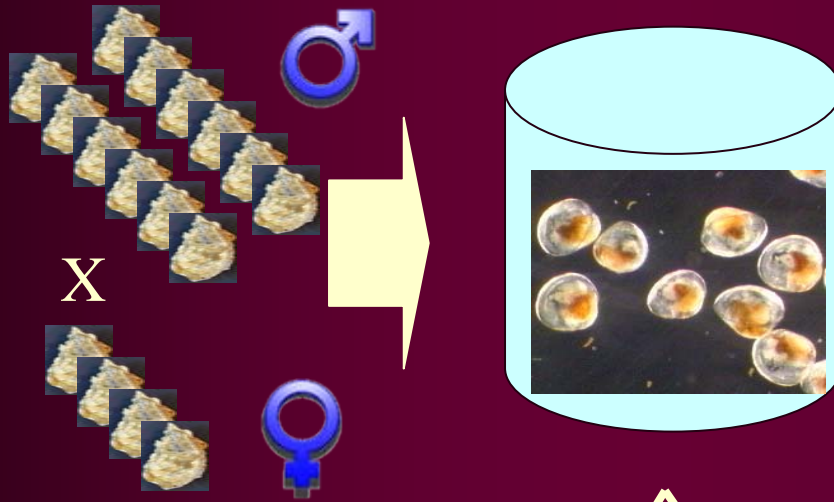
Mixed-family approach : microsatellite-based parentage analysis

One set of 3 PCR-multiplexed markers
Cg108 + Cg49 + L10

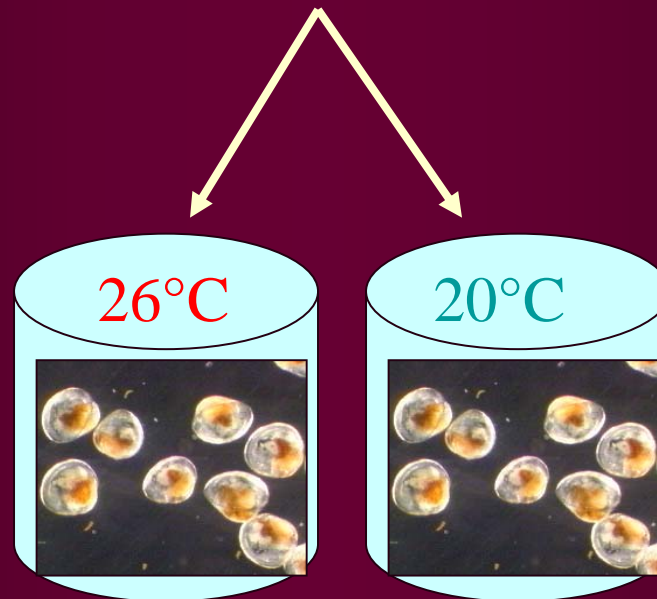


- More families
- Homogeneous rearing conditions
- G x E ?

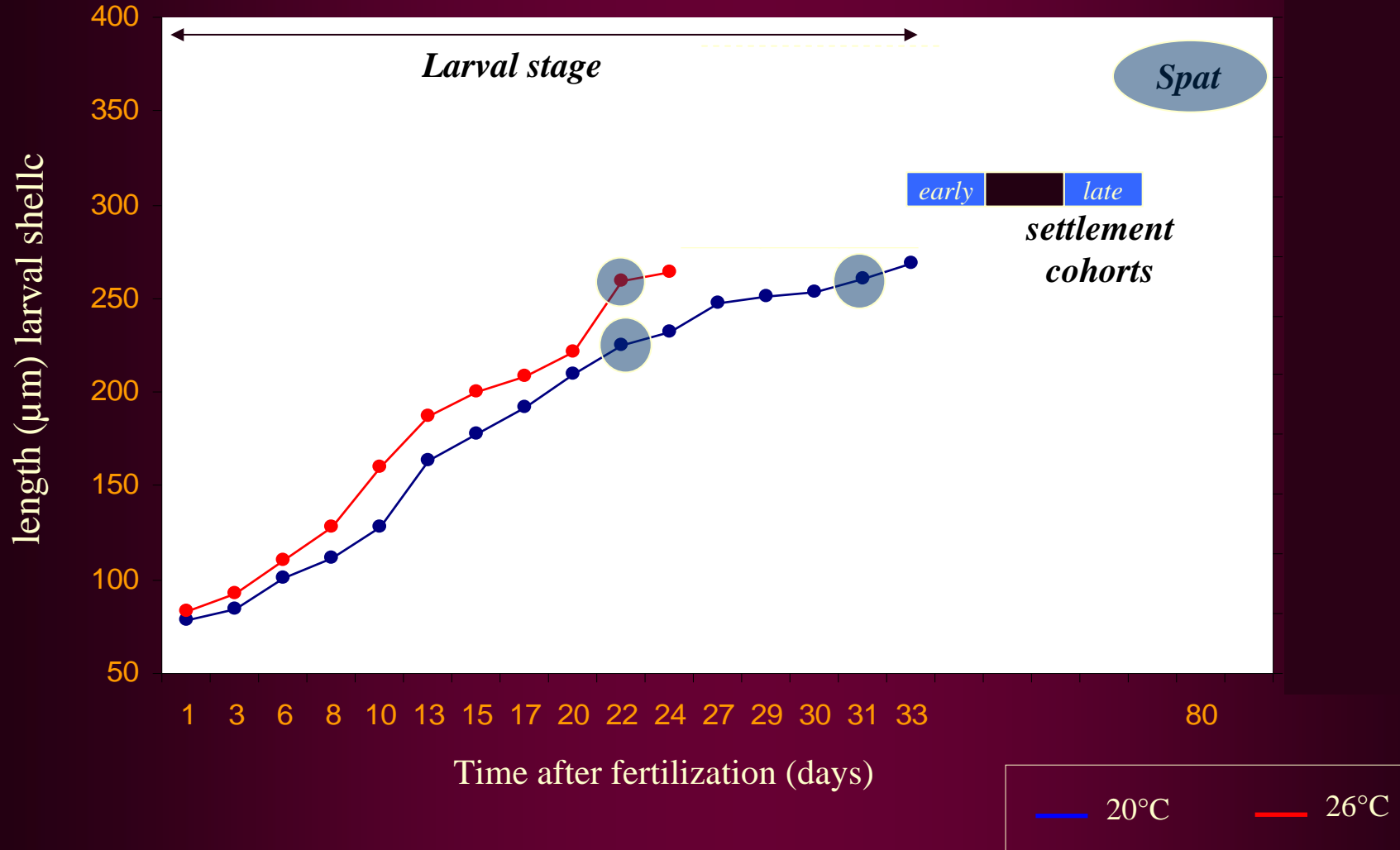
“Wild” versus “hatchery” conditions ?



4 females x 12 males cross



Phenotypic trend & sampling



Results

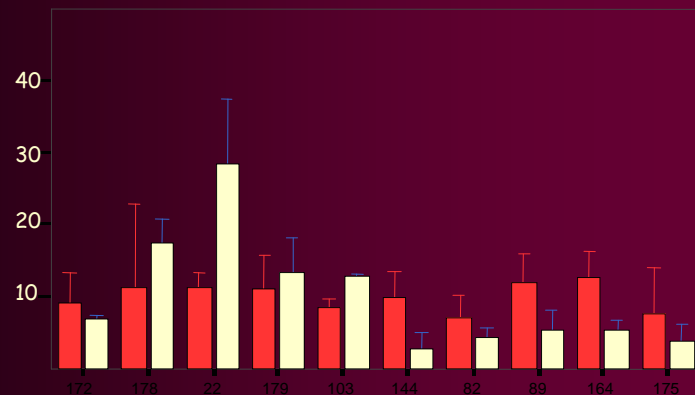
Studied traits based on individual larvae assignment data

A Parental contributions

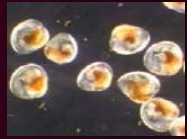
SAS macro Glimmix
Littell et al., 1996

B Larval growth

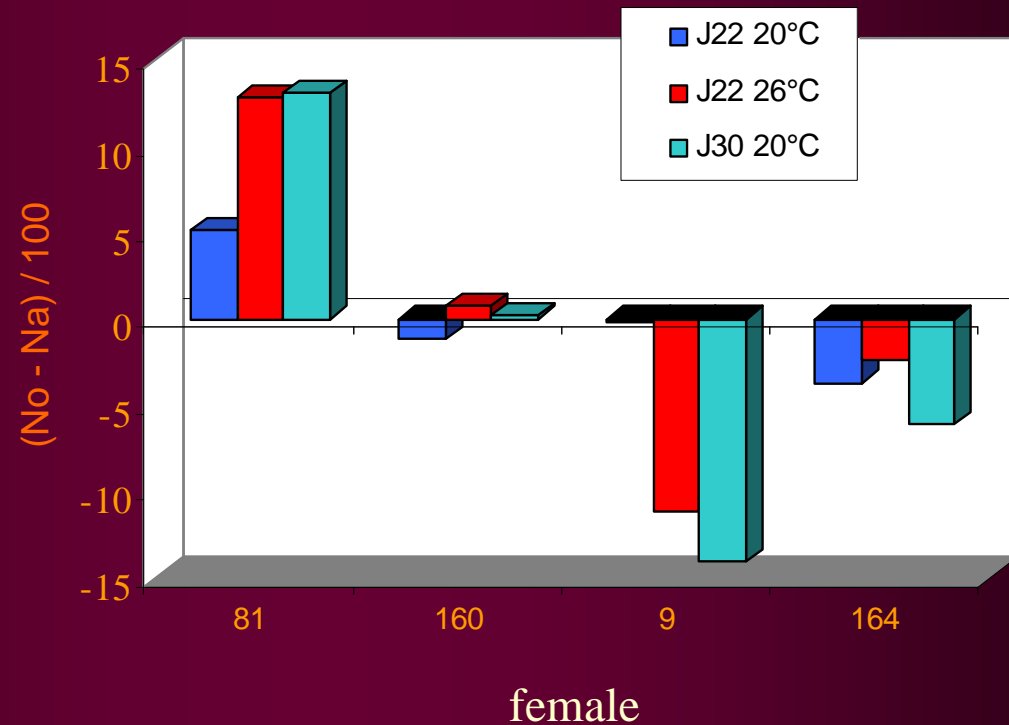
SAS/STAT® Proc Mixed



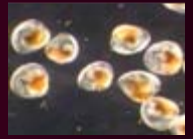
A Variance of female reproductive success



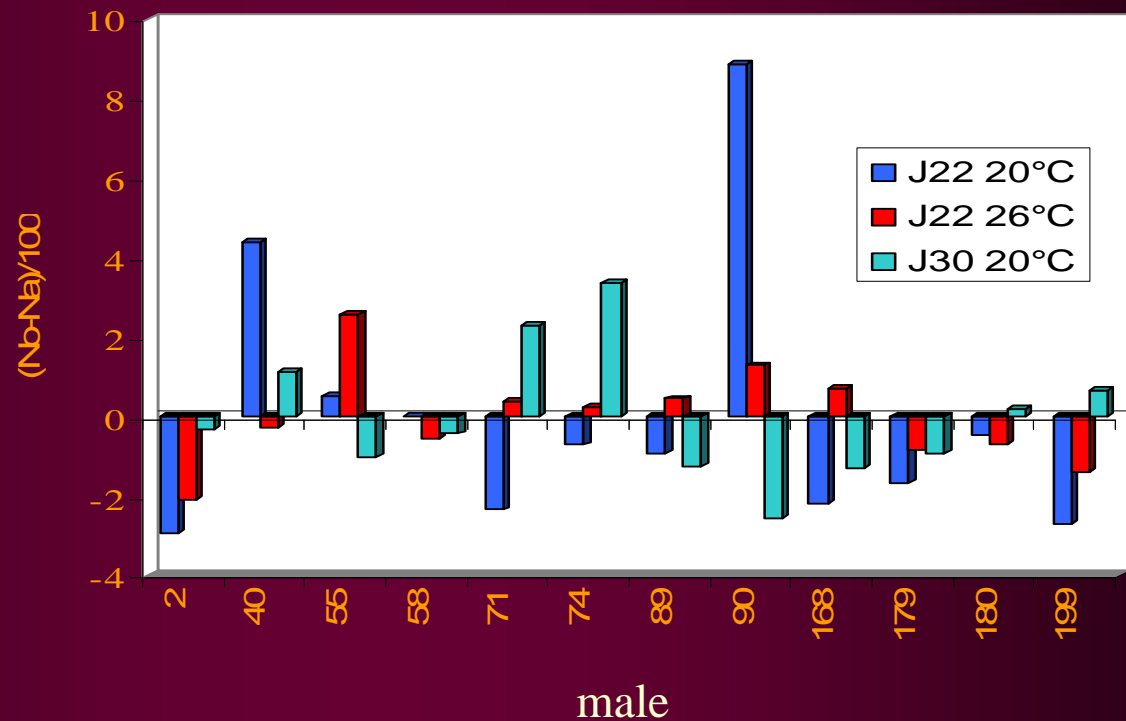
Observed maternal contributions relative to mean hatching rate at Day 1



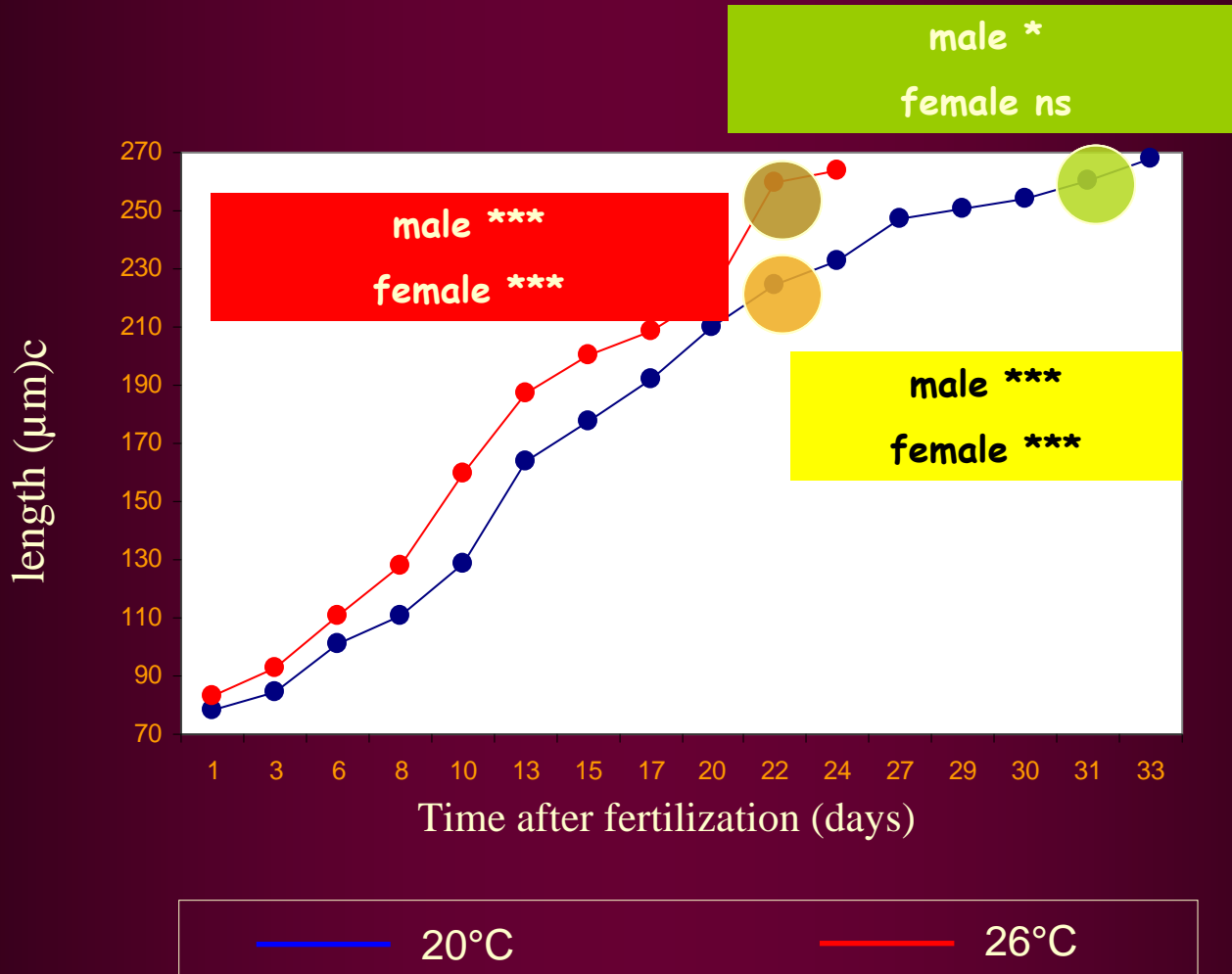
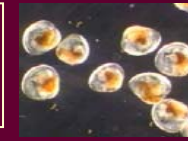
A Variance of male reproductive success



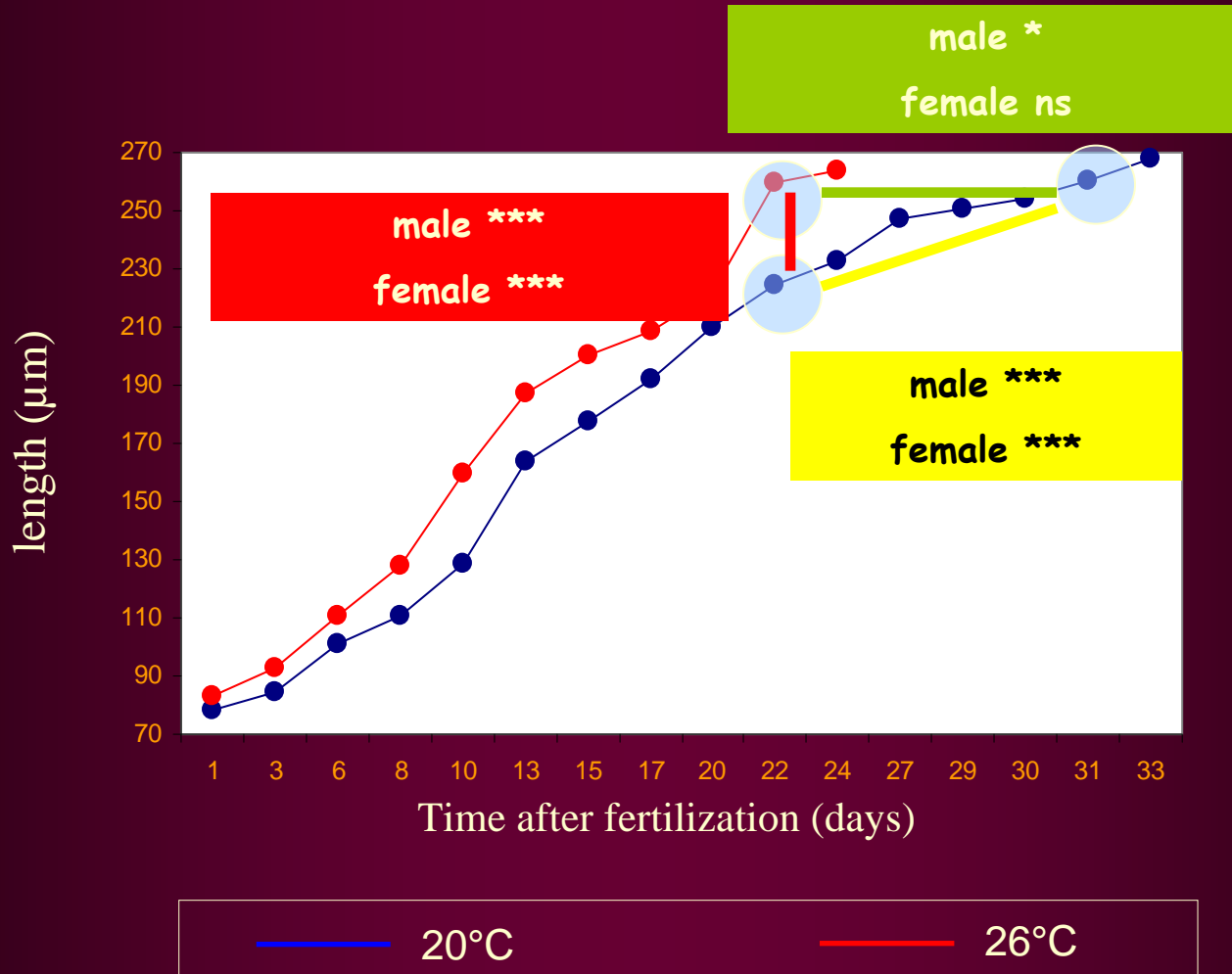
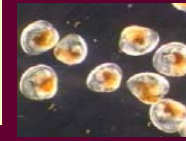
Observed paternal contributions relative to mean hatching rate at Day 1



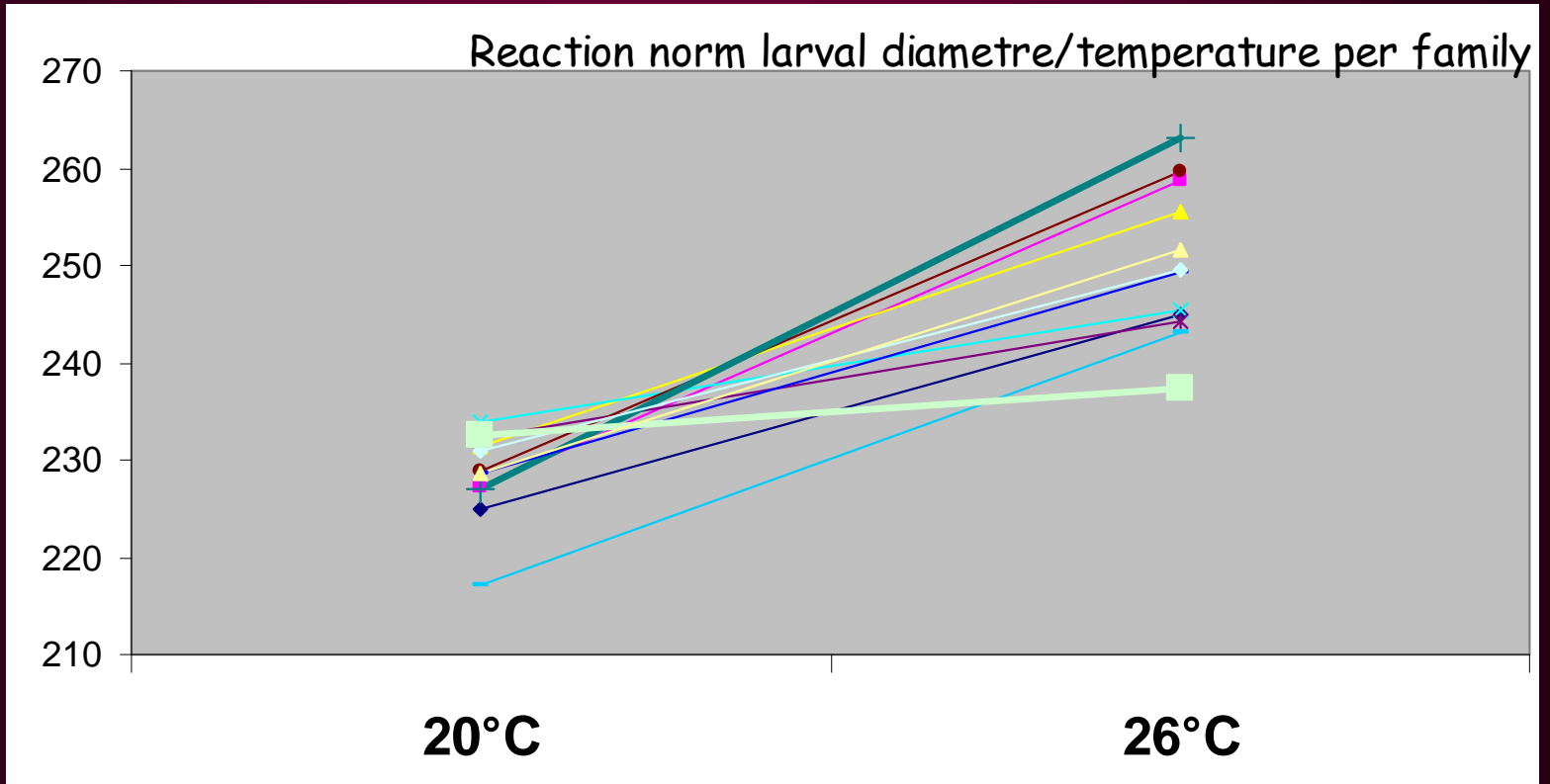
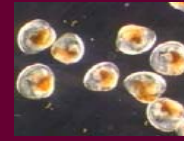
A Parental contributions



A Parental contributions



B Larval size



Male

ns

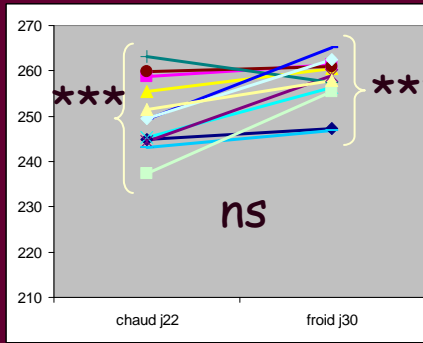
$p < 0.05$

Female

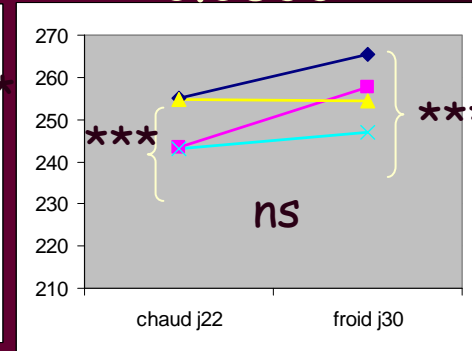
ns

$p < 0.05$

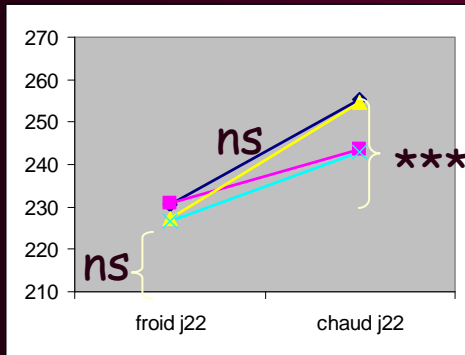
0.7518



0.0833

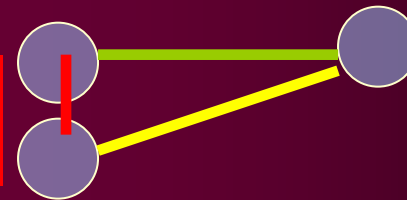


0.1307

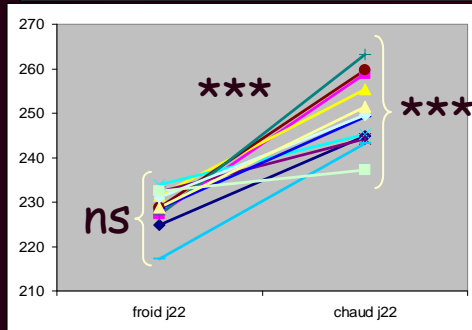


male ***
female ns

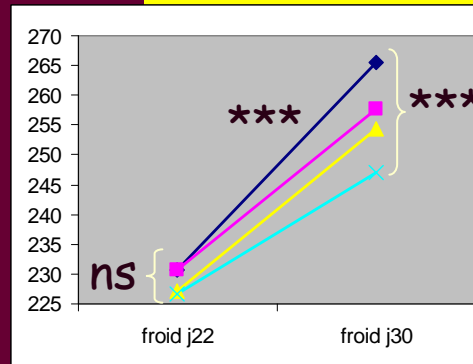
male ns
female ns



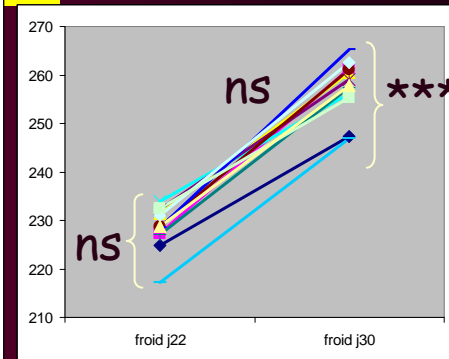
male ns
female ***



0.0006

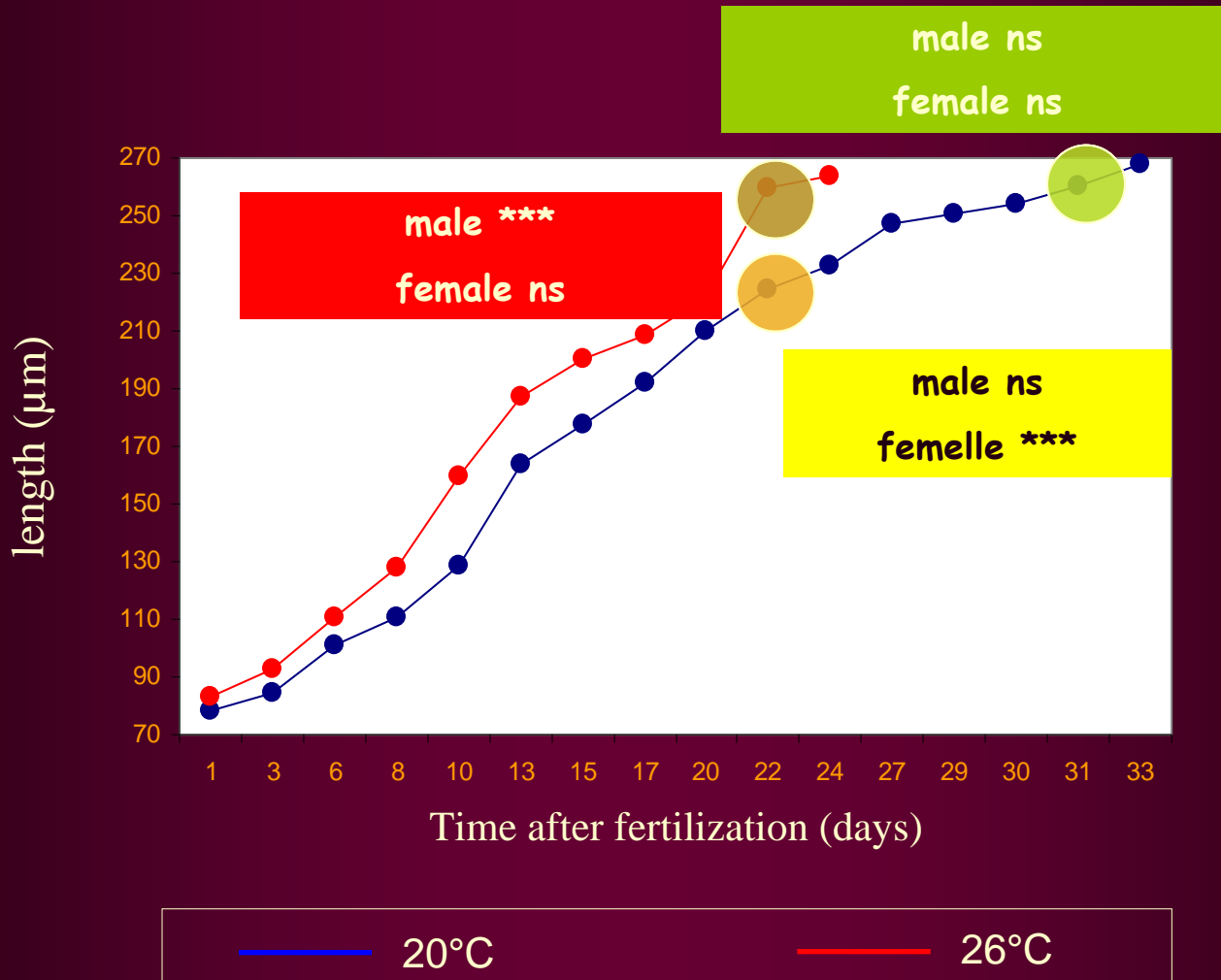
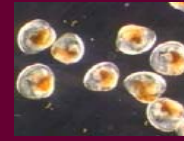


0.001

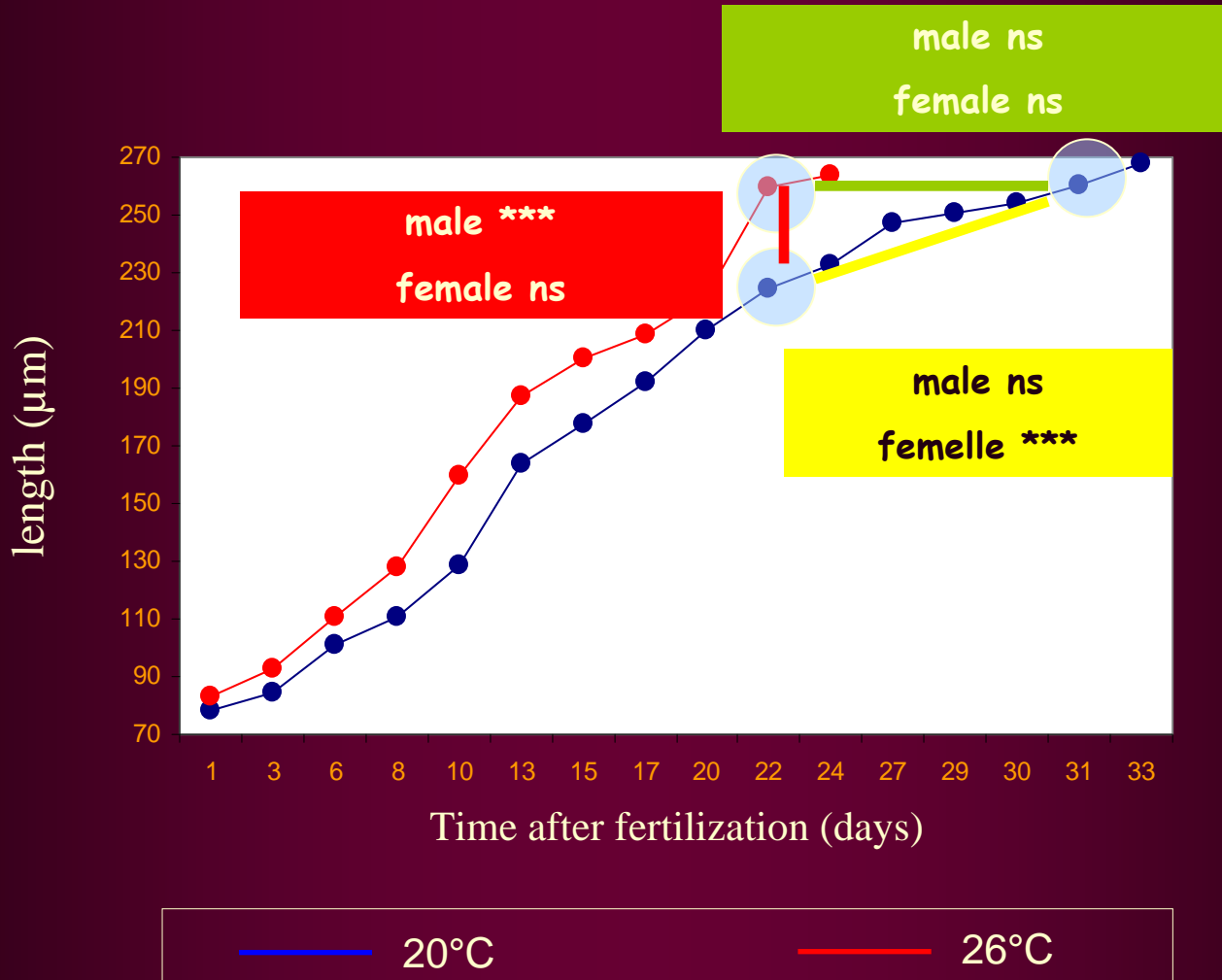
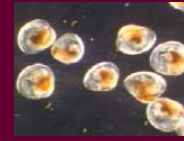


0.4386

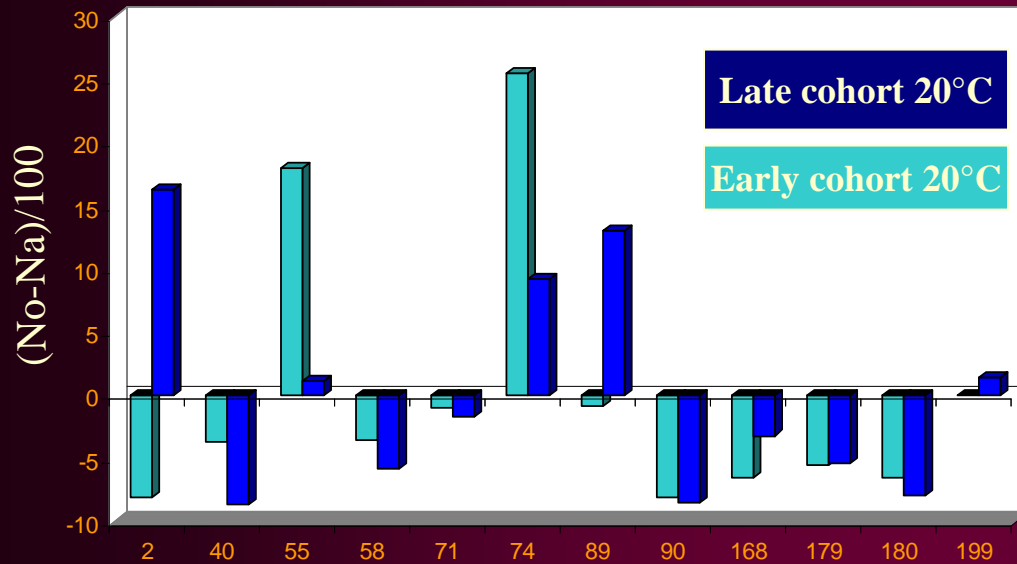
B Larval size



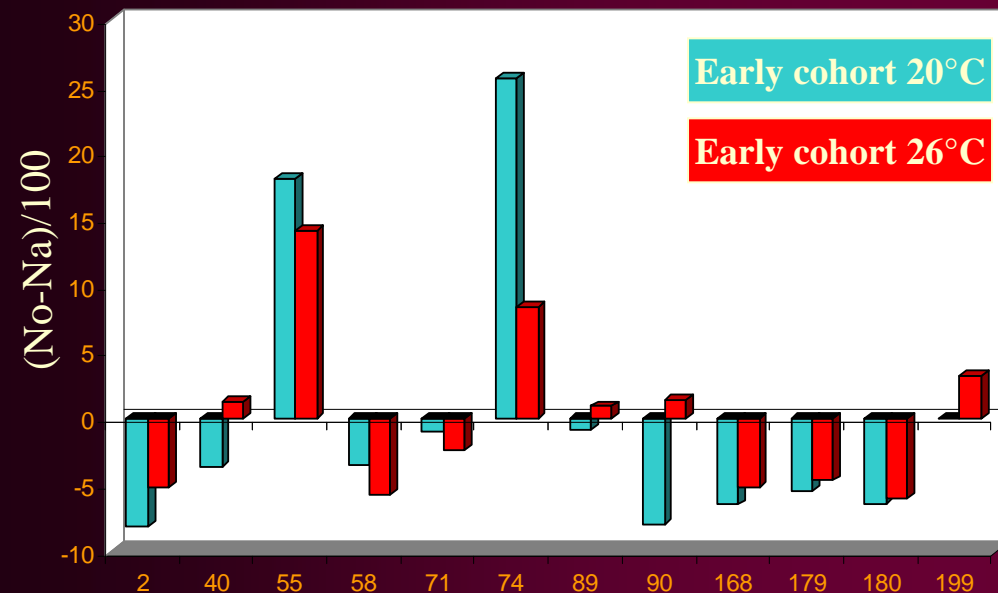
B Larval size



Paternal contributions at day 80 (spat)

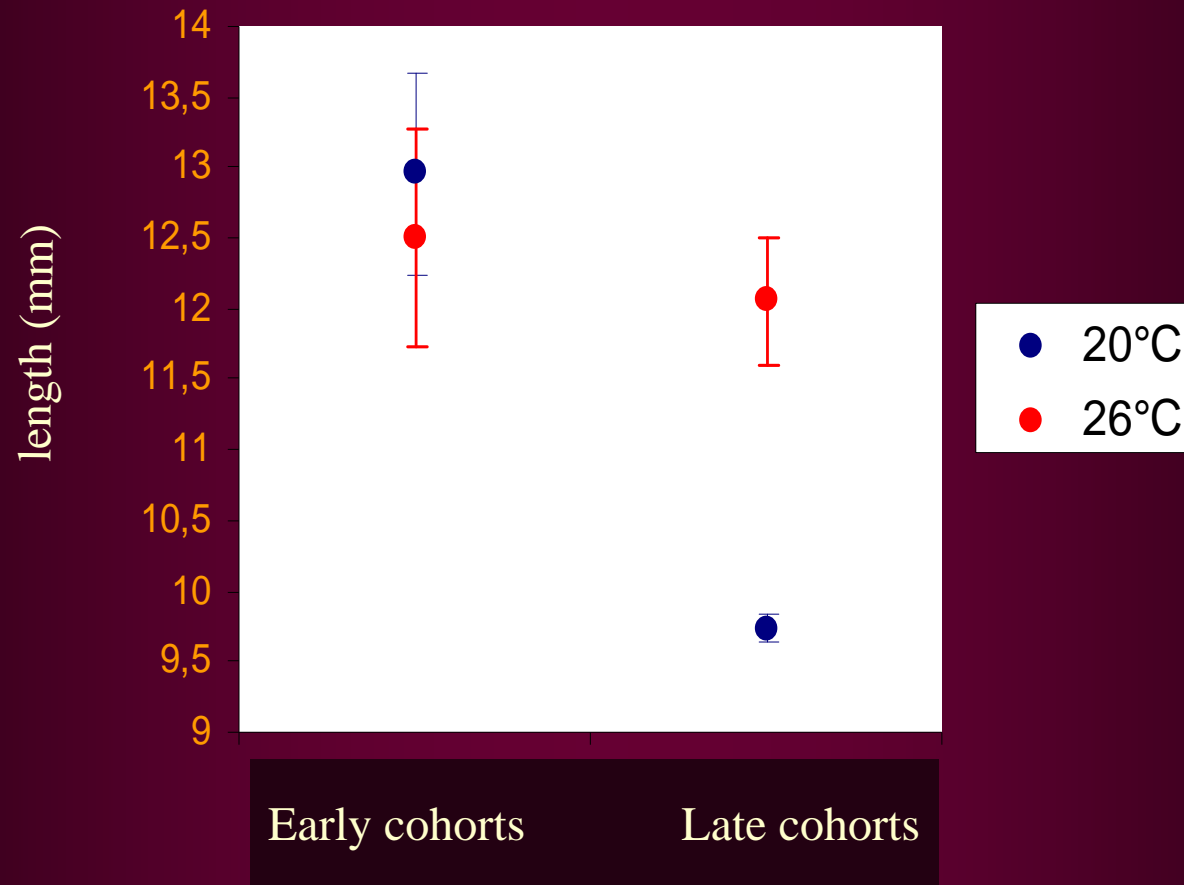


Significantly different contributions between early and late cohorts at 20°C (same result at 26°C)

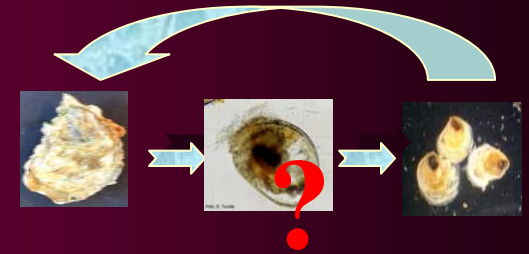


Significantly different contributions between early cohorts at 20°C and 26°C (same result for late cohort)

Spat growth



Conclusion



TECHNICALLY

- As individual tagging is impossible at early life stages, marker-based parentage analysis of mixed families represents an efficient tool to study genetics of larval traits

SELECTION AT LARVAL STAGE ?

- Significant differences are observed between progenies
 - Temperature influences the expression of genetic variability for growth and survival