

Global change and aquatic ecosystems: An opportunity to combine fundamental and applied researches

Simon Blanchet
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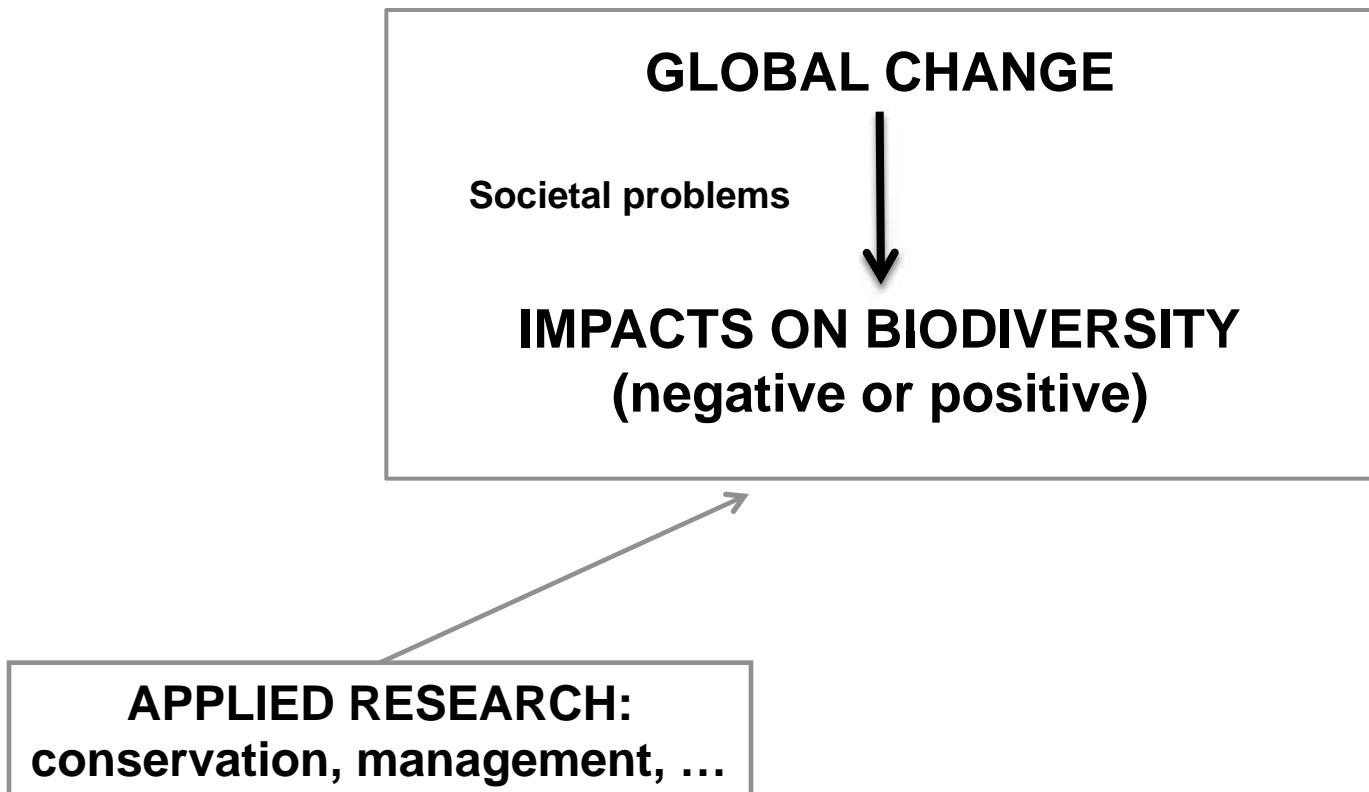
**AS MOST ECOSYSTEMS,
FRESHWATERS ARE IMPACTED BY MULTIPLE STRESSES**

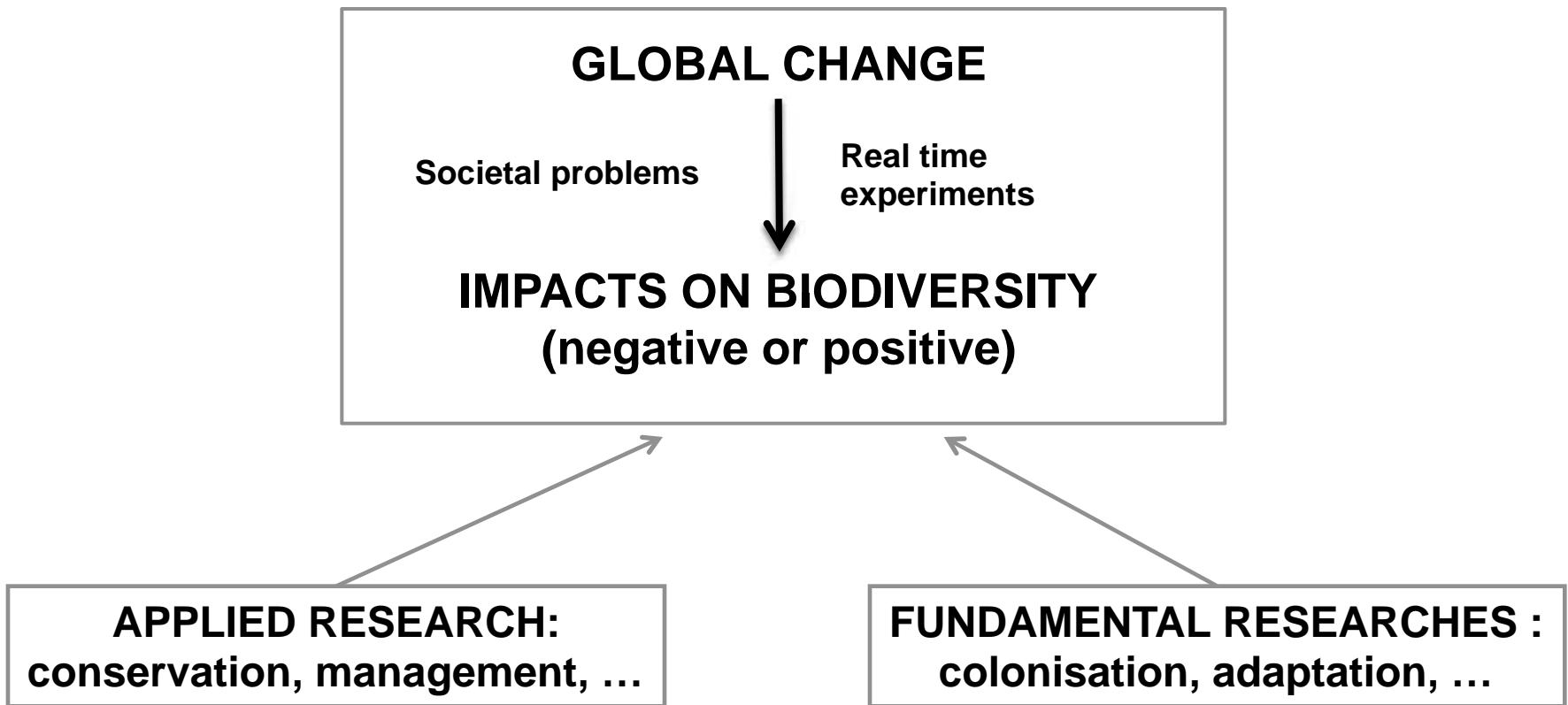


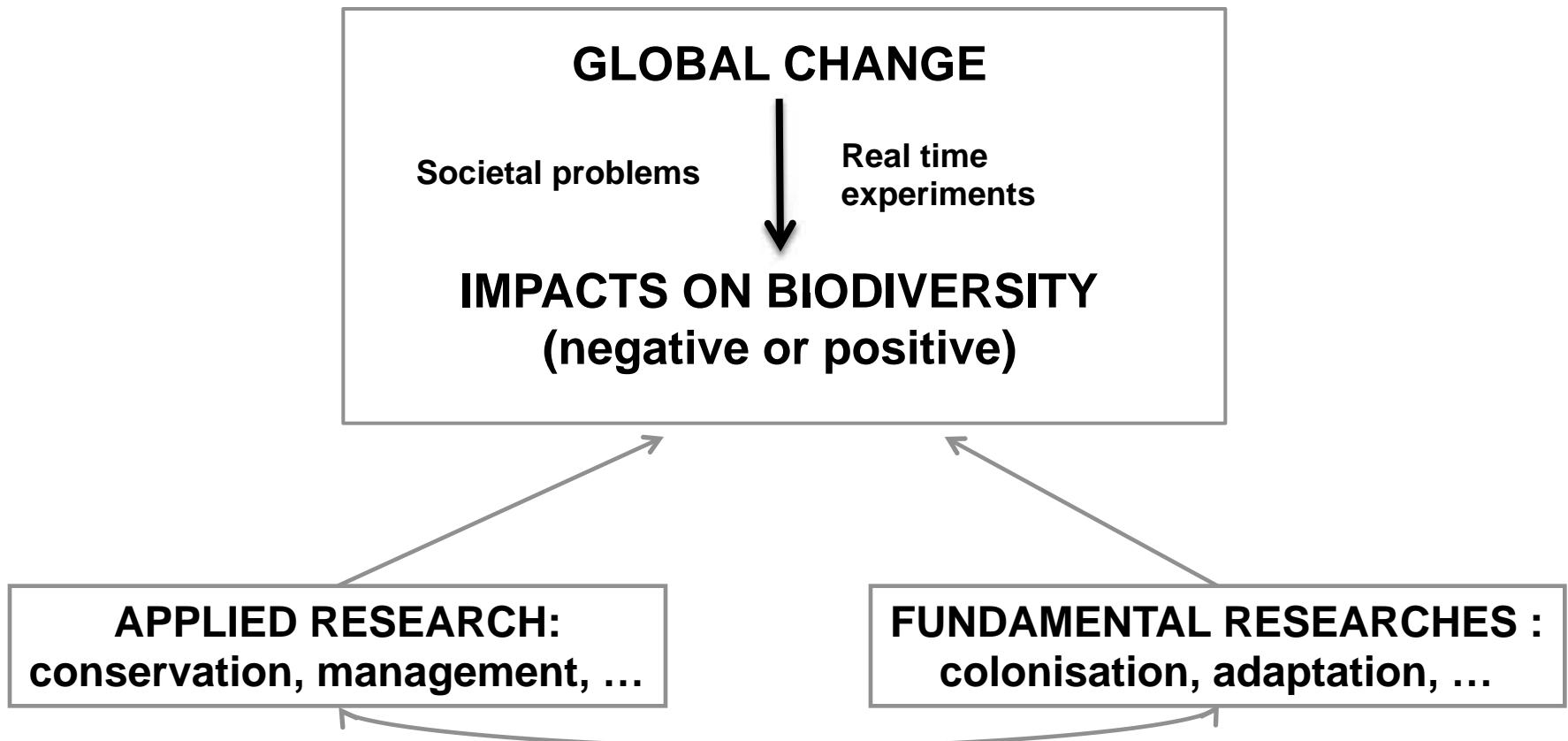
GLOBAL CHANGE



IMPACTS ON BIODIVERSITY
(negative or positive)







A UNIQUE FRAMEWORK TO COMBINE APPLIED AND FUNDAMENTAL
RESEARCHES



Two research axes

Ecology and evolution of host-parasite interactions
Biological invasions

Intraspecific diversity in river networks
Conservation and habitat fragmentation

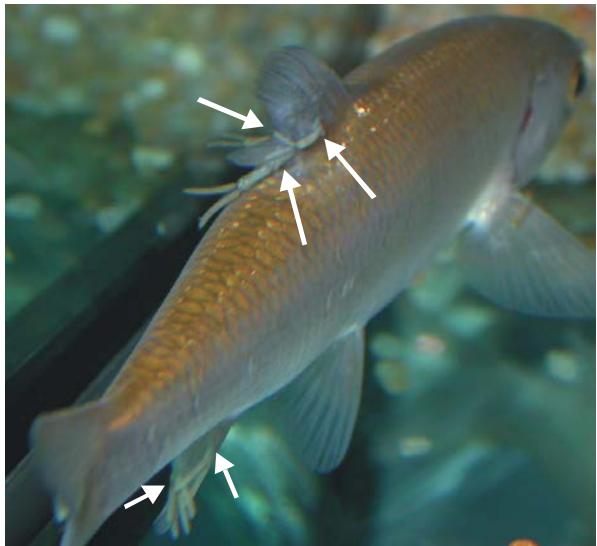
Both applied and fundamental questions
Molecular tools, empirical surveys, simulations, experiments



- 1) PATHWAYS OF INVASION FOR A NEGLECTED PARASITE**
- 2) ENVIRONMENTAL AND GENETIC BASES OF HOST DEFENSES**
- 3) GENOMIC BASES OF HOST DEFENSES**



THE TRACHELIASTES-DACE INTERACTIONS:



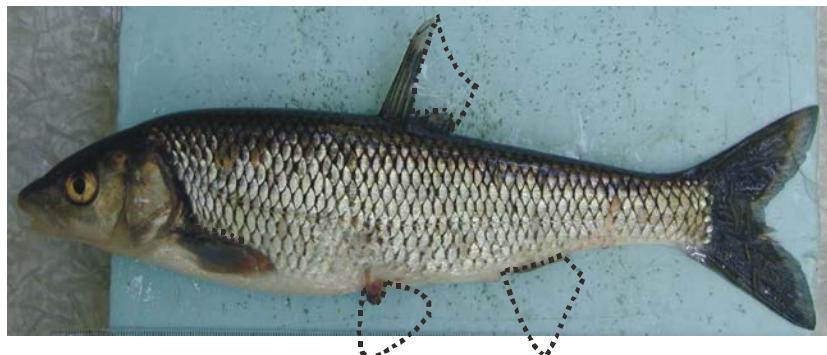
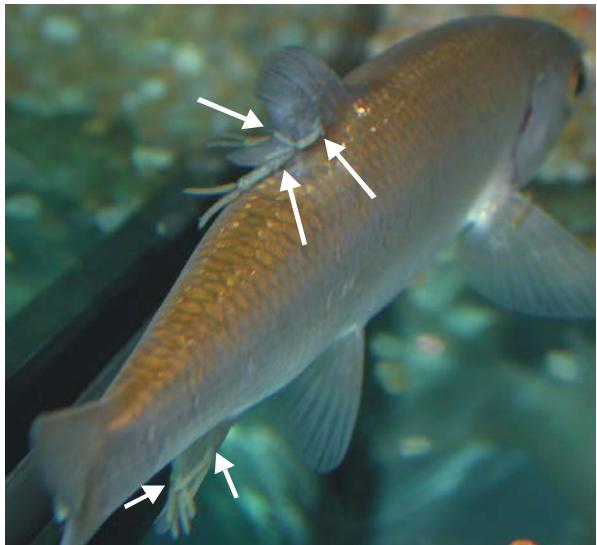
Dace (*Leuciscus sp*)



Copepod (*Trachelastes polycolpus*)

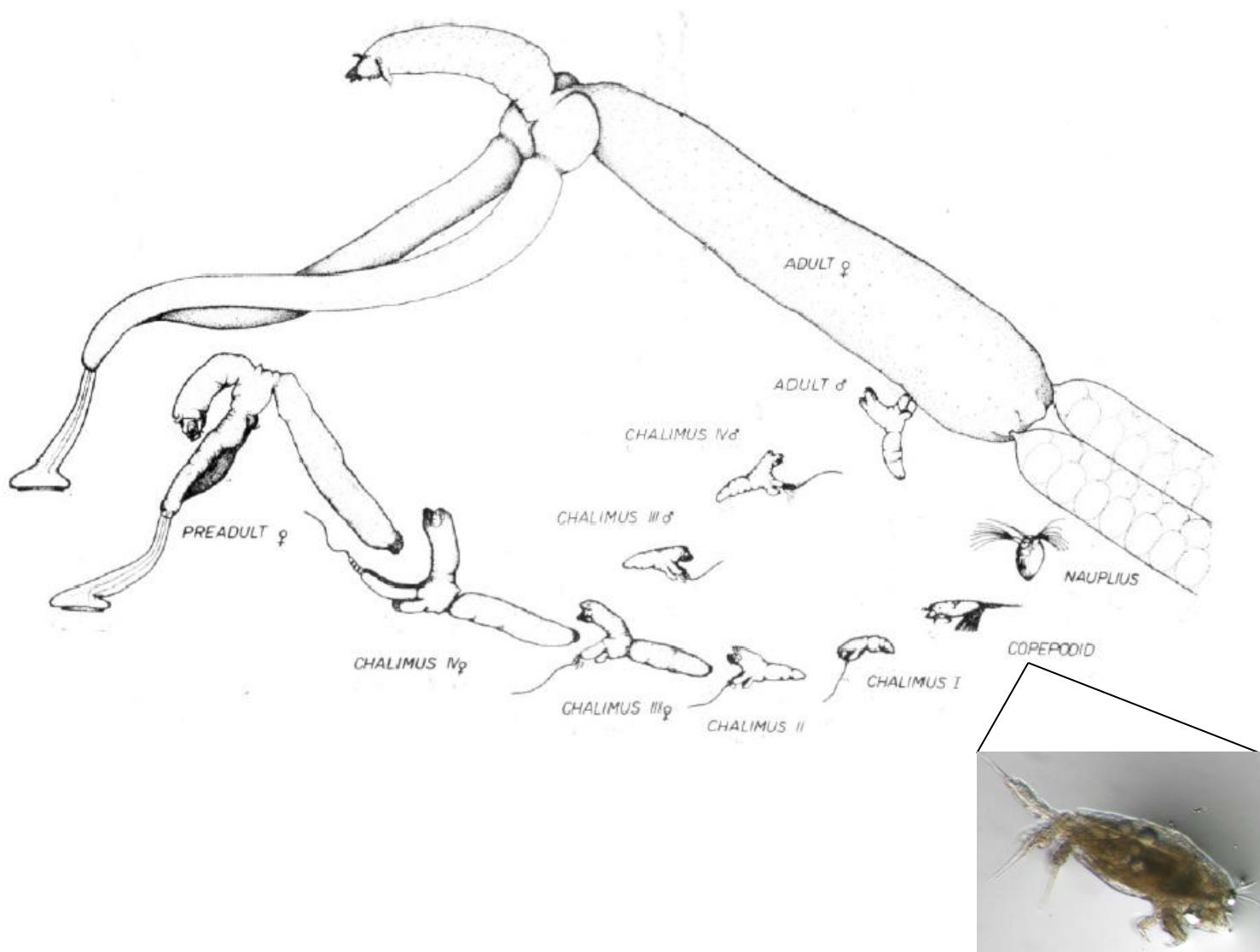


THE TRACHELIASTES-DACE INTERACTIONS:



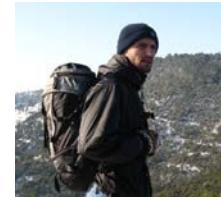


LIFE CYCLE (DIRECT CYCLE, A SINGLE HOST SPECIES):



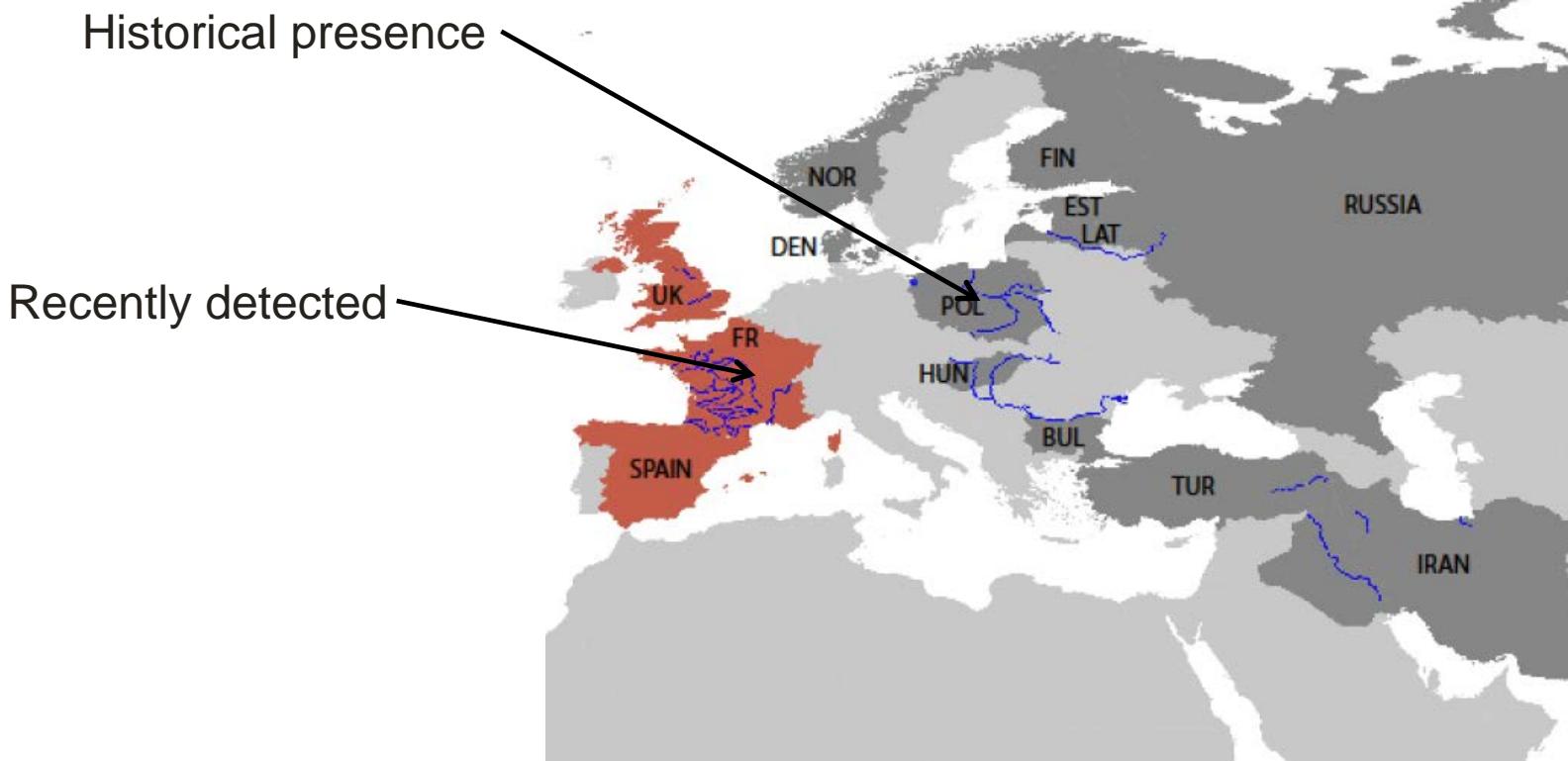
(I) PATHWAYS OF INVASION

- Widespread in the North-Eastern part of the Palearctic
- Detected since the 1930' in the UK, the 1960' in France



Olivier Rey

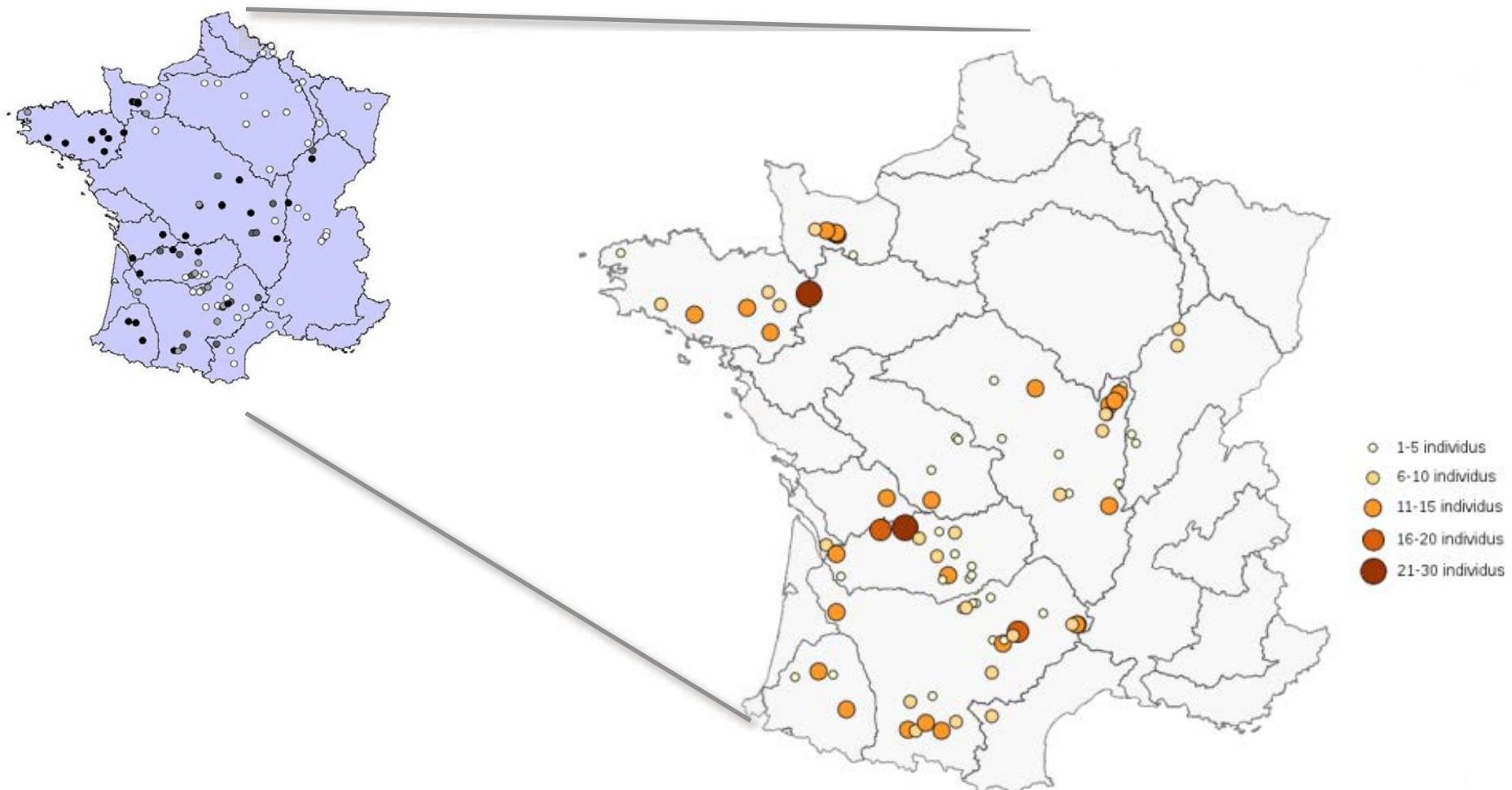
Lisa Fourtune



Is *T. polycolpus* a non-native species *in France*?
What is its invasion history? (potential sources are unknown)

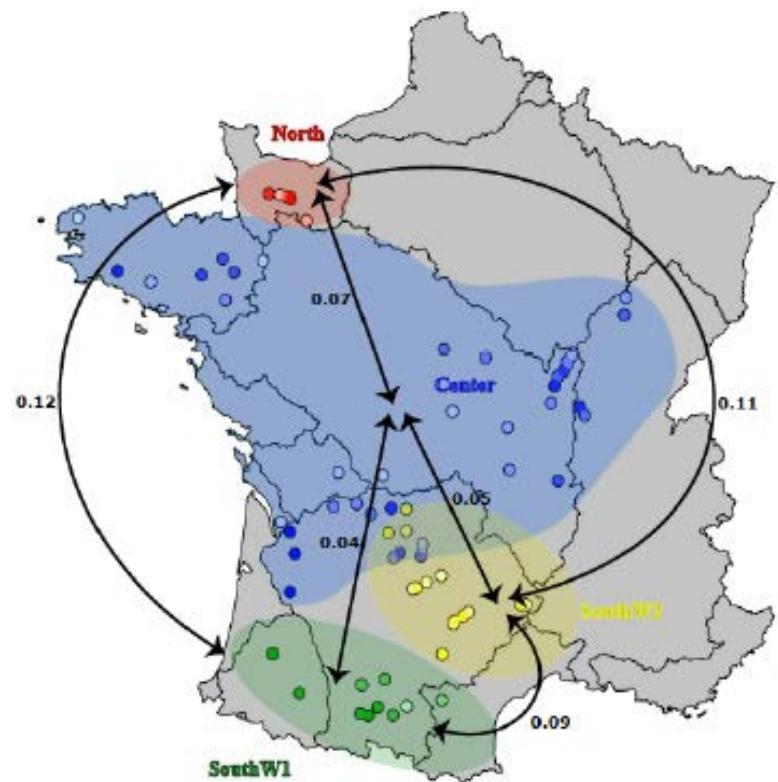
(I) PATHWAYS OF INVASION

SAMPLING ACROSS FRANCE:
673 individuals, 86 sites, 61 rivers, 16 microsatellite loci

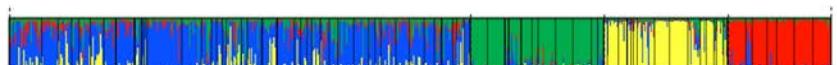


(I) PATHWAYS OF INVASION

FOUR MAIN GENETIC CLUSTERS (*Structure, Pritchard et al. 2000*)



Two possible types of scenarios:



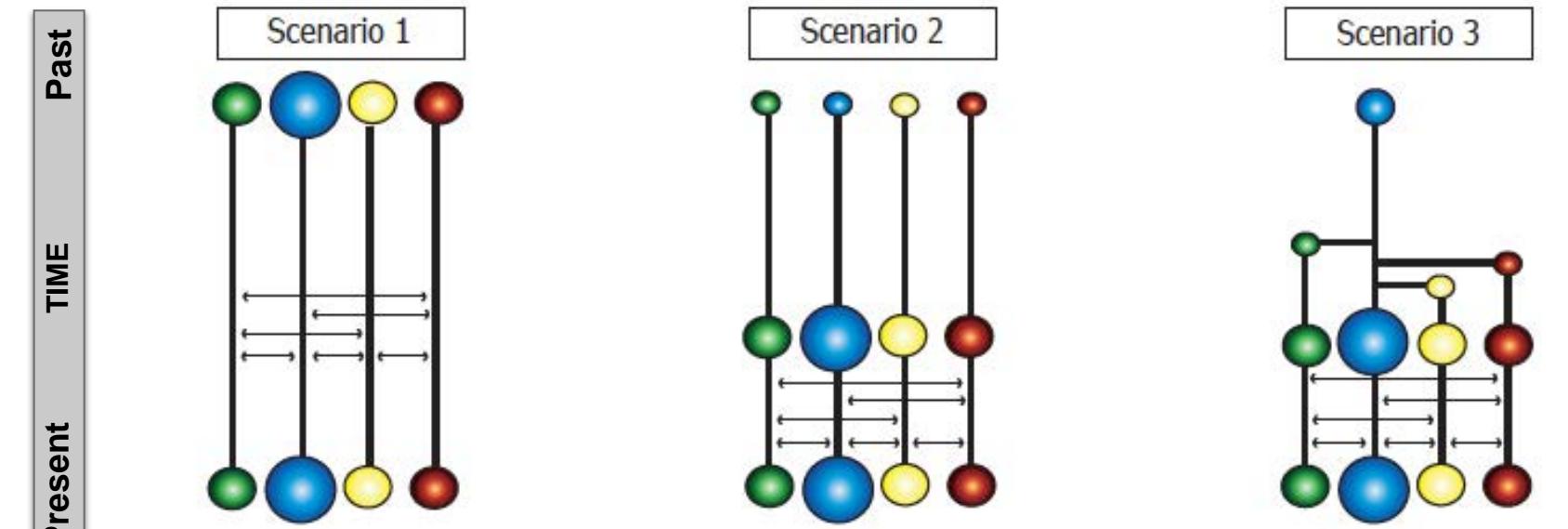
« Native » : historical presence in france, recent expansion

« Non-native » : introduction and recent expansion

(I) PATHWAYS OF INVASION



Native scenarios: 3 models



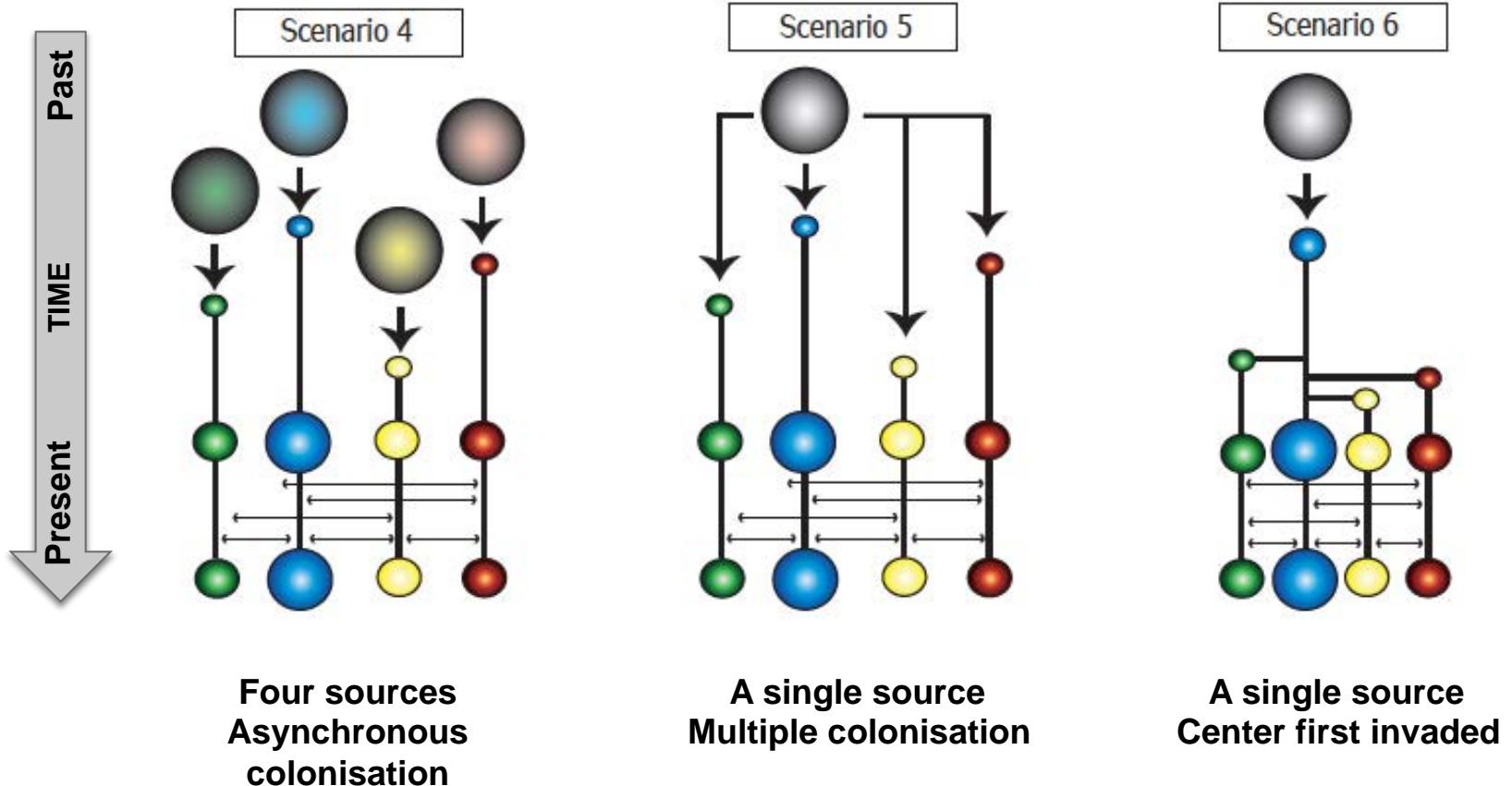
The four clusters historically exist
Tracheliastes discovered only recently
Stabilité (S1) vs. exponential growth (S2)

Only the Center cluster
historically exists
Recent colonisation of
new basins

(I) PATHWAYS OF INVASION



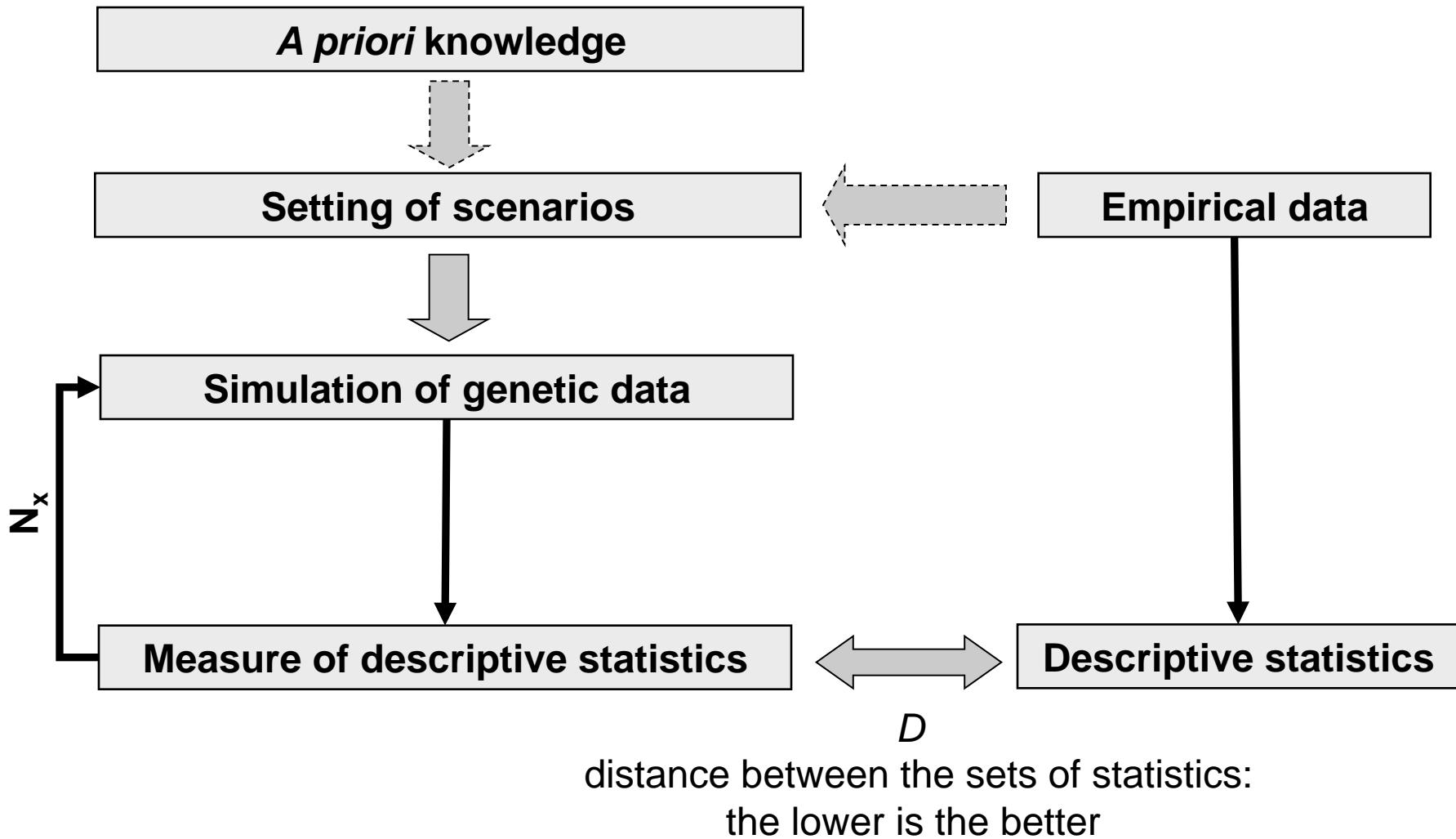
Non-native scenarios: 3 models



(I) PATHWAYS OF INVASION



SIMULATION AND MODEL COMPARISON: « ABC » APPROACH

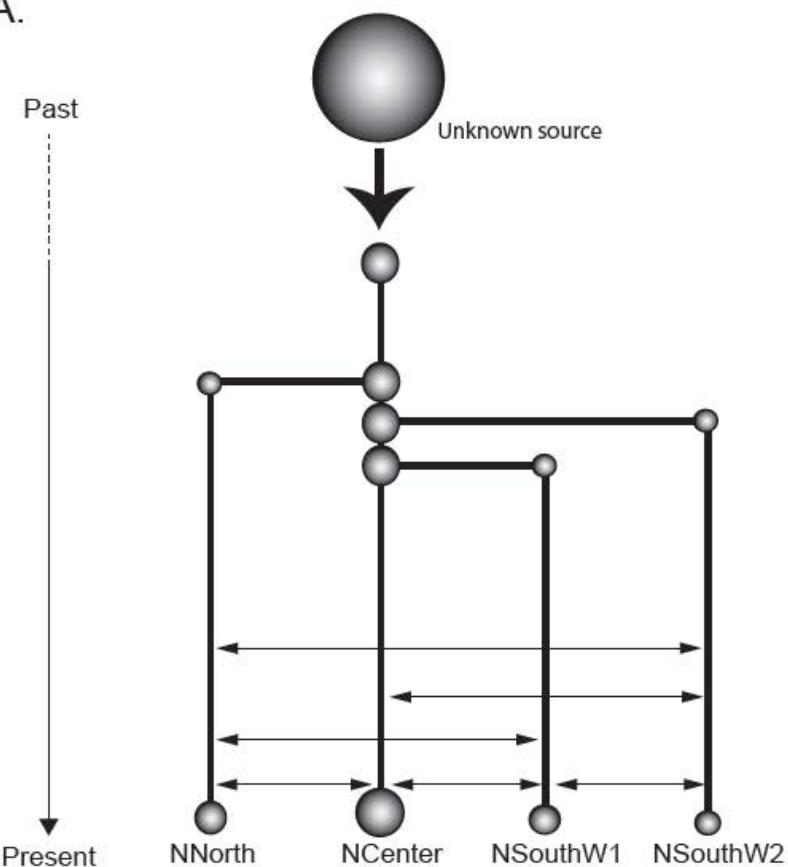


distance between the sets of statistics:
the lower is the better

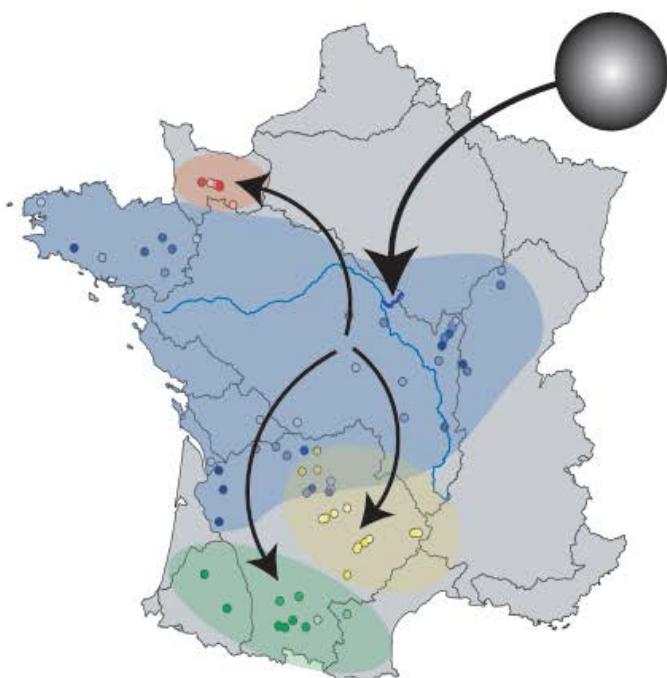
(I) PATHWAYS OF INVASION

→ One of the « non-native » scenario is most likely:

A.



B.

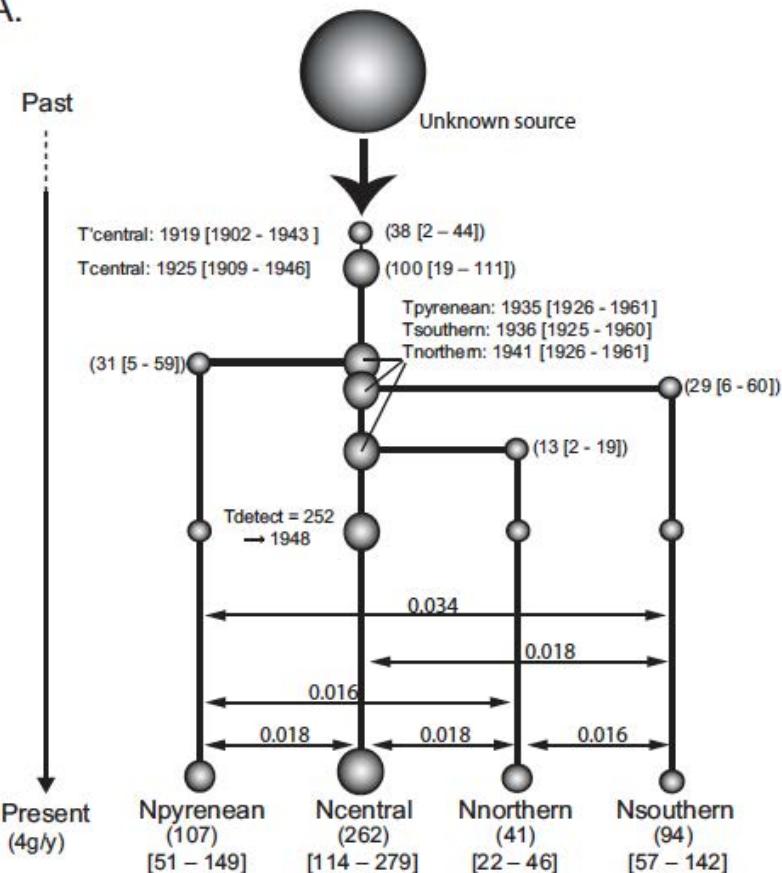


Tracheliaastes has been introduced in Center France in the Loire river from a single unknown source, then spread to other river basins

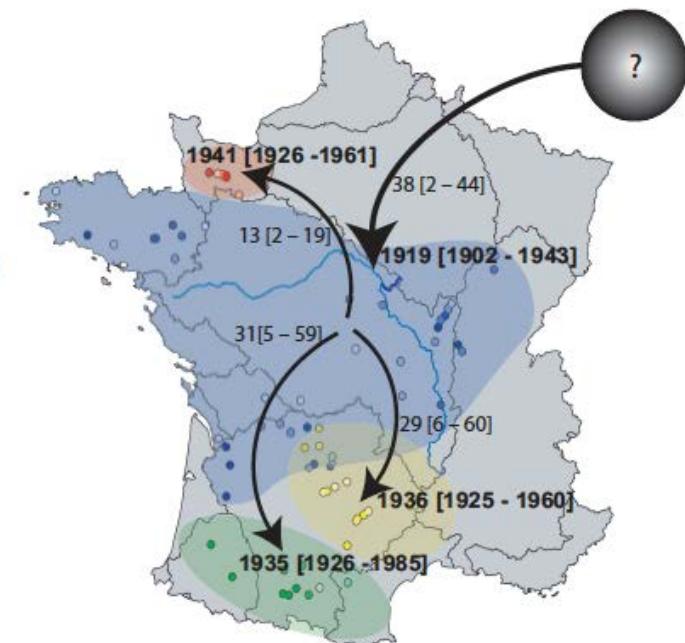
(I) PATHWAYS OF INVASION

→ Further simulations are ran to infer key parameter values:

A.

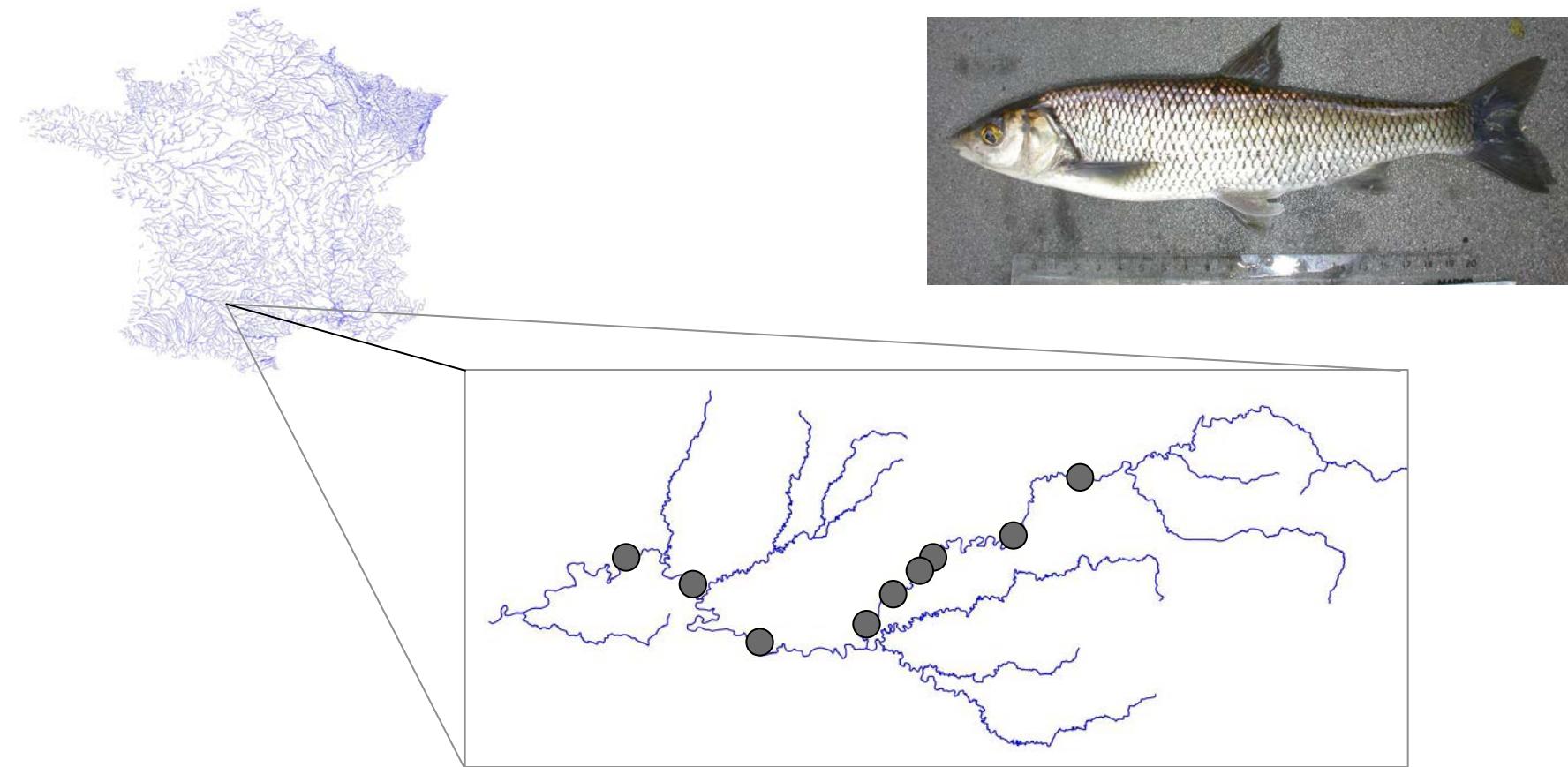


B.



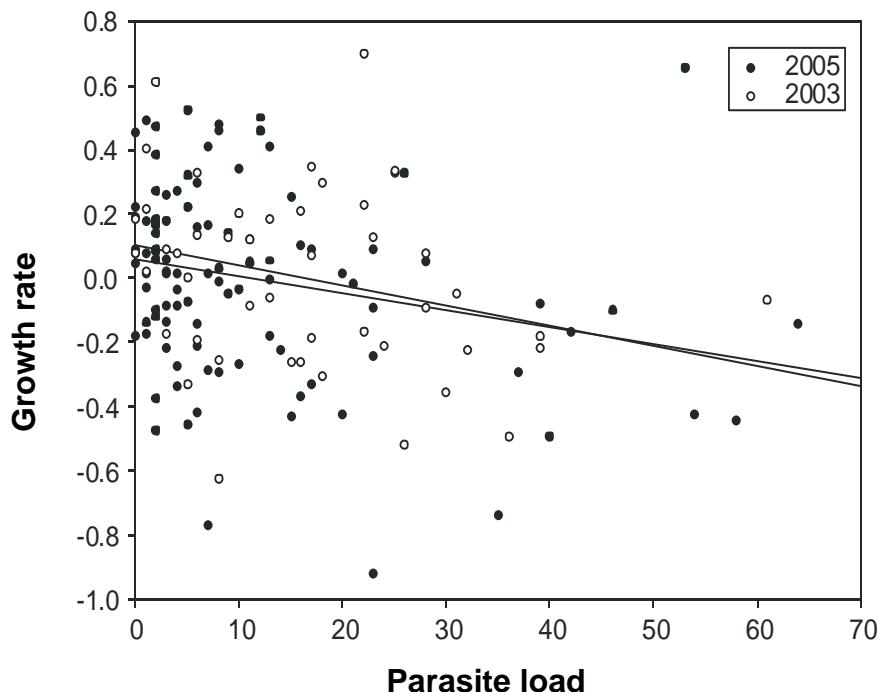
Tracheliaastes first arrived in the 1920's (observed in the UK in 1930) from a few numbers of founders (20). It quickly colonised other river basins, i.e. 15 years later.

LONG-TERM SURVEY ON NATURAL POPULATIONS: VIAUR AND CÉLÉ RIVERS



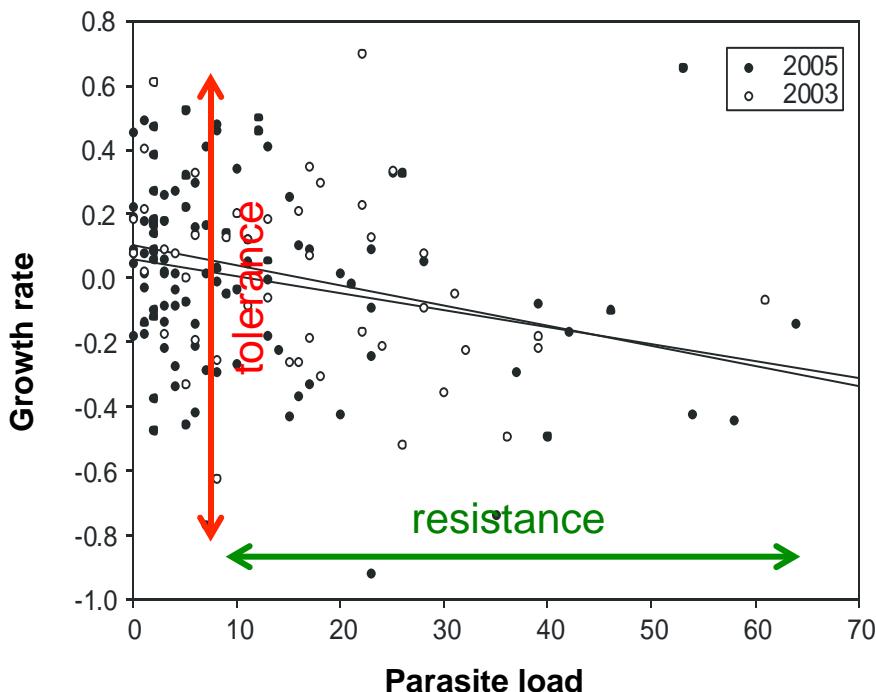
**8 sampling sites from 2003 to 2018 x 2 rivers:
Tissue samples – biometry – parasitic indices**

LONG-TERM SURVEY ON NATURAL POPULATIONS: VIAUR AND CÉLÉ RIVERS



- The parasite affects the dace individual fitness (evidences for population effects – selective mortality)

LONG-TERM SURVEY ON NATURAL POPULATIONS: VIAUR AND CÉLÉ RIVERS



- The parasite affects the dace individual fitness (evidences for population effects – selective mortality)
- Large inter-individual variance in terms of resistance and tolerance to the parasite



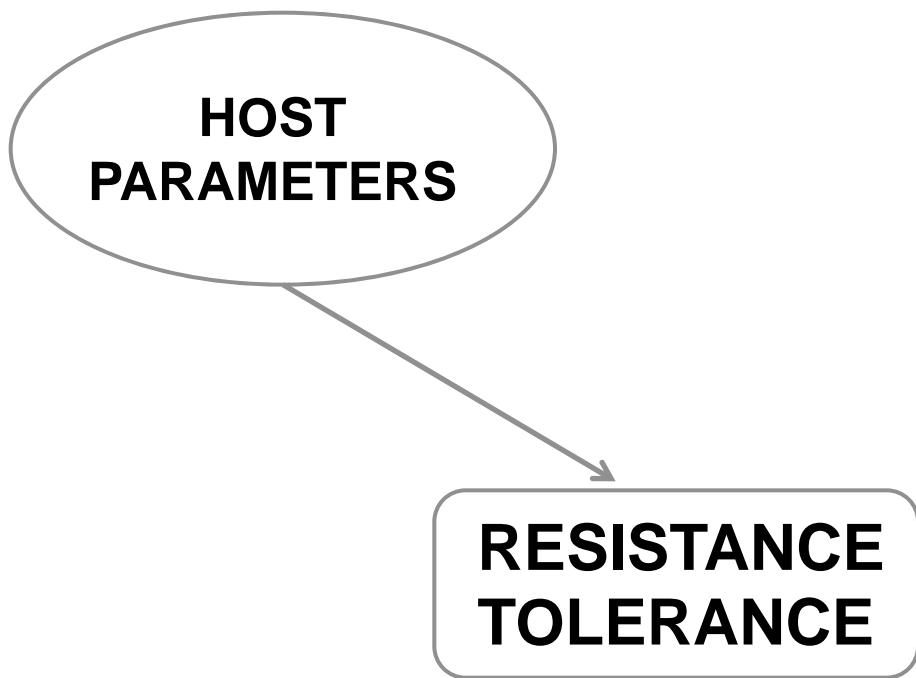
GENETIC AND ENVIRONMENTAL BASES



Maxime Cardon



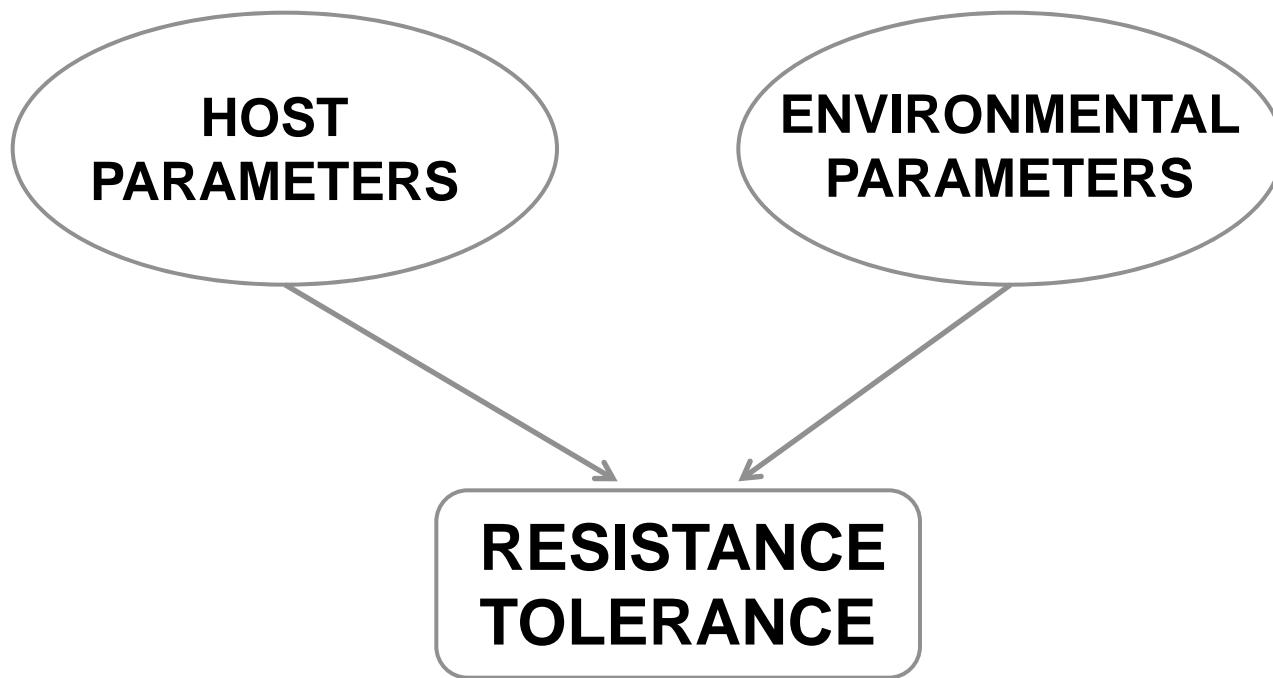
GENETIC AND ENVIRONMENTAL BASES



1) "HOST" MODEL



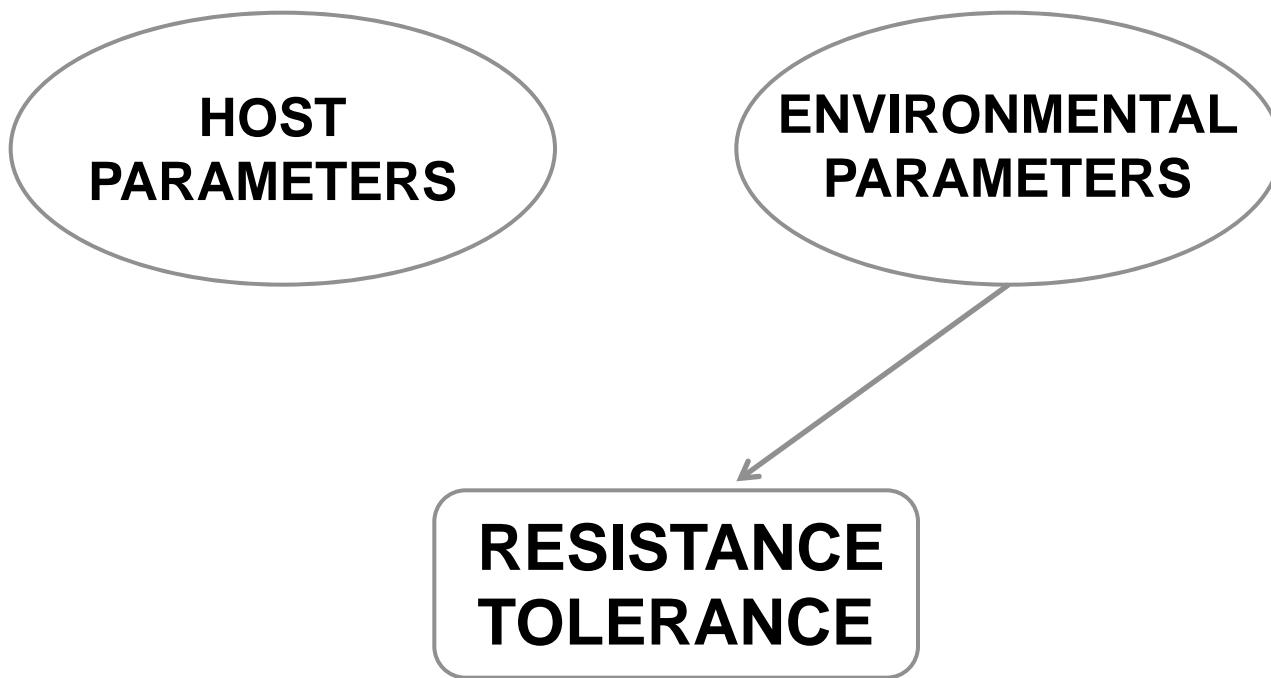
GENETIC AND ENVIRONMENTAL BASES



- 1) "HOST" MODEL
- 2) "HOST – ENVIRONMENT" MODEL



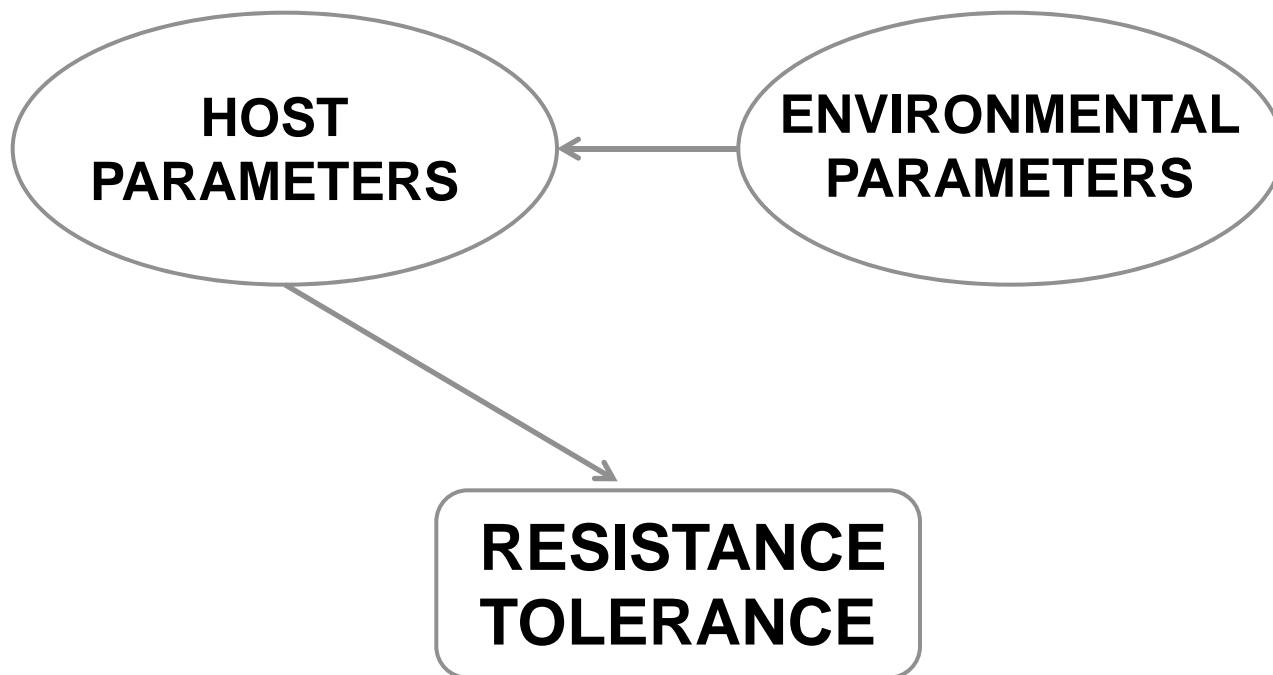
GENETIC AND ENVIRONMENTAL BASES



- 1) "HOST" MODEL
- 2) "HOST – ENVIRONMENT" MODEL
- 3) "DIRECT ENVIRONMENT" MODEL



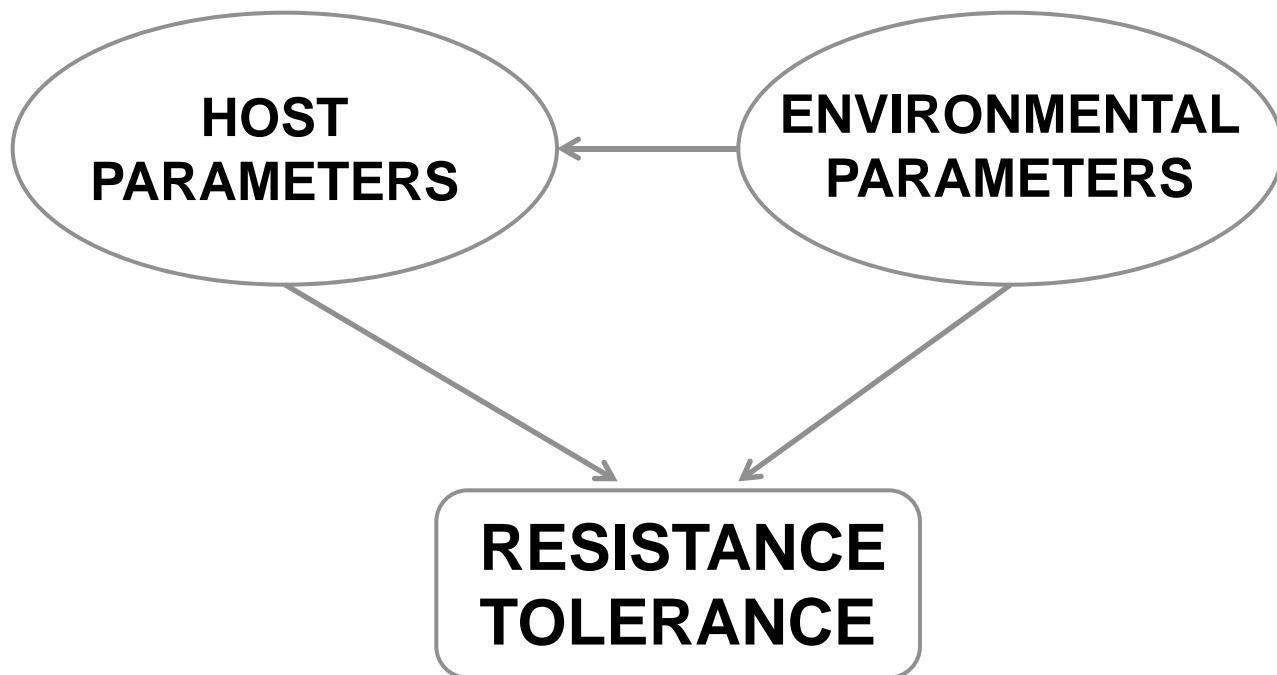
GENETIC AND ENVIRONMENTAL BASES



- 1) "HOST" MODEL
- 2) "HOST – ENVIRONMENT" MODEL
- 3) "DIRECT ENVIRONMENT" MODEL
- 4) "INDIRECT ENVIRONMENT" MODEL



GENETIC AND ENVIRONMENTAL BASES



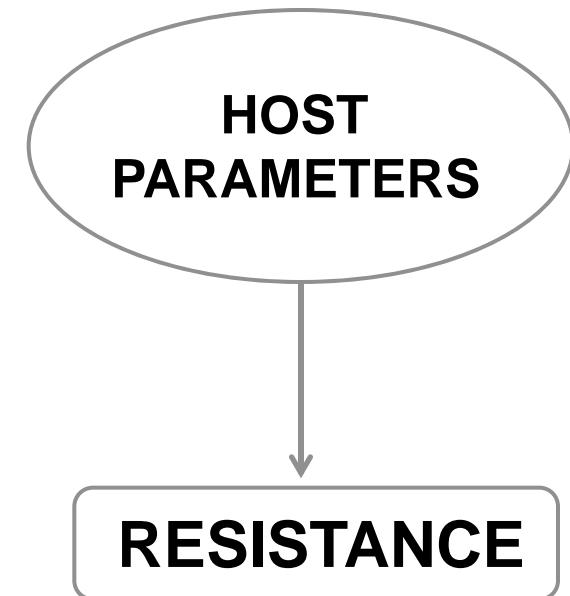
- 1) "HOST" MODEL
- 2) "HOST – ENVIRONMENT" MODEL
- 3) "DIRECT ENVIRONMENT" MODEL
- 4) "INDIRECT ENVIRONMENT" MODEL
- 5) "HOST – DIRECT + INDIRECT ENVIRONMENT" MODEL

SEM
+
AIC



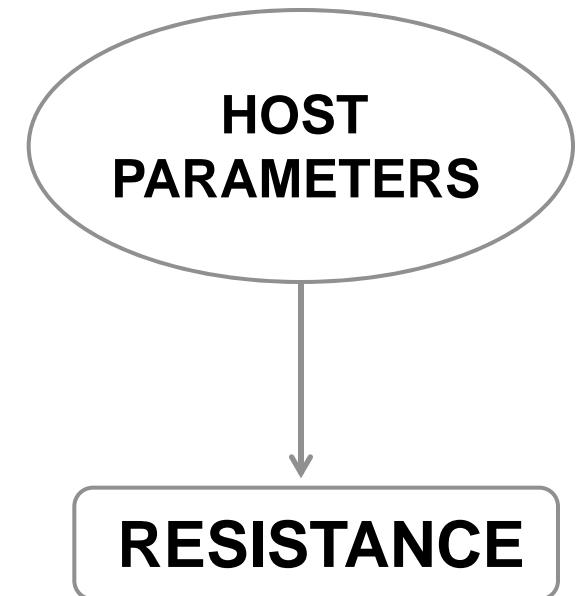
GENETIC AND ENVIRONMENTAL BASES

“HOST” MODELS

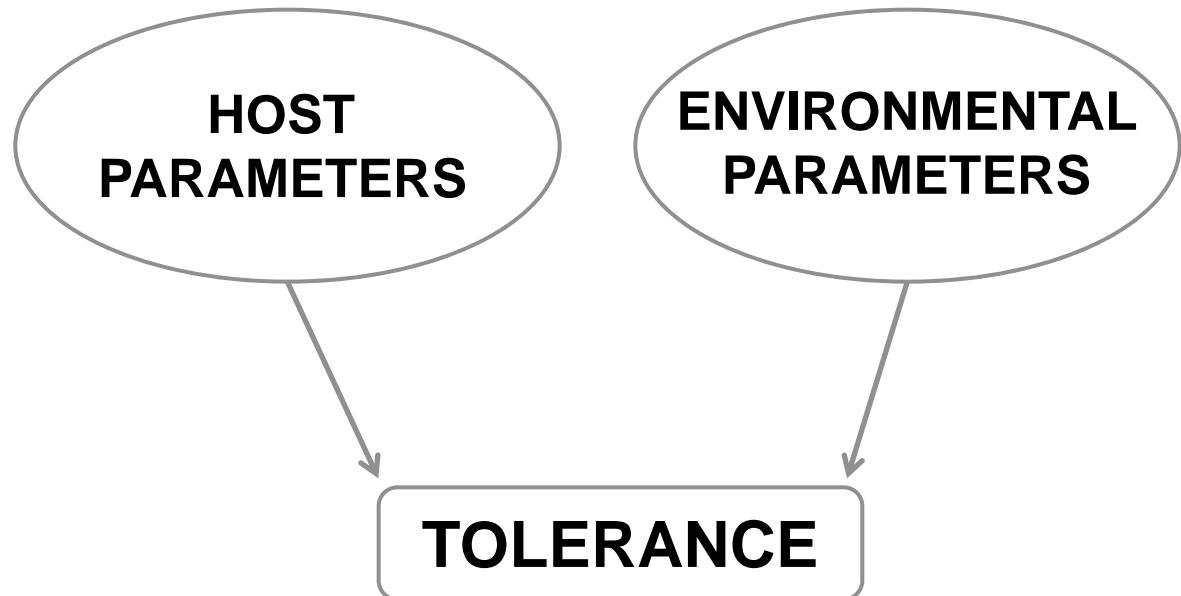


GENETIC AND ENVIRONMENTAL BASES

“HOST” MODELS



“HOST + ENVIRONMENT” MODELS



- ENVIRONMENTAL BASES FOR TOLERANCE (thermal regime)
- GENETIC BASES FOR BOTH RESISTANCE AND TOLERANCE?

(III) RESISTANCE AND TOLERANCE

GENETIC BASES (HERITABLE)

Molecular data => inferring the parental links (pedigrees)



Elise Mazé

PEDIGREE - JOBS - Mozilla Firefox

Echier Editer Affichage Historique Marque-pages Outils

hebinger.biology.dal.ca:5000/Pedigree/cgi-bin/PedigreeResults.cgi

Les plus visités À la une BiblioVIE Dictionnaire anglais ISI Web of Knowledge France Inter Montagne - Prévisions ENT Rennes Le Monde dico synonymes

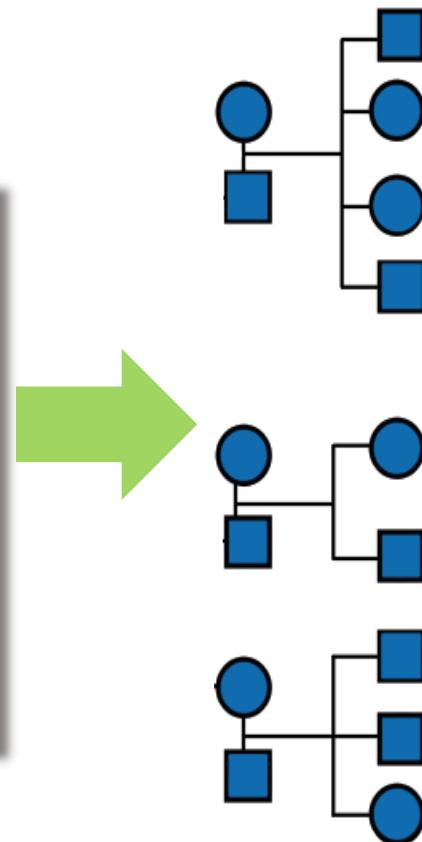
PEDIGREE - Jobs



PEDIGREE - JOBS
(Cnrs - Maze)

Please note: your jobs will be held for 365 days. Past this delay, they will be erased.
Learn how you can save jobs for [later replay](#).

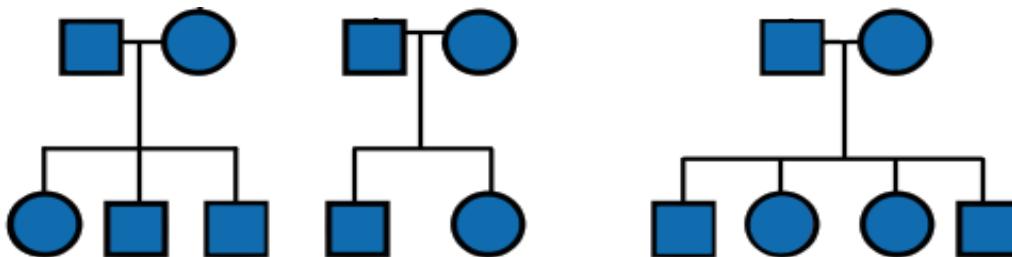
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2012-2-14_11_15_4720locus	Thu May 31 15:26:30 2012	100.0% done in 168. mn	View details Delete
2012-2-17_15_15_0813marqueurs	Thu May 31 15:26:31 2012	100.0% done in 162. mn	View details Delete
2012-2-24_16_23_15globalbis	Thu May 31 15:26:32 2012	100.0% done in 5085. mn	View details Delete
2012-2-24_16_26_110markeur	Thu May 31 15:26:48 2012	100.0% done in 989. mn	View details Delete
2012-2-28_12_36_25global2loc	Thu May 31 15:26:50 2012	100.0% done in 329. mn	View details Delete
2012-2-28_12_37_43	Thu May 31 15:26:54 2012	100.0% done in 327. mn	View details Delete
2012-2-28_18_06_49globalrebris	Thu May 31 15:26:58 2012	100.0% done in 838. mn	View details Delete
2012-2-8_12_52_54	Thu May 31 15:27:07 2012	100.0% done in 195. mn	View details Delete
2012-3-14_10_12_23noFSC-W5	Thu May 31 15:27:09 2012	100.0% done (now in run 10, 0. mn to go)	View details Delete
2012-3-15_13_00_44	Thu May 31 15:27:13 2012	100.0% done (now in run 10, 0. mn to go)	View details Delete
2012-3-15_13_02_12restart-FSC vers noFSC	Thu May 31 15:27:17 2012	100.0% done (now in run 10, 0. mn to go)	View details Delete
2012-3-1_10_32_56globalFSC	Thu May 31 15:27:22 2012	100.0% done in 1018. mn	View details Delete
2012-3-1_10_37_01global-noFSC	Thu May 31 15:27:30 2012	100.0% done in 753. mn	View details Delete
2012-3-1_17_58_39weight	Thu May 31 15:27:35 2012	100.0% done in 1021. mn	View details Delete
2012-3-2_16_09_58W5-FSC-restart-temp	Thu May 31 15:28:01 2012	100.0% done (now in run 10, 0. mn to go)	View details Delete
2012-3-2_16_11_55W10-FSC-restart-temp	Thu May 31 15:28:09 2012	100.0% done (now in run 10, 0. mn to go)	View details Delete



~ 250 FULL-SIB FAMILIES (2-4 INDIV / FAM)

(III) RESISTANCE AND TOLERANCE

GENETIC BASES (HERITABLE)



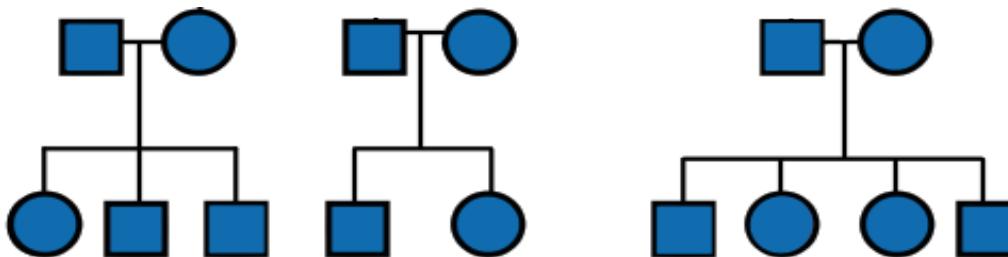
RESISTANCE 1 2 1 10 14

TOLERANCE 9 6 7 3 5

7 5 3 6

2 6 6 9

GENETIC BASES (HERITABLE)



RESISTANCE

1 2 1 10 14

TOLERANCE

9 6 7 3 5

7 5 3 6

2 6 6 9

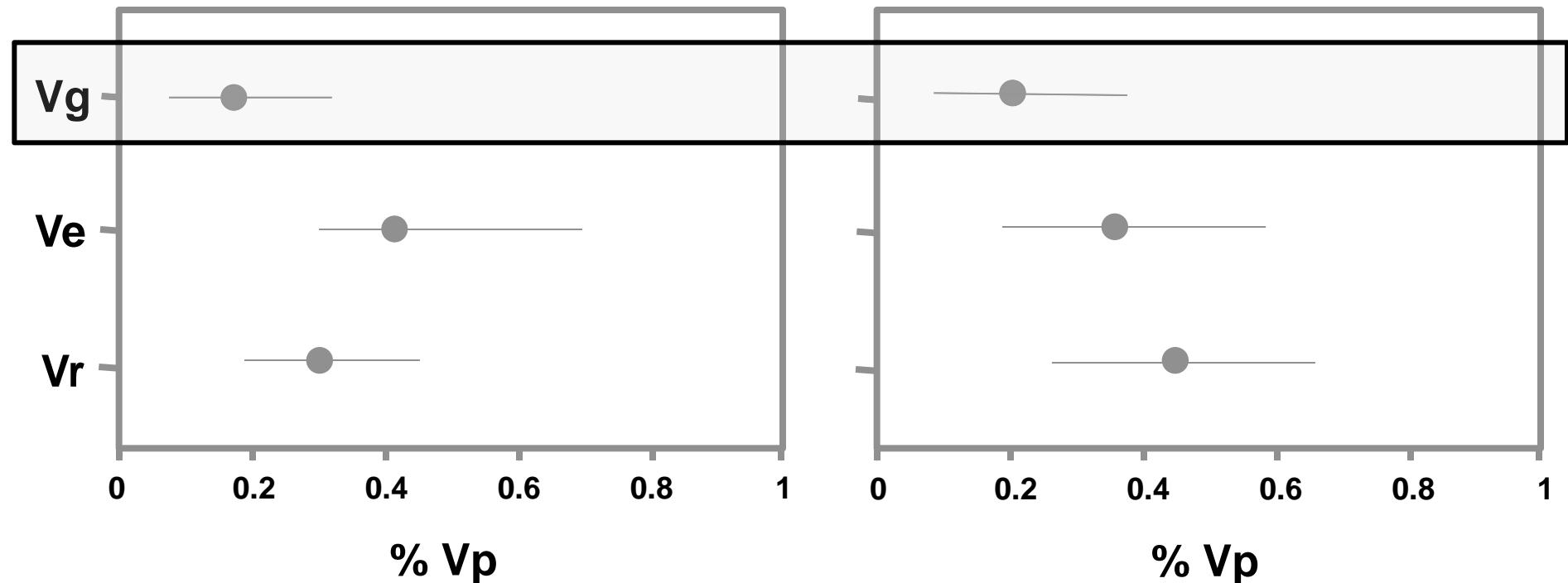
“ANIMAL MODELS” :

$$V_p = V_g + V_e + V_r$$

$$\Rightarrow H^2 = V_g / V_p$$

RESISTANCE

TOLERANCE



- SIGNIFICANT HERITABILITY VALUES FOR BOTH TRAITS
 - GENETIC BASES FOR BOTH DEFENSIVE TRAITS
- BASES FOR HOST ADAPTATION TO THIS NEW SELECTIVE PRESSURE



GOING INTO THE PHYSIOLOGICAL PATHWAYS OF RESISTANCE



Eglantine
Mathieu-Bégné

(IV) THE GENOMIC BASES OF RESISTANCE



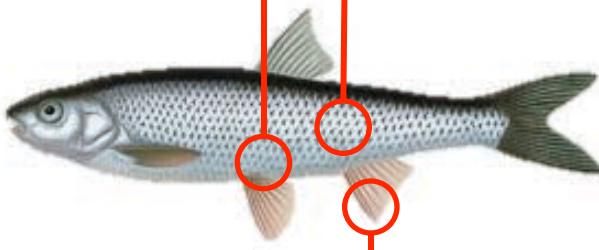
GOING INTO THE PHYSIOLOGICAL PATHWAYS OF RESISTANCE



Eglantine
Mathieu-Bégné

4 healthy vs.
4 parasitized

kidney spleen



RNA-seq

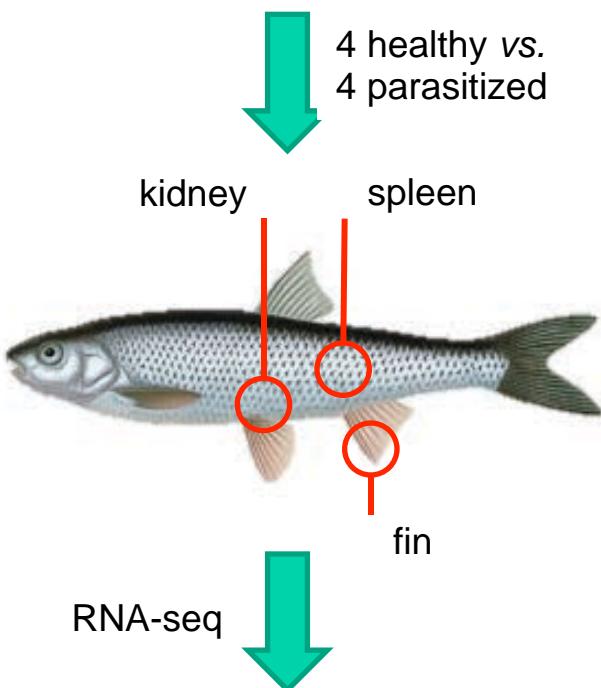
Gene expression profile
Biological functions



GOING INTO THE PHYSIOLOGICAL PATHWAYS OF RESISTANCE



Eglantine
Mathieu-Bégné



Gene expression profile
Biological functions

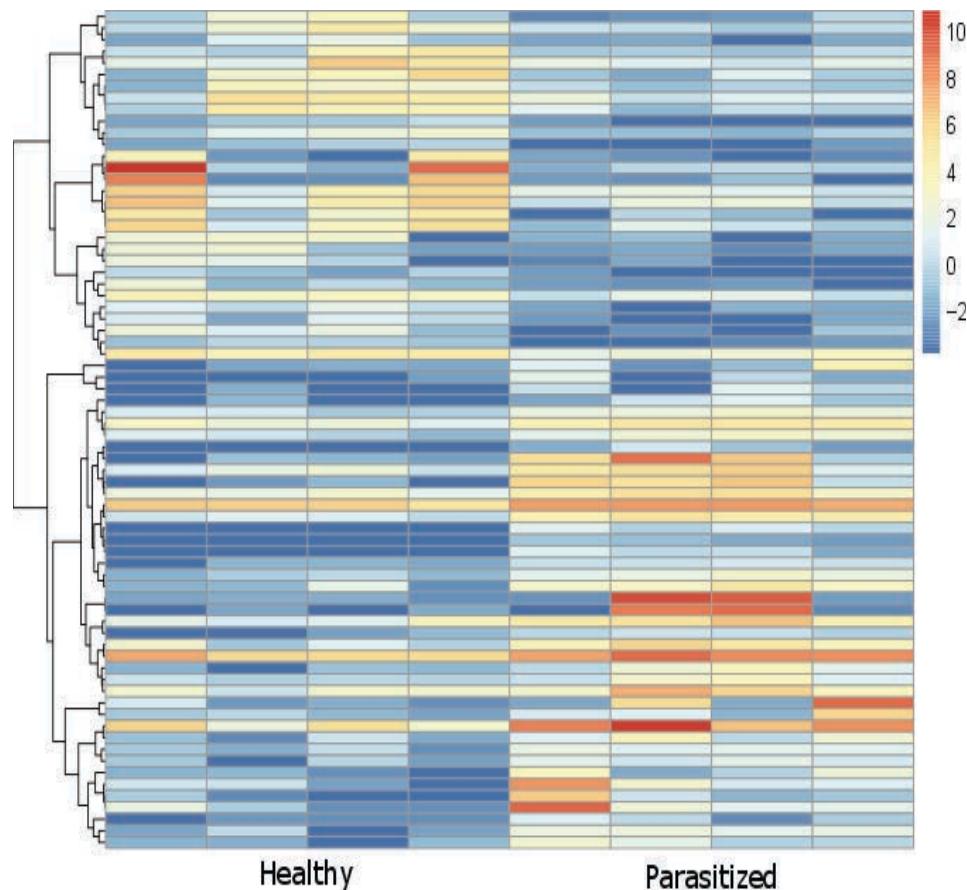
Understanding the physiological responses to an ectoparasite:

- **local (fin) response or general response?**
- **If general, is the response tissue-specific?**

(IV) THE GENOMIC BASES OF RESISTANCE



Genes expression profile



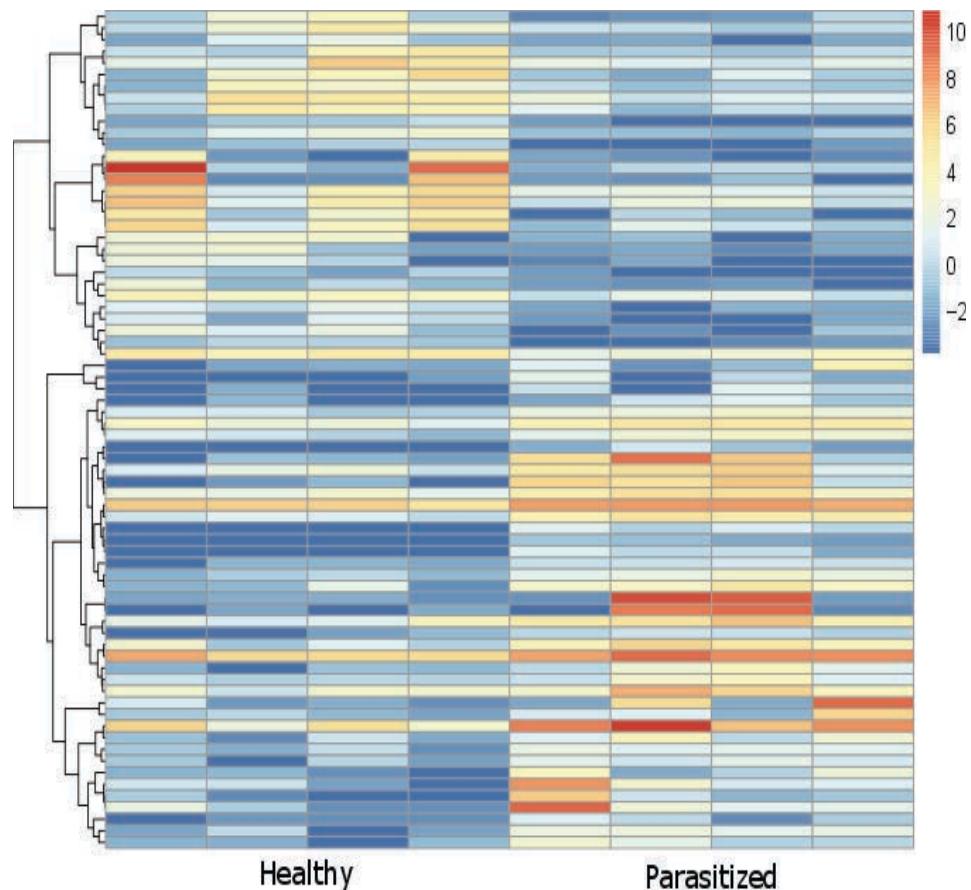
Heat map of genes expression profile:
example of the fin tissue

→ Some genes are differentially expressed depending on the health status

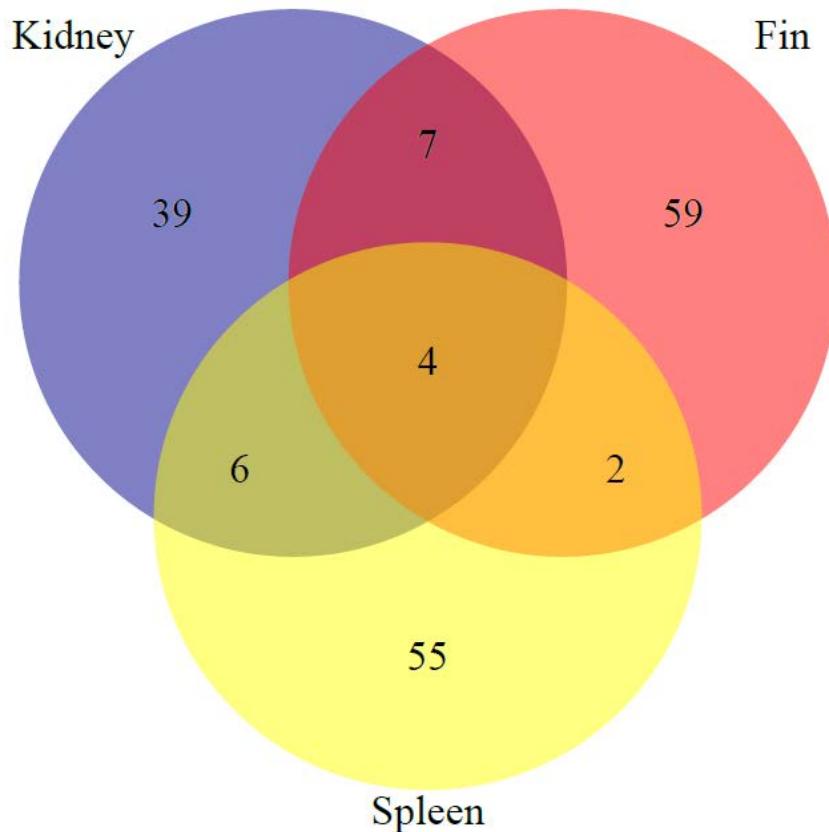
(IV) THE GENOMIC BASES OF RESISTANCE



Genes expression profile



Heat map of genes expression profile:
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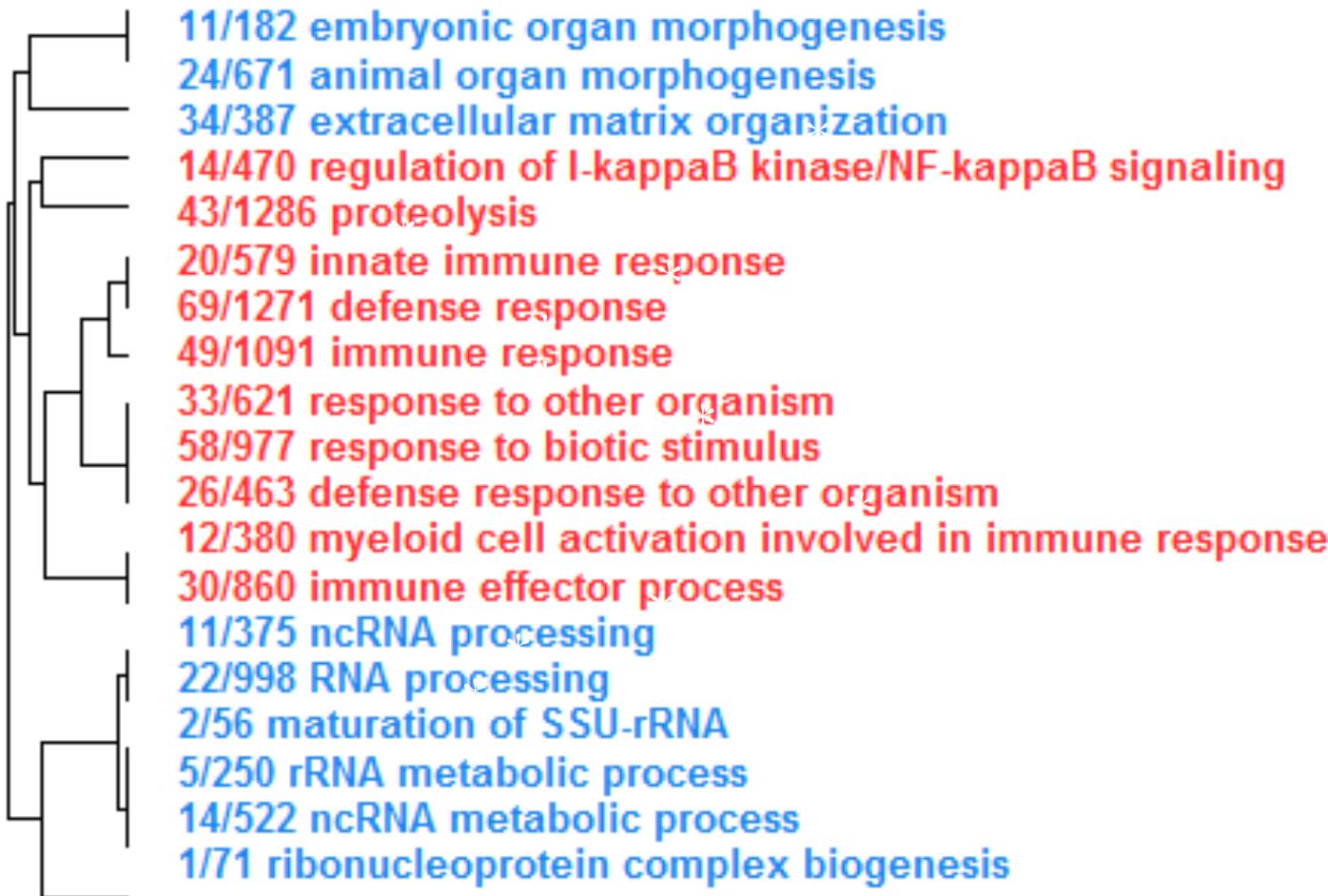


- Some genes are differentially expressed depending on the health status
- Host response is tissue specific



Biological functions involved

Fins



- Generalized immune response in parasitized fishes
- Metabolism/Immunity trade-offs



⇒ A NEWLY INTRODUCED SPECIES (< 200 generations)
 ⇒ SIGNIFICANT PATHOGENIC EFFECTS
 ⇒ POTENTIAL FOR HOST ADAPTATION



PARASITES = NEW SELECTIVE PRESSURE
= REAL-TIME ADAPTATION



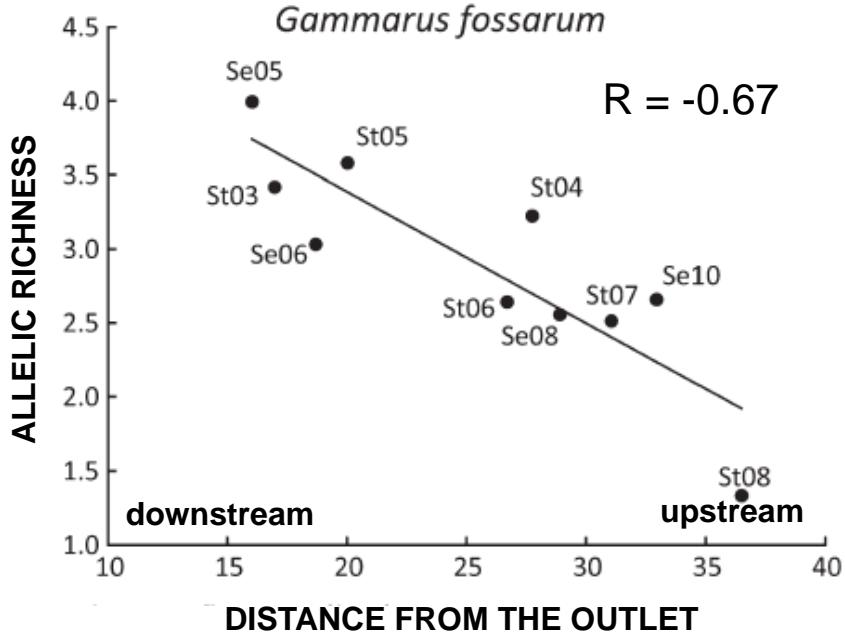
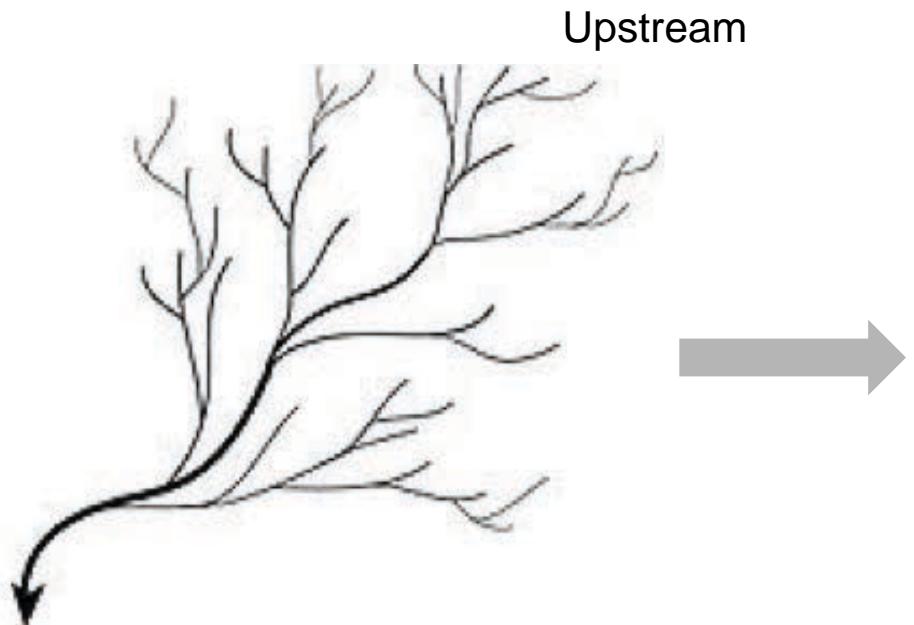
- 1) RIVER NETWORKS AND PATTERNS OF INTRASPECIFIC DIVERSITY**
- 2) ECOLOGICAL CONSEQUENCES OF INTRASPECIFIC DIVERSITY**
- 3) QUANTIFYING THE INFLUENCE OF HABITAT FRAGMENTATION**



INCREASE IN GENETIC DIVERSITY DOWNSTREAM (IGDD)



Ivan Paz-Vinas



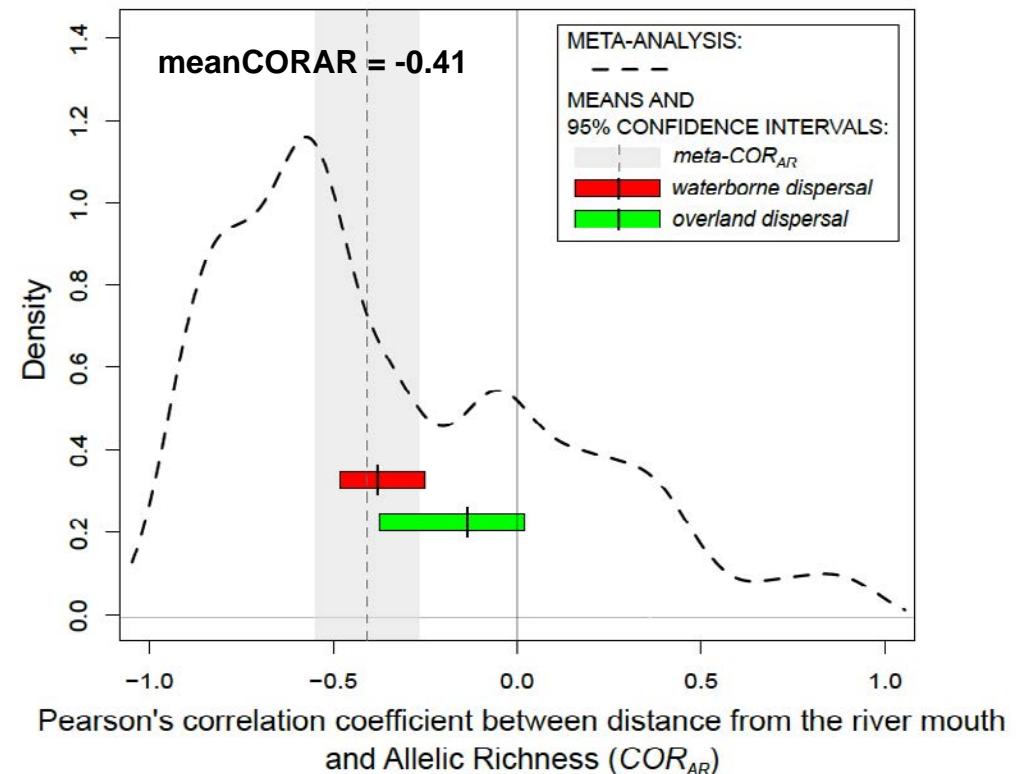
IS THAT A GENERAL PATTERN (RULE) FOUND ACROSS TAXA?



IGDD: A META-ANALYTIC TEST (79 case studies)

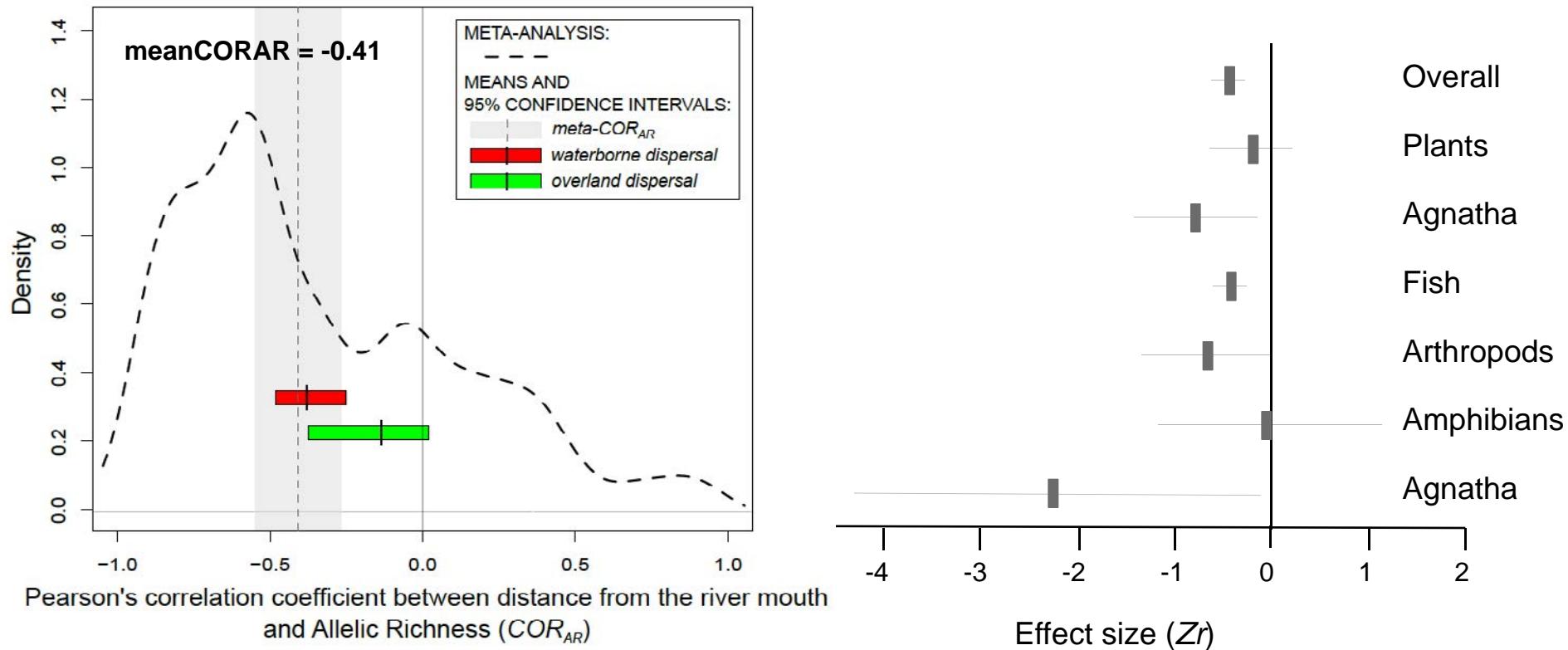


IGDD: A META-ANALYTIC TEST (79 case studies)





IGDD: A META-ANALYTIC TEST (79 case studies)

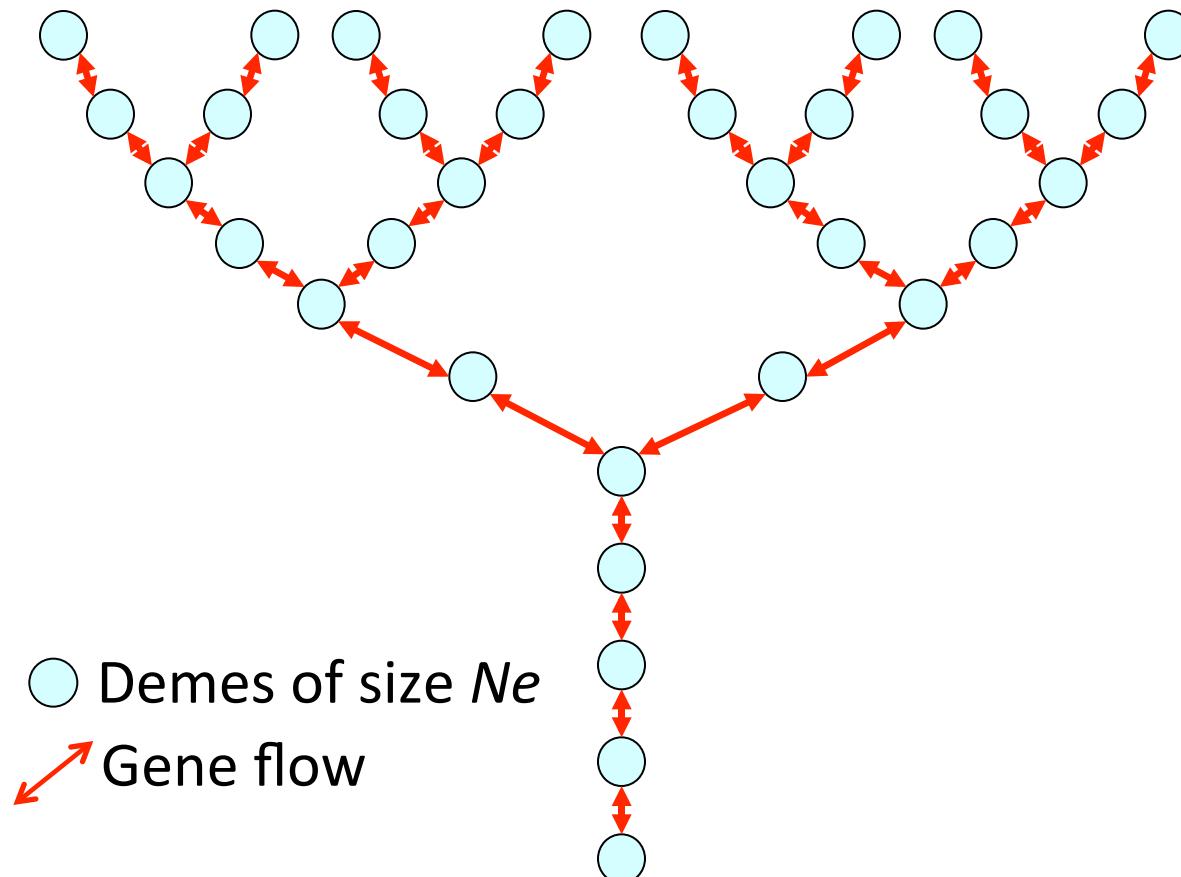


THE PATTERN HOLDS TRUE FOR SEVERAL TAXA

WHAT ARE THE PROCESSES BEHIND THIS GENERAL PATTERN?

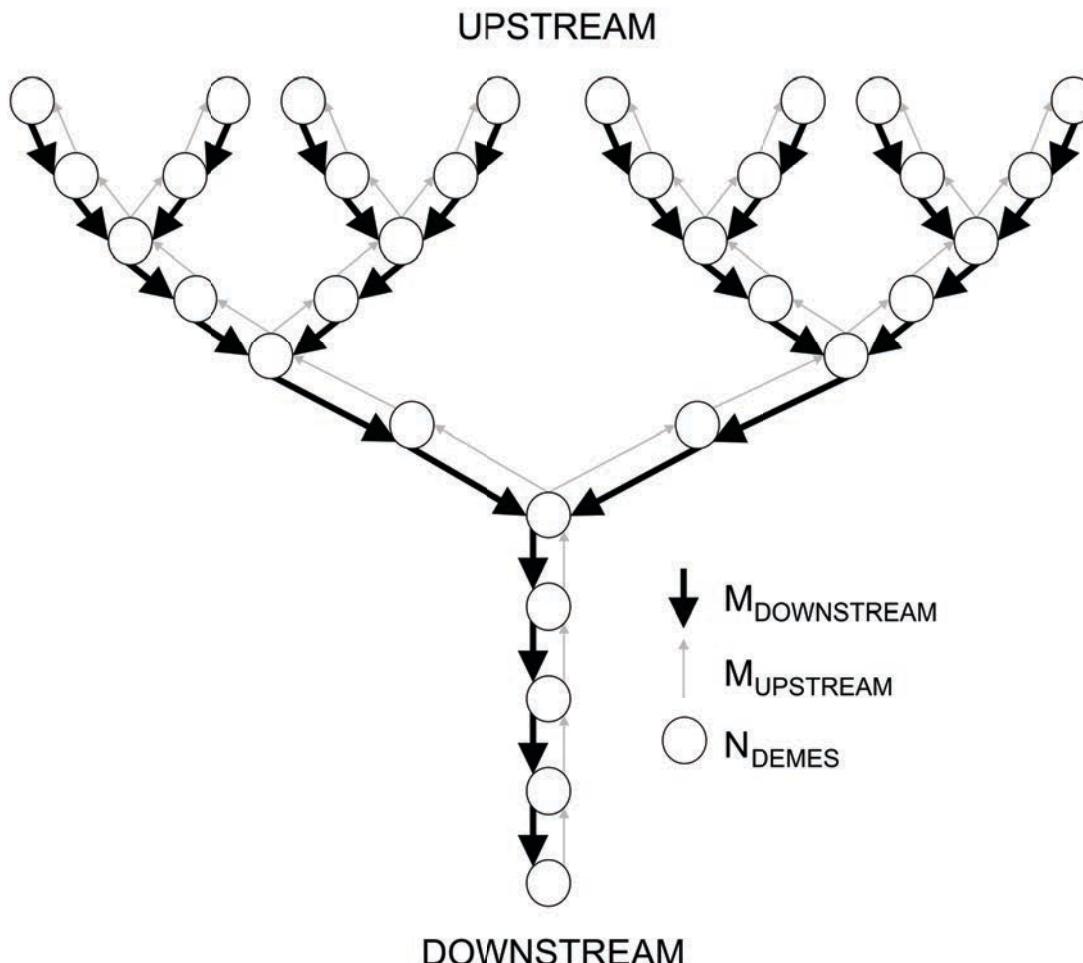


SIMULATIONS OF NEUTRAL GENETIC DIVERSITY IN RIVER NETWORKS





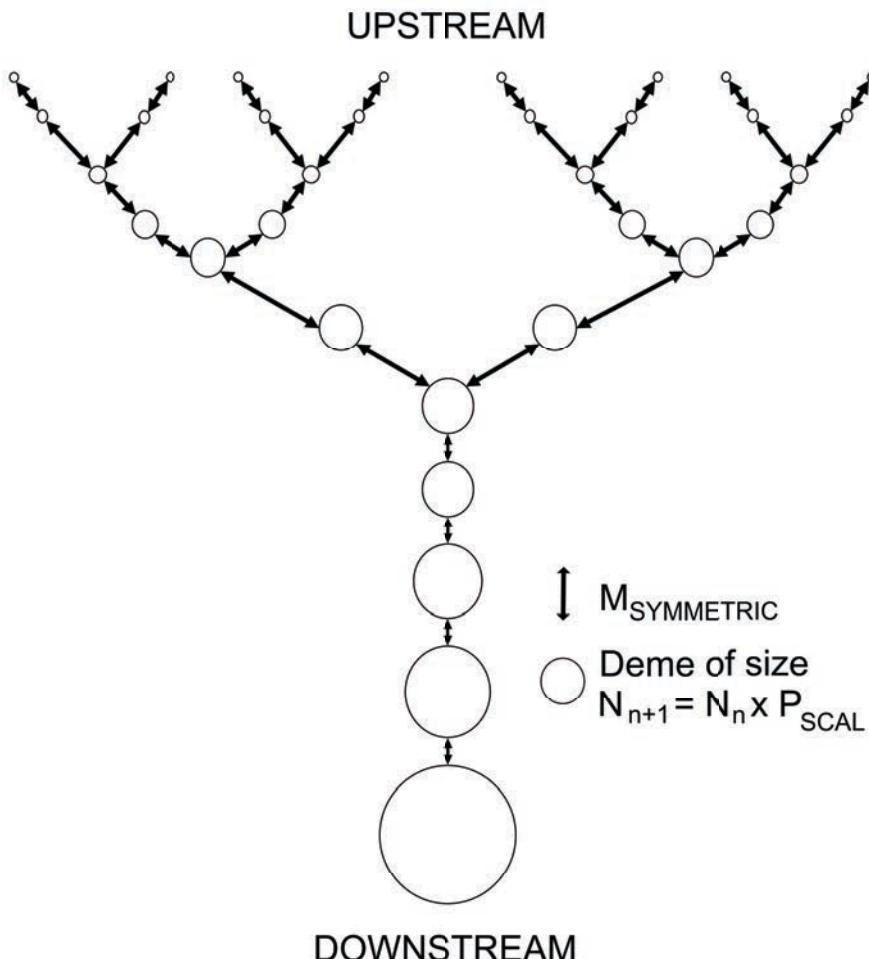
(A) ASYMMETRIC GENE FLOW MODEL



ACCUMULATION OF ALLELES DOWNSTREAM DUE TO
ASYMMETRIC GENE FLOW (ASYMM MODEL)



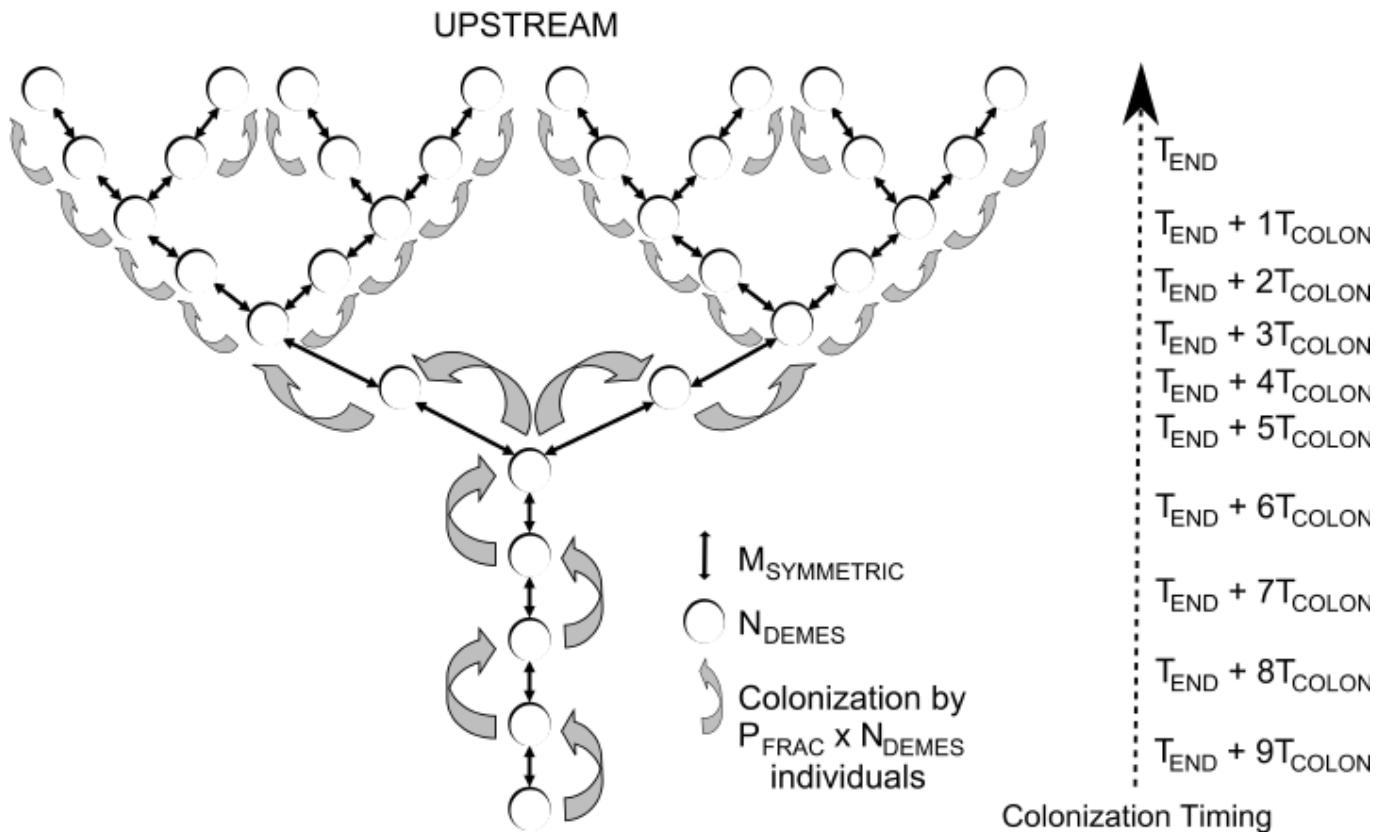
(C) DIFFERENTIAL IN N_e MODEL



HIGHER N_e DOWNSTREAM FAVOUR INCREASE GENETIC DIVERSITY DOWNSTREAM (DIFFNE MODEL)



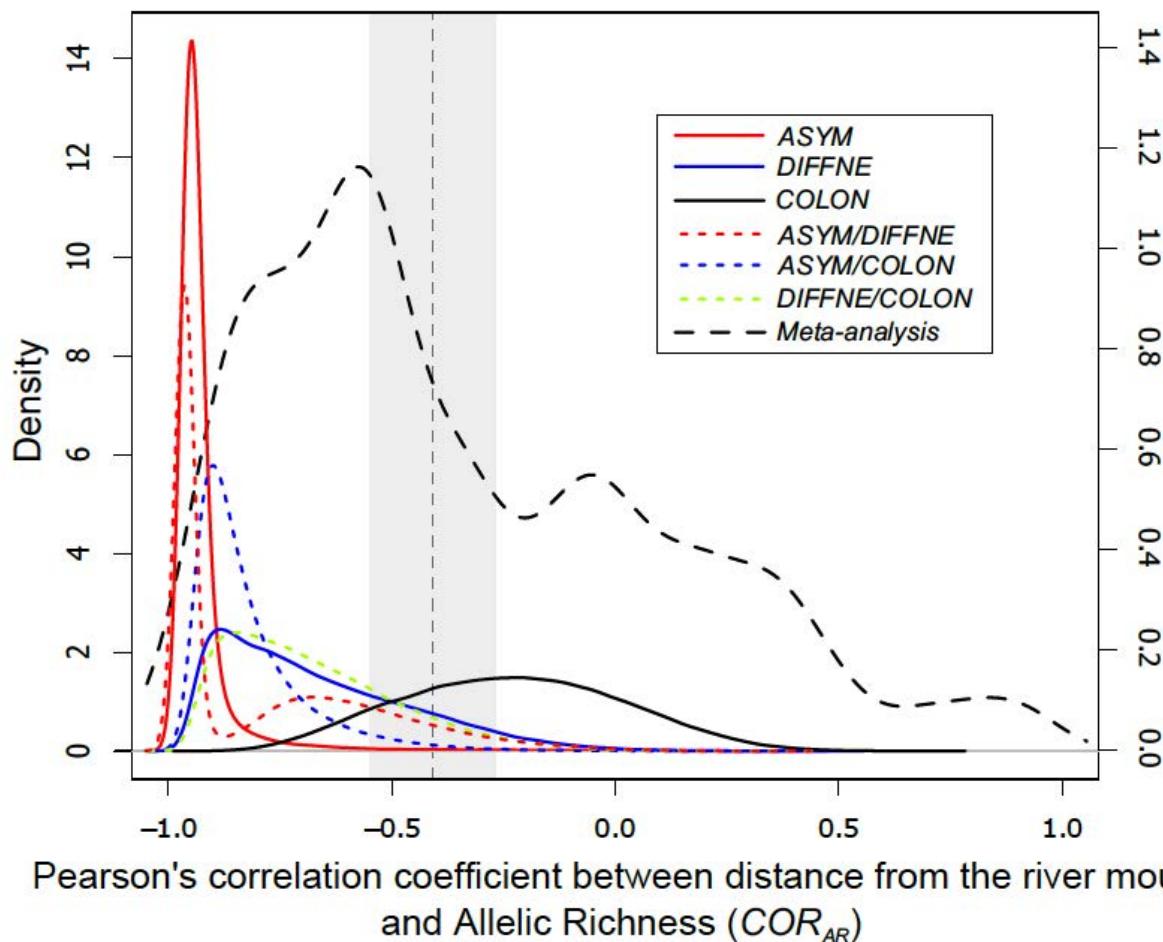
(B) COLONISATION MODEL



COLONISATION PROCESS BEGINNING DOWNSTREAM: LOSS OF ALLELES ALONG THE PROCESS (COLON MODEL)



SIMULATIONS UNDER ALL THESE POSSIBLE MODELS



ALL PROCESSES CAN GENERATE IGDD (IN THEORY), EITHER INDIVIDUALLY OR IN INTERACTION



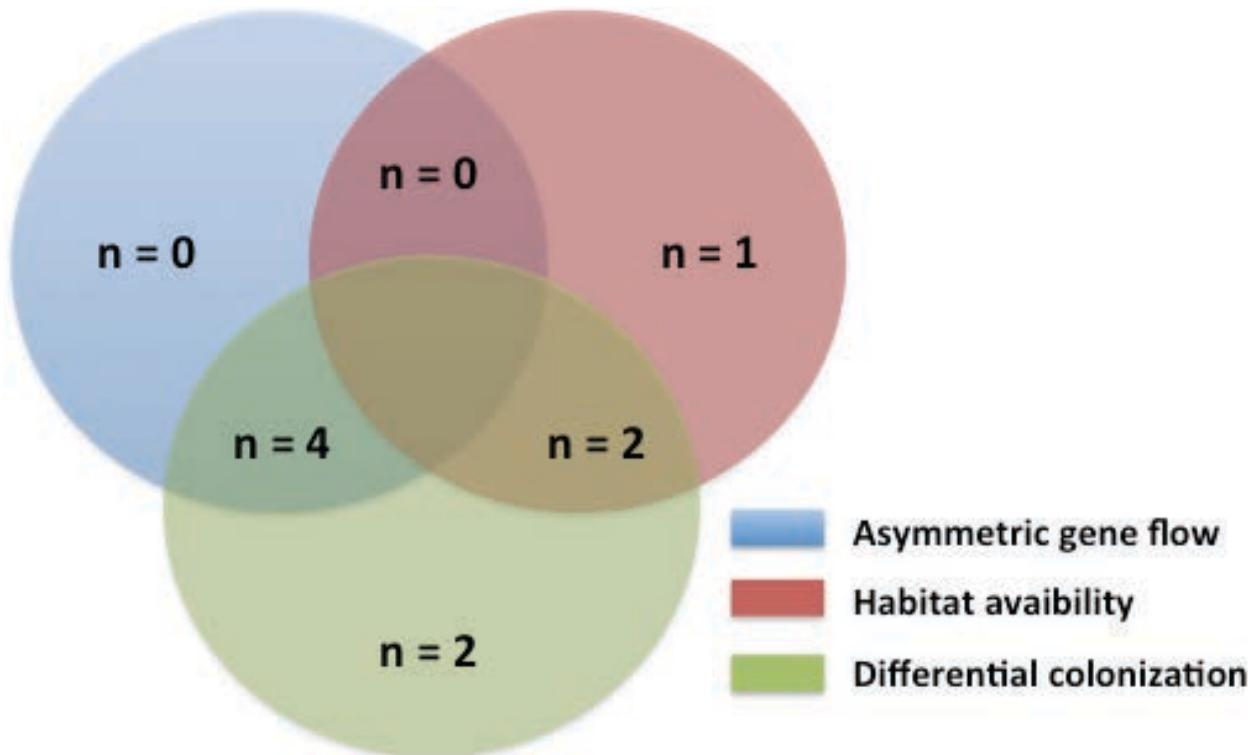
ABC APPROACH TO INFER PROCESSES IN THE WILD:

12 EMPIRICAL CASE STUDIES (fish, invertebrates...)



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12 EMPIRICAL CASE STUDIES (fish, invertebrates...)



**COLONISATION LEGACY AS AN IMPORTANT PROCESS
GENERATING PATTERNS OF GENETIC DIVERSITY IN THE WILD**



INTRASPECIFIC DIVERSITY VARIES SPATIALLY. DOES IT MATTER FOR ECOLOGICAL PROCESSES?



Allan Raffard



INTRASPECIFIC DIVERSITY VARIES SPATIALLY. DOES IT MATTER FOR ECOLOGICAL PROCESSES?

- do diverging populations have similar effects on ecosystem functioning?
- Are these effects of similar magnitude than climatic variation?



Allan Raffard

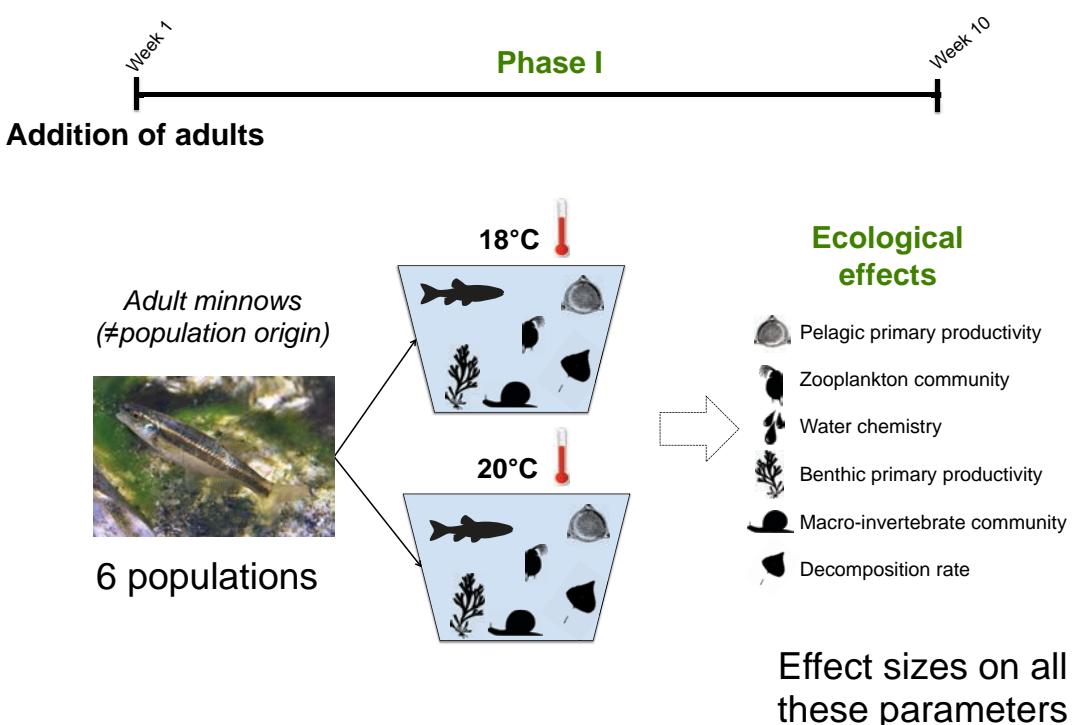


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Allan Raffard



(II) ECOLOGICAL CONSEQUENCES OF INTRASPECIFIC DIVERSITY

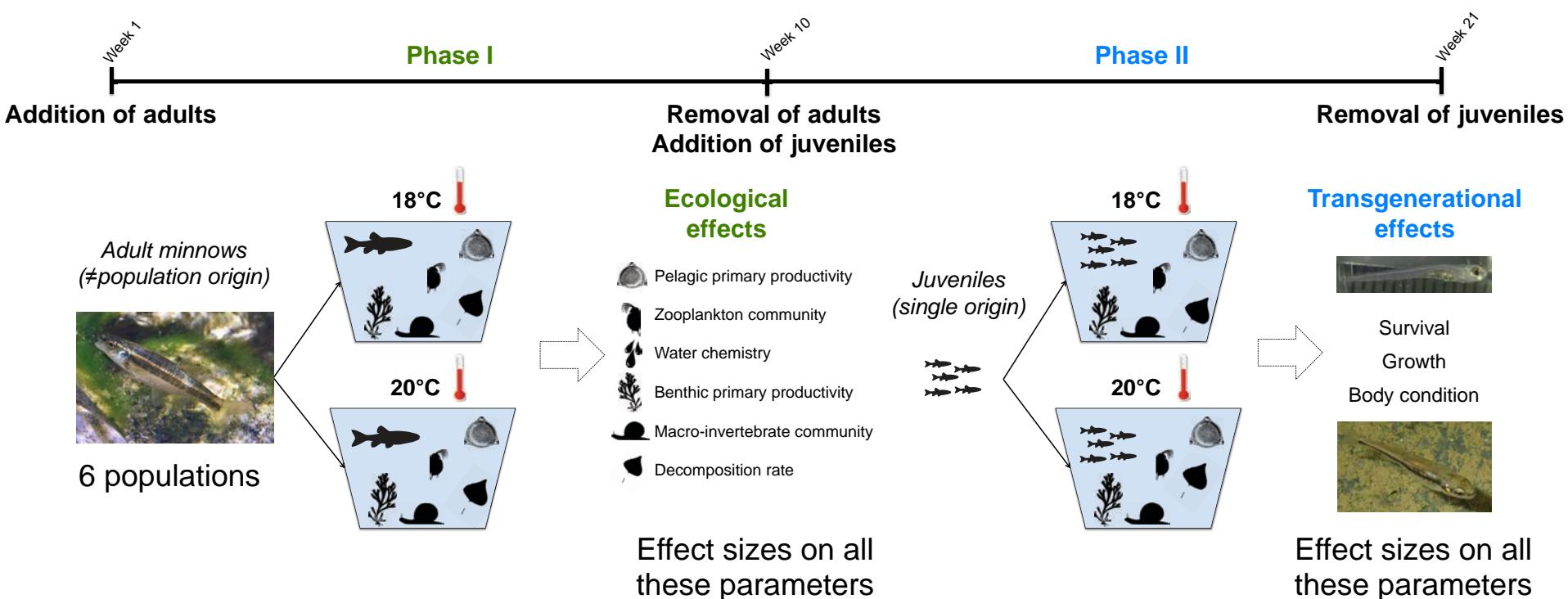


INTRASPECIFIC DIVERSITY VARIES SPATIALLY. DOES IT MATTER FOR ECOLOGICAL PROCESSES?

- do diverging populations have similar effects on ecosystem functioning?
- Are these effects of similar magnitude than climatic variation?

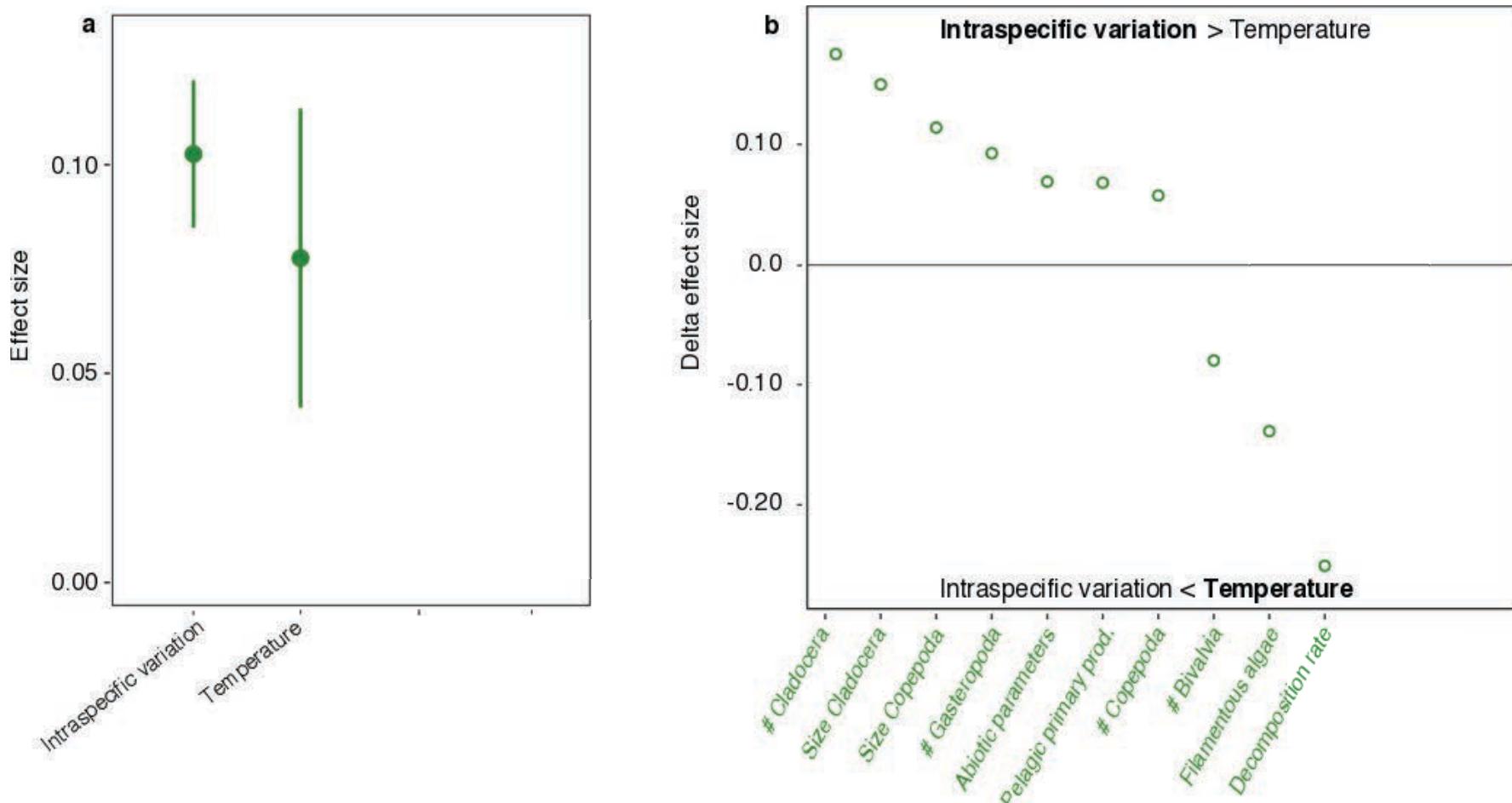


Allan Raffard





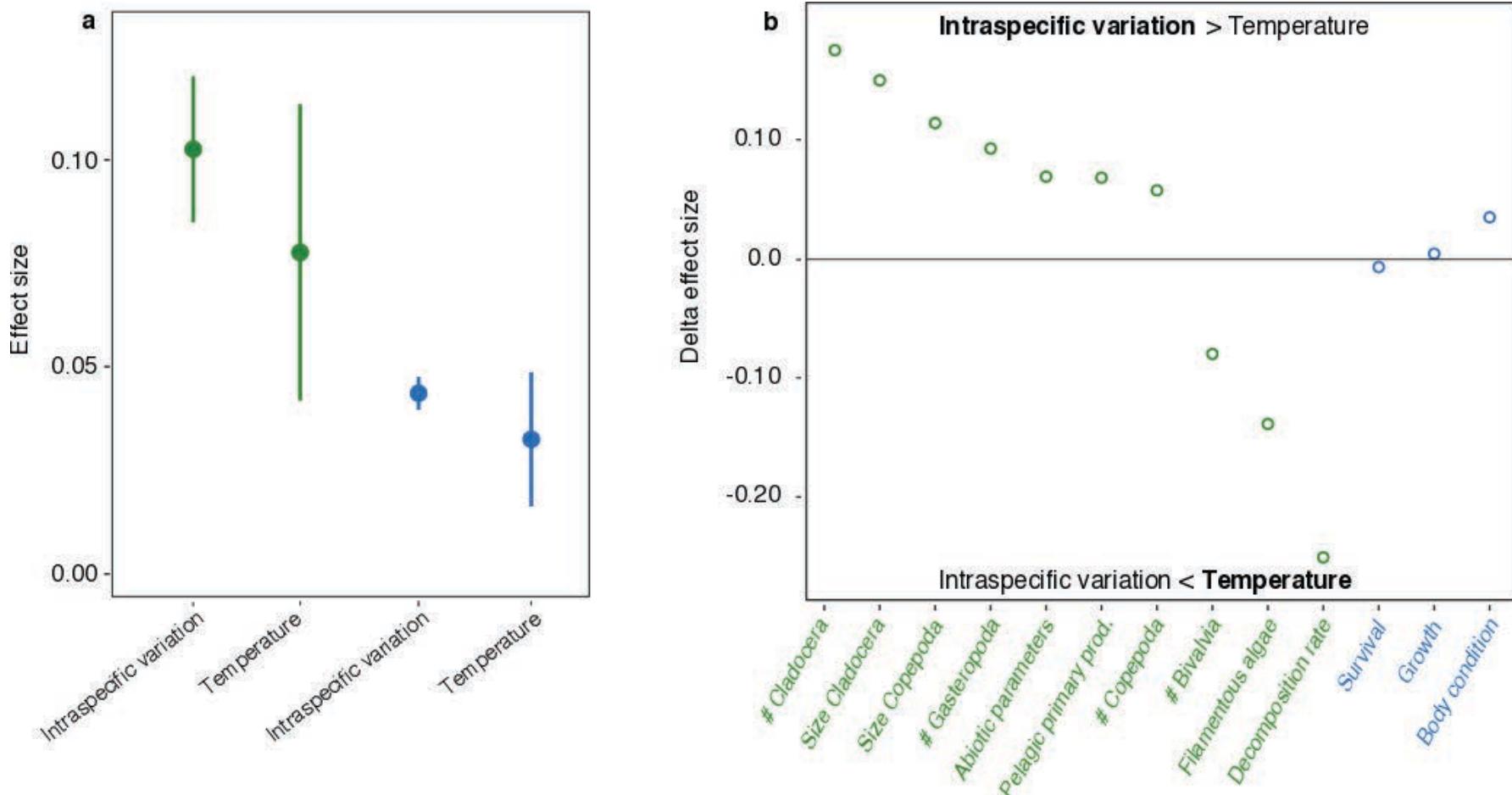
INTRASPECIFIC DIVERSITY STRONGLY IMPACTS ECOLOGY



ID HAS ECOLOGICAL EFFECTS OF SIMILAR STRENGTH THAN WARMING



INTRASPECIFIC DIVERSITY STRONGLY IMPACTS ECOLOGY...AND “EVOLUTION”.

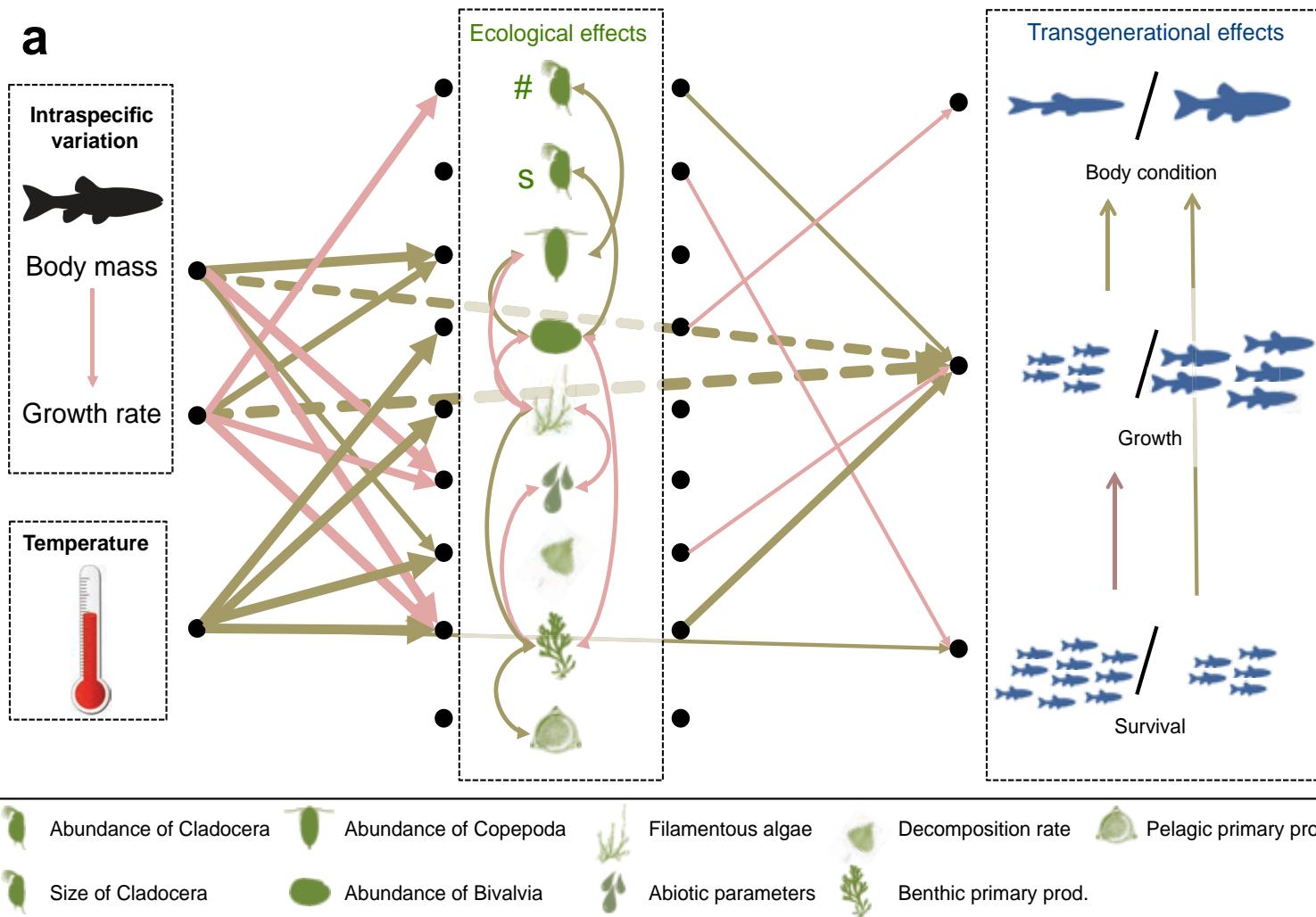


ID HAS ECOLOGICAL EFFECTS OF SIMILAR STRENGTH THAN WARMING LEADING TO ECO-EVO FEEDBACKS

(II) ECOLOGICAL CONSEQUENCES OF INTRASPECIFIC DIVERSITY



a



ID IS NOT DISTRIBUTED HOMOGENEOUSLY, AND THIS CAN HAVE CONSEQUENCES FOR ECOSYSTEM FUNCTIONING (AND EVOLUTION)

(III) ID AS A INDICATOR OF FRAGMENTATION



MANY OBSTACLES ALONG RIVERS: MAINLY WEIRS

Restoring connectivity by erasing or managing (fishpass) weirs and dams: costly. Hierarchizing actions is needed.





MANY OBSTACLES ALONG RIVERS: MAINLY WEIRS

Restoring connectivity by erasing or managing (fishpass) weirs and dams: costly. Hierarchizing actions is needed.



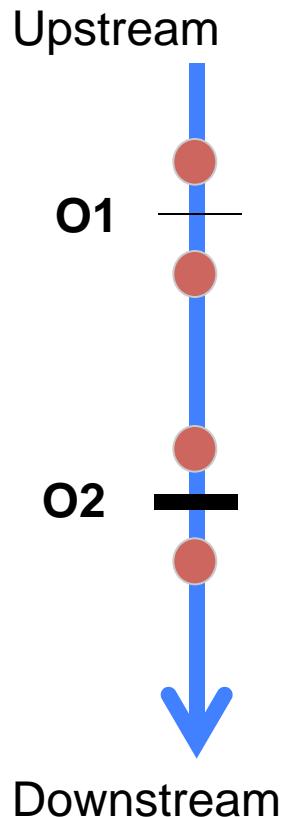
Using genetic differentiation (below-to-above design) to identify the most problematic weirs. But!

- How to take into account the age of the obstacle?
- How to take into account the size of populations?

(III) ID AS A INDICATOR OF FRAGMENTATION



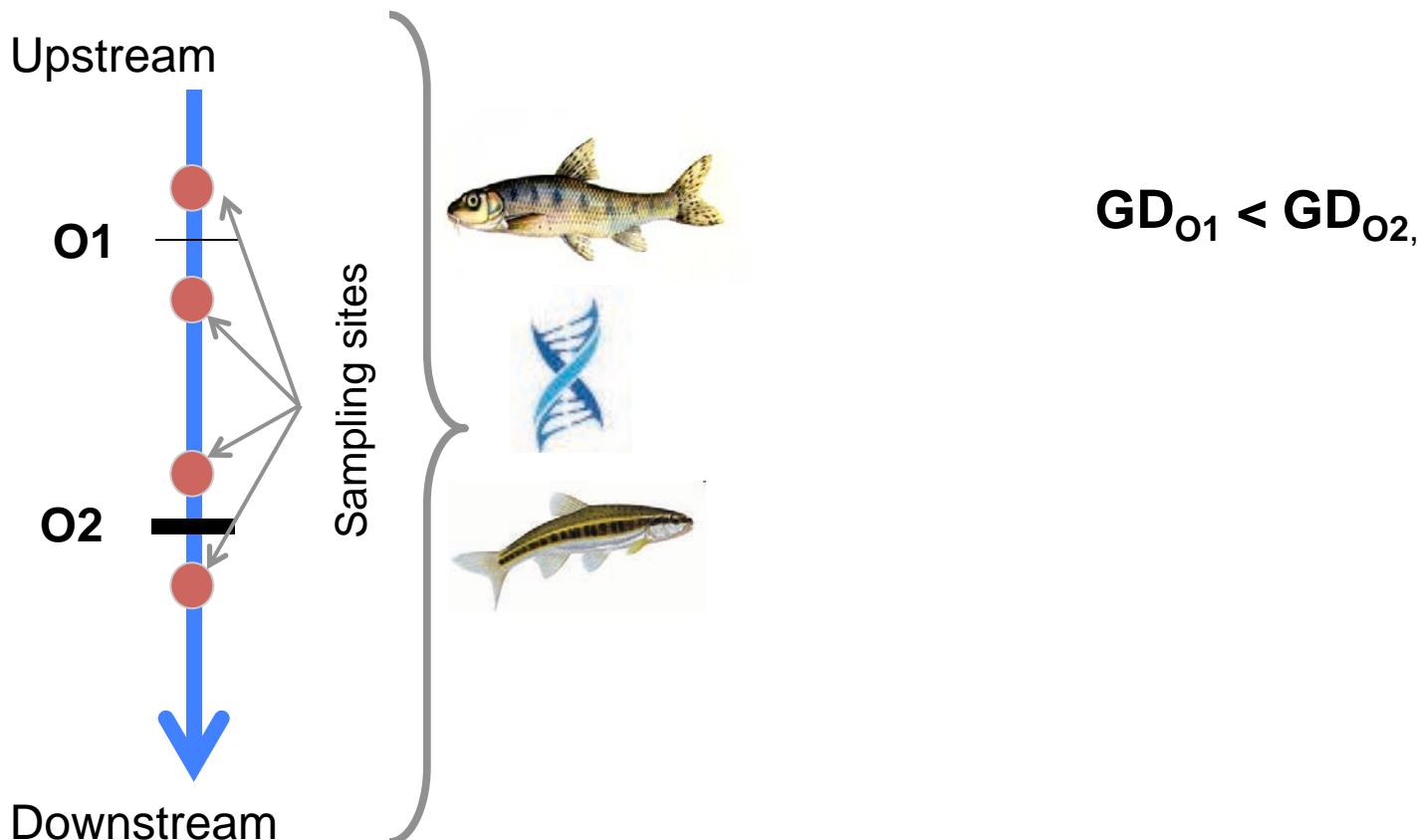
A below-to-above design quantifying genetic differentiation :



(III) ID AS A INDICATOR OF FRAGMENTATION



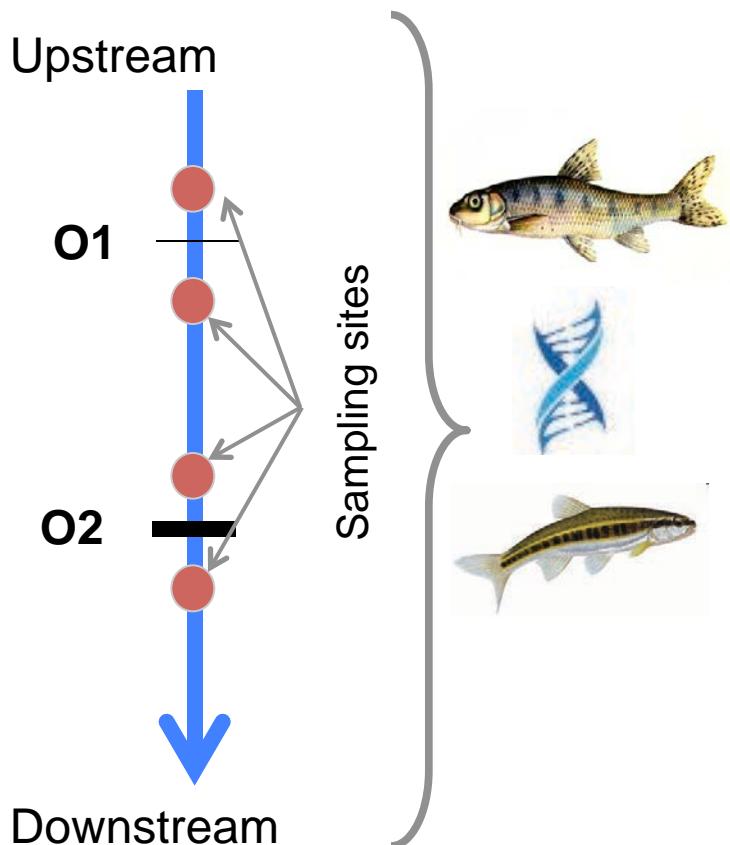
A below-to-above design quantifying genetic differentiation :



(III) ID AS A INDICATOR OF FRAGMENTATION



A below-to-above design quantifying genetic differentiation :



$$GD_{O1} < GD_{O2},$$

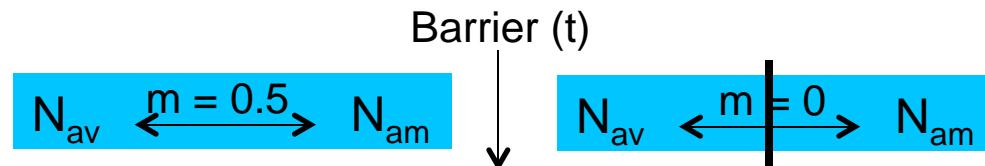
if:

- O1 and O2 of the same age
- Population size in O1 = O2

Designing an index of fragmentation (F) accounting for the age of obstacles and the local population size

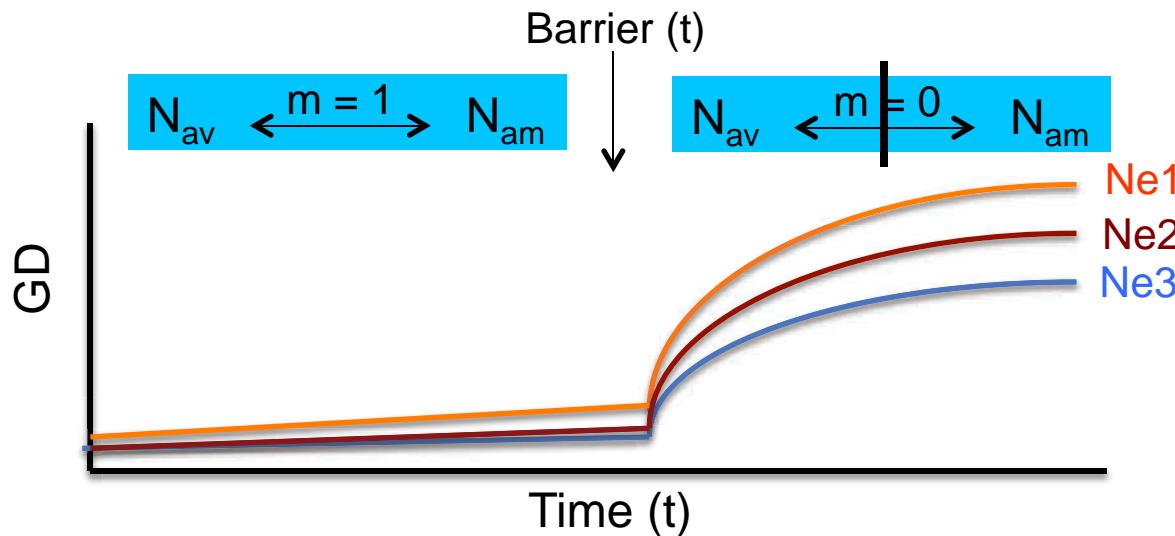
(III) ID AS A INDICATOR OF FRAGMENTATION

Step 1: Simulations. Calculating expected GD (eGD) if the barrier is total ($m=0$, maximum expected effect) according to N_e and Age (t)



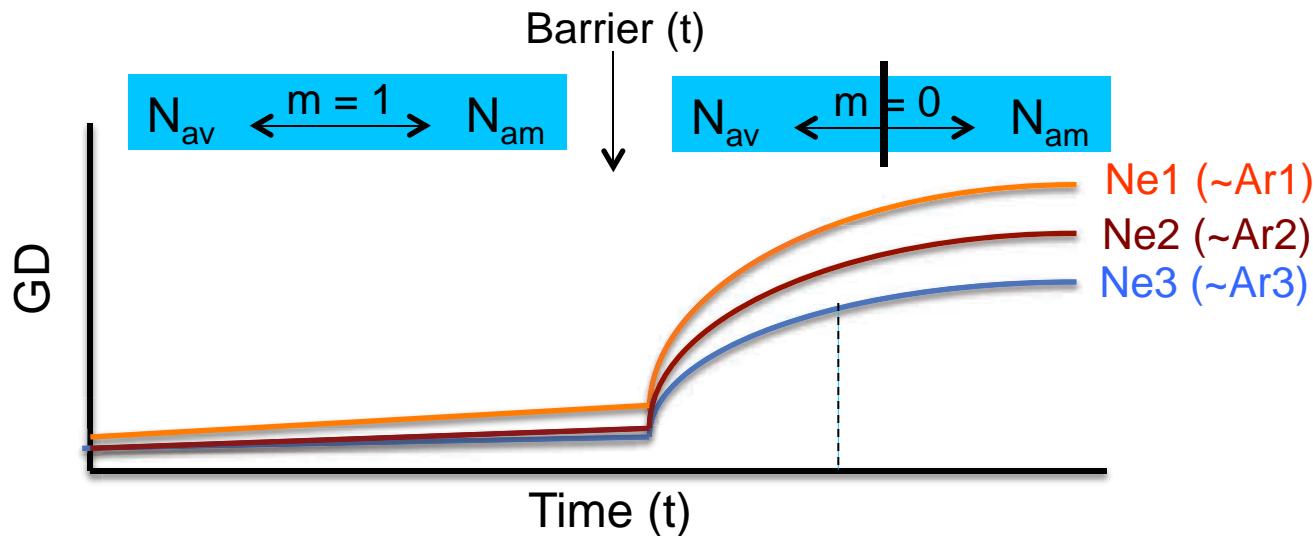
(III) ID AS A INDICATOR OF FRAGMENTATION

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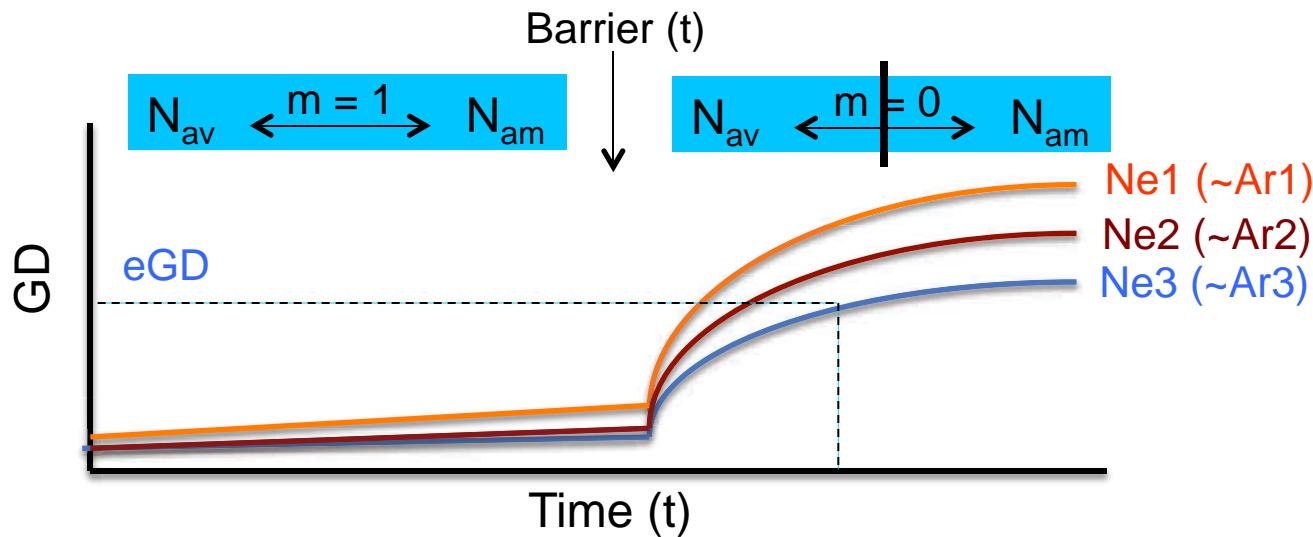
(III) ID AS A INDICATOR OF FRAGMENTATION

Step 1: Simulations. Calculating expected GD (eGD) if the barrier is total ($m=0$, maximum expected effect) according to N_e and Age (t)



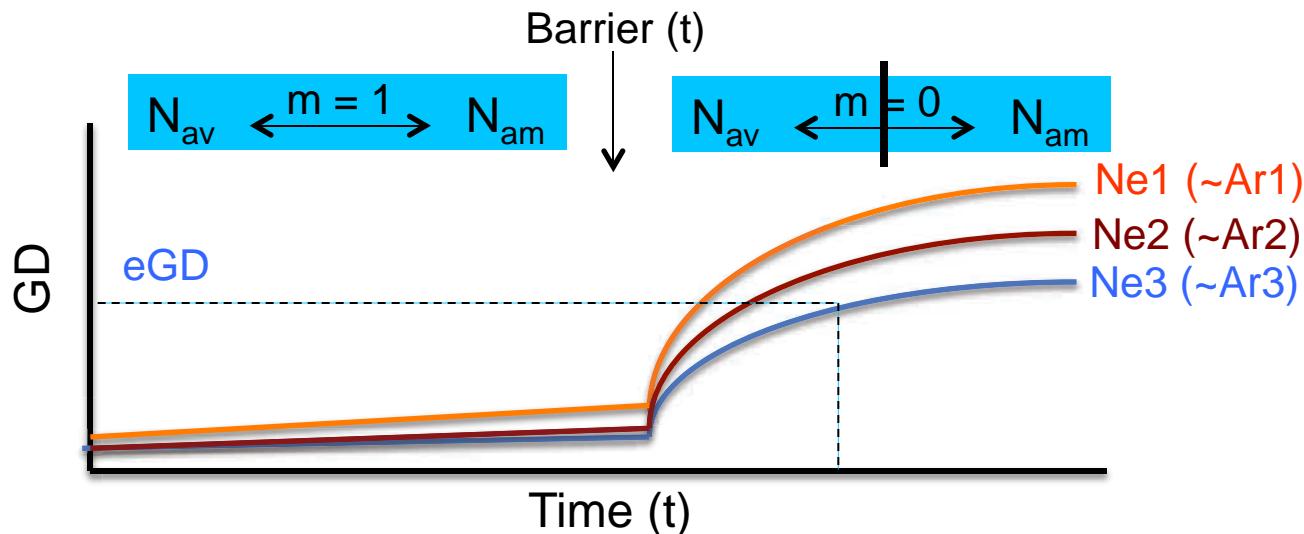
(III) ID AS A INDICATOR OF FRAGMENTATION

Step 1: Simulations. Calculating expected GD (eGD) if the barrier is total ($m=0$, maximum expected effect) according to N_e and Age (t)

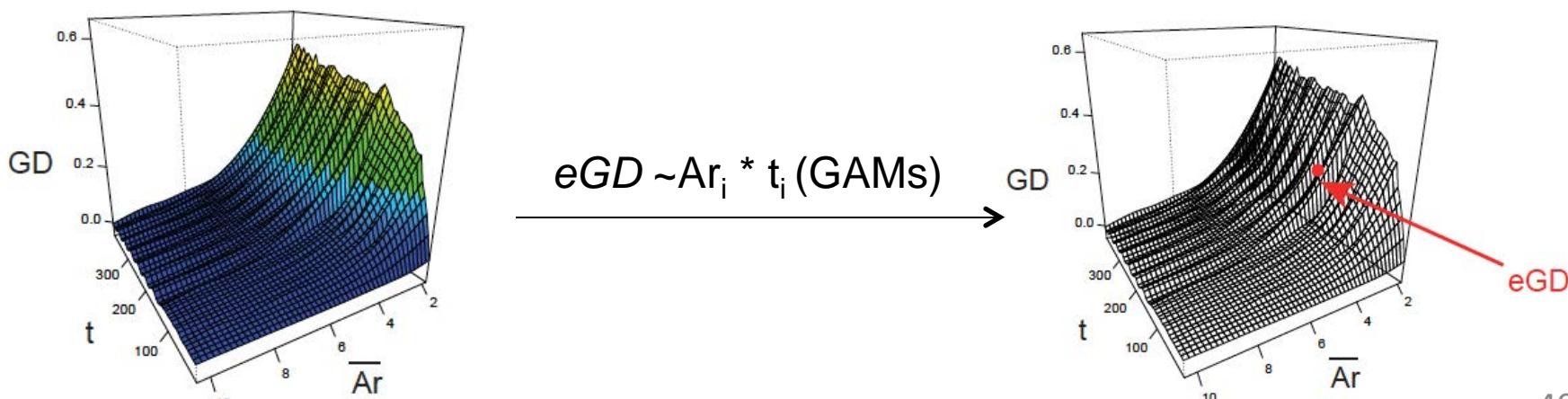


(III) ID AS A INDICATOR OF FRAGMENTATION

Step 1: Simulations. Calculating expected GD (eGD) if the barrier is total ($m=0$, maximum expected effect) according to Ne and Age (t)



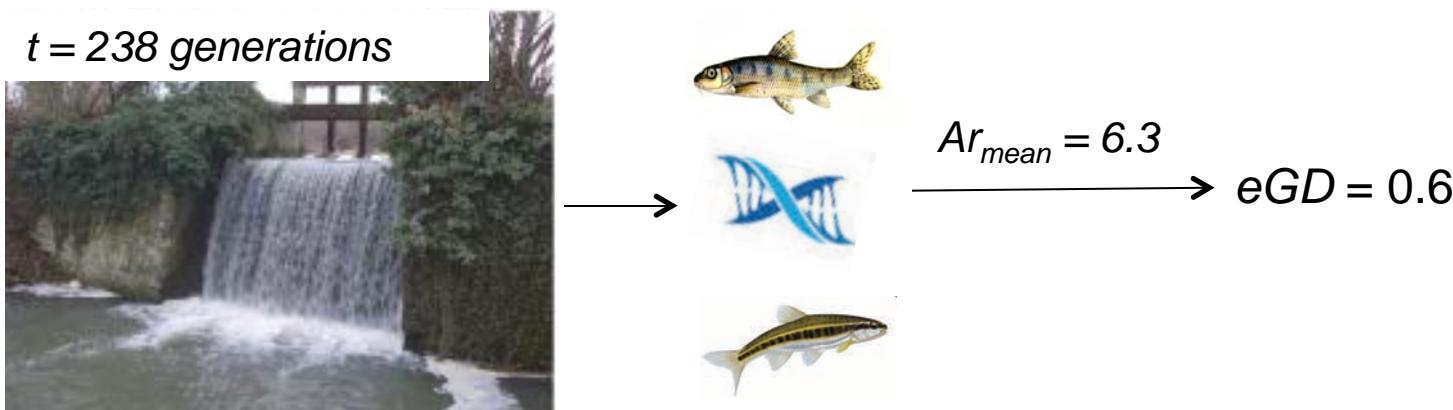
Step 2: Calibrating models (from simulations) to predict eGD from any Ne (Ar) and t



(III) ID AS A INDICATOR OF FRAGMENTATION



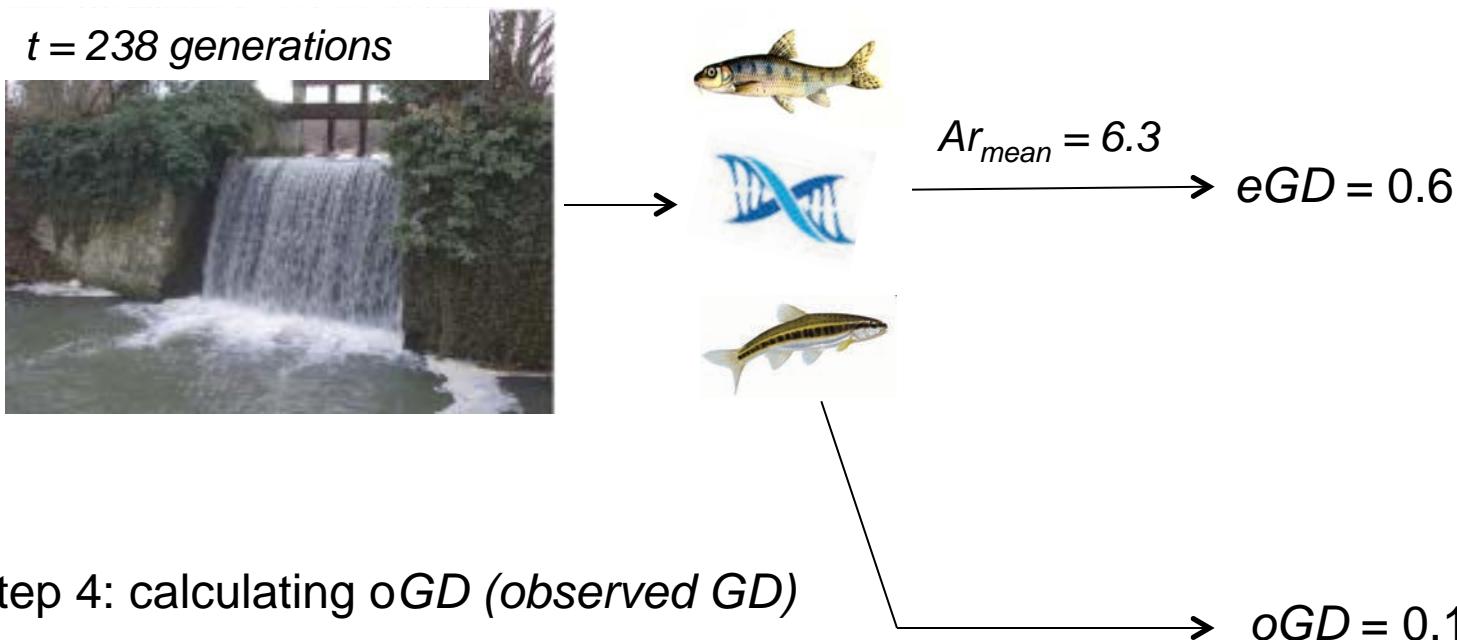
Step 3: using the models to estimate eGD from empirical Ar and t values



(III) ID AS A INDICATOR OF FRAGMENTATION



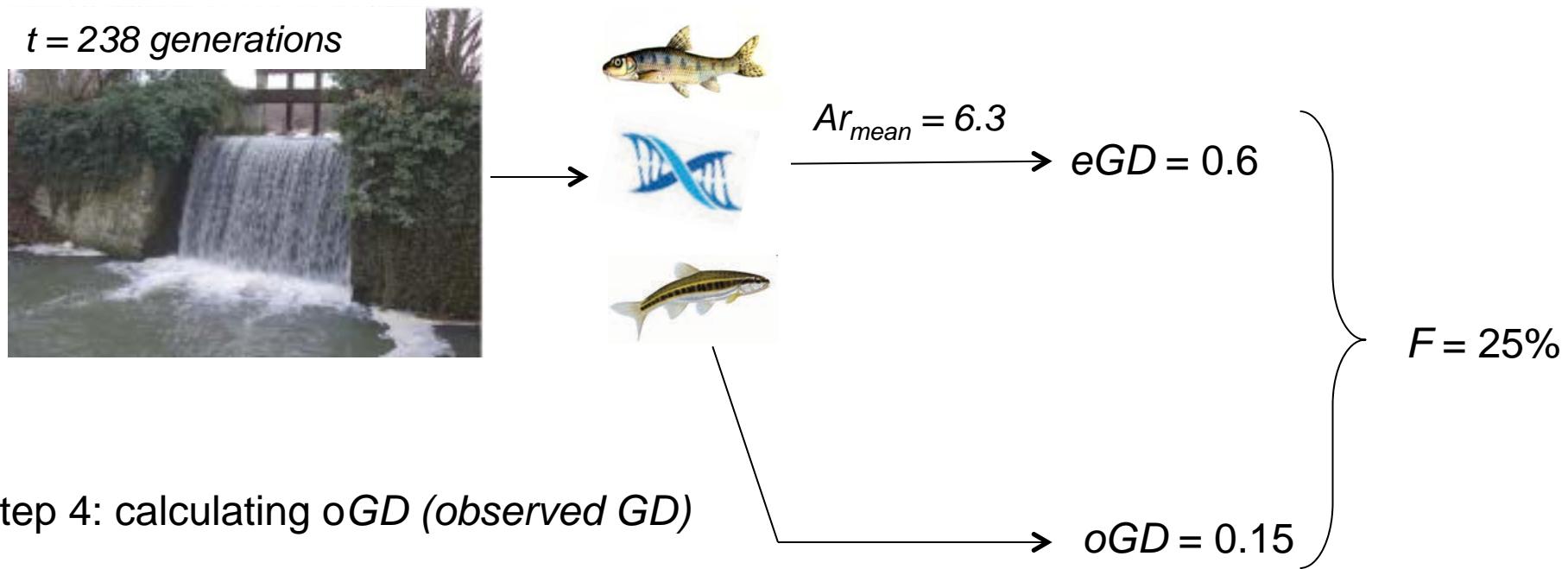
Step 3: using the models to estimate eGD from empirical Ar and t values



(III) ID AS A INDICATOR OF FRAGMENTATION



Step 3: using the models to estimate *eGD* from empirical *Ar* and *t* values



Step 4: calculating *oGD* (*observed GD*)

Step 5: calculating the fragmentation index: $F = [oGD/eGD]*100$

Percentage of an expected maximal effect, given N_e and t



(III) ID AS A INDICATOR OF FRAGMENTATION

Validation using independent simulations.

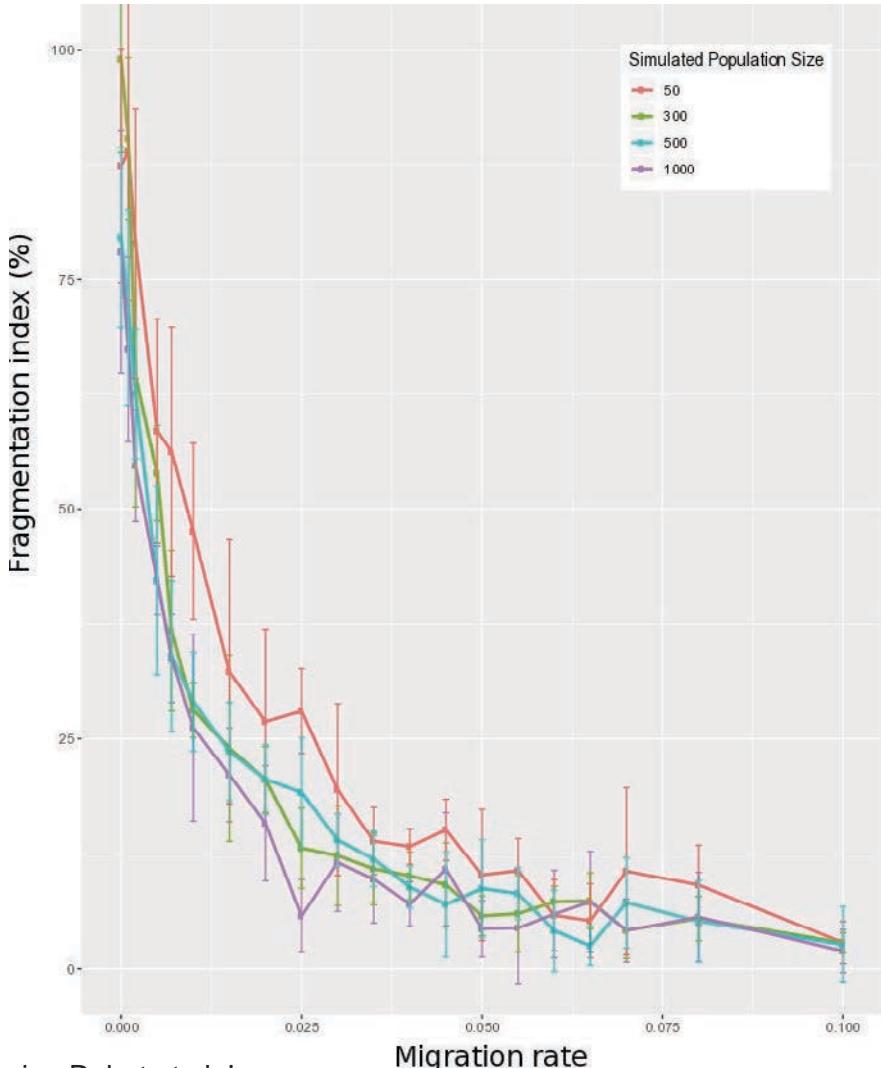
$$N_{av} < \boxed{N_{am}} \\ m = 0.2 - 0$$

(III) ID AS A INDICATOR OF FRAGMENTATION

Validation using independent simulations.

$$N_{av} < \boxed{ } > N_{am}$$

$$m = 0.2 - 0$$

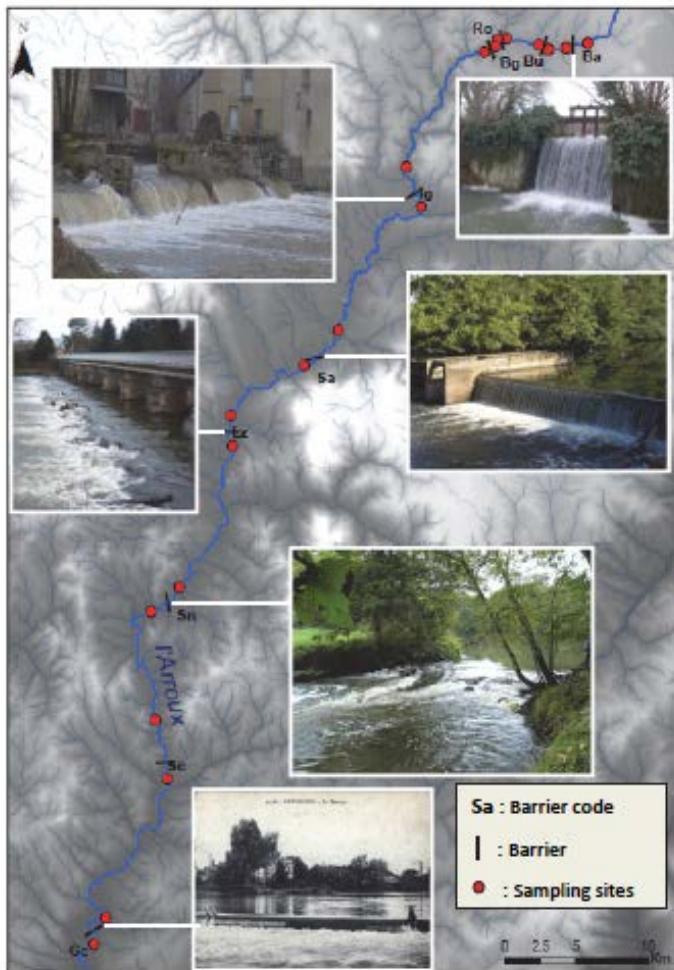


The index is close to 100% when $m = 0$ (total barrier)

The index decreases very quickly and is rapidly closed to 0% (no barrier effect detected when $m > 0.1$)

(III) ID AS A INDICATOR OF FRAGMENTATION

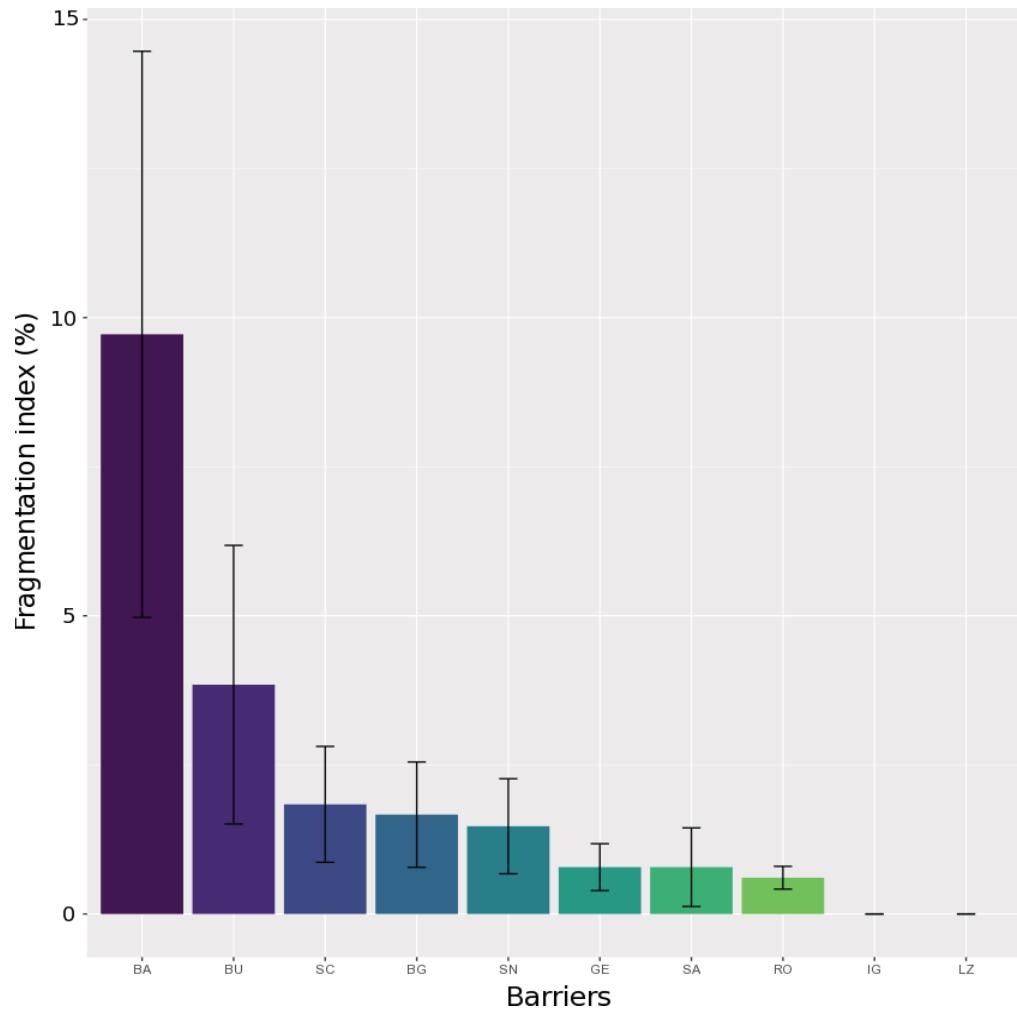
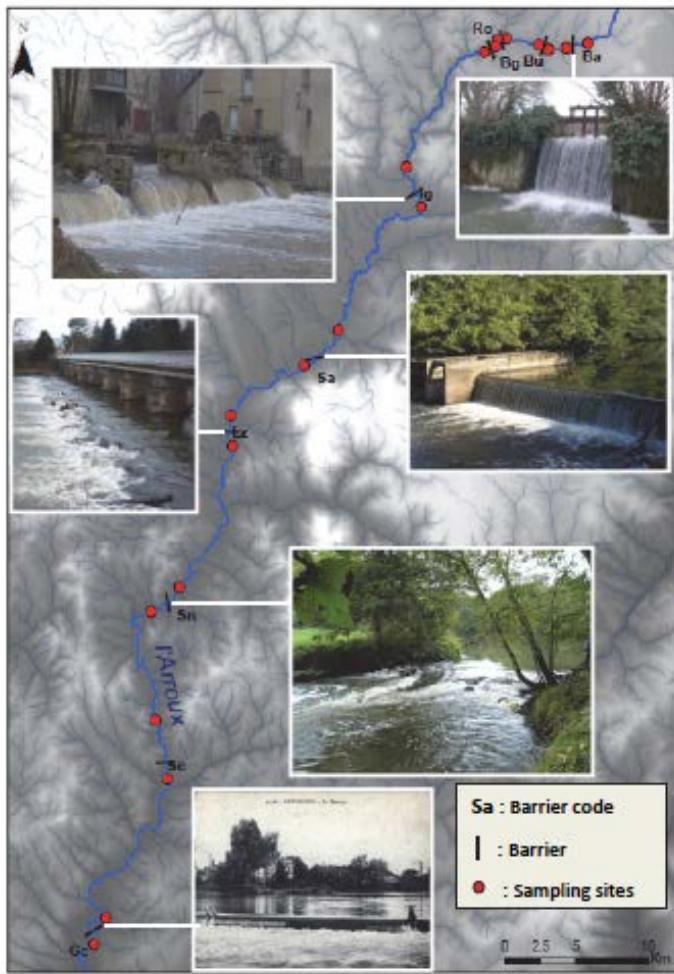
An empirical test on 10 obstacle along a river (Arroux)



(III) ID AS A INDICATOR OF FRAGMENTATION



An empirical test on 10 obstacle along a river (Arroux)



The index has relatively value (weirs are not impassables)

Variability among barriers: hierarchisation



- ⇒ DIVERSITY VARIES ALONG NETWORKS, PATTERNS ARE REPEATABLE
- ⇒ DECIPHERING THESE PROCESSES IS POSSIBLE
- ⇒ DIVERSITY IS NOT ECOLOGICALLY TRIVIAL. IT HAS STRONG IMPACTS ON ECOLOGICAL DYNAMICS
- ⇒ CONSERVATION OF THESE EVOLUTIONARY AND ECOLOGICAL SIGNIFICANT UNITS IS REQUIRED
- ⇒ IT IS ALSO A USEFUL INDICATOR FOR SOME HUMAN PRESSURES

ACKNOWLEDGMENTS

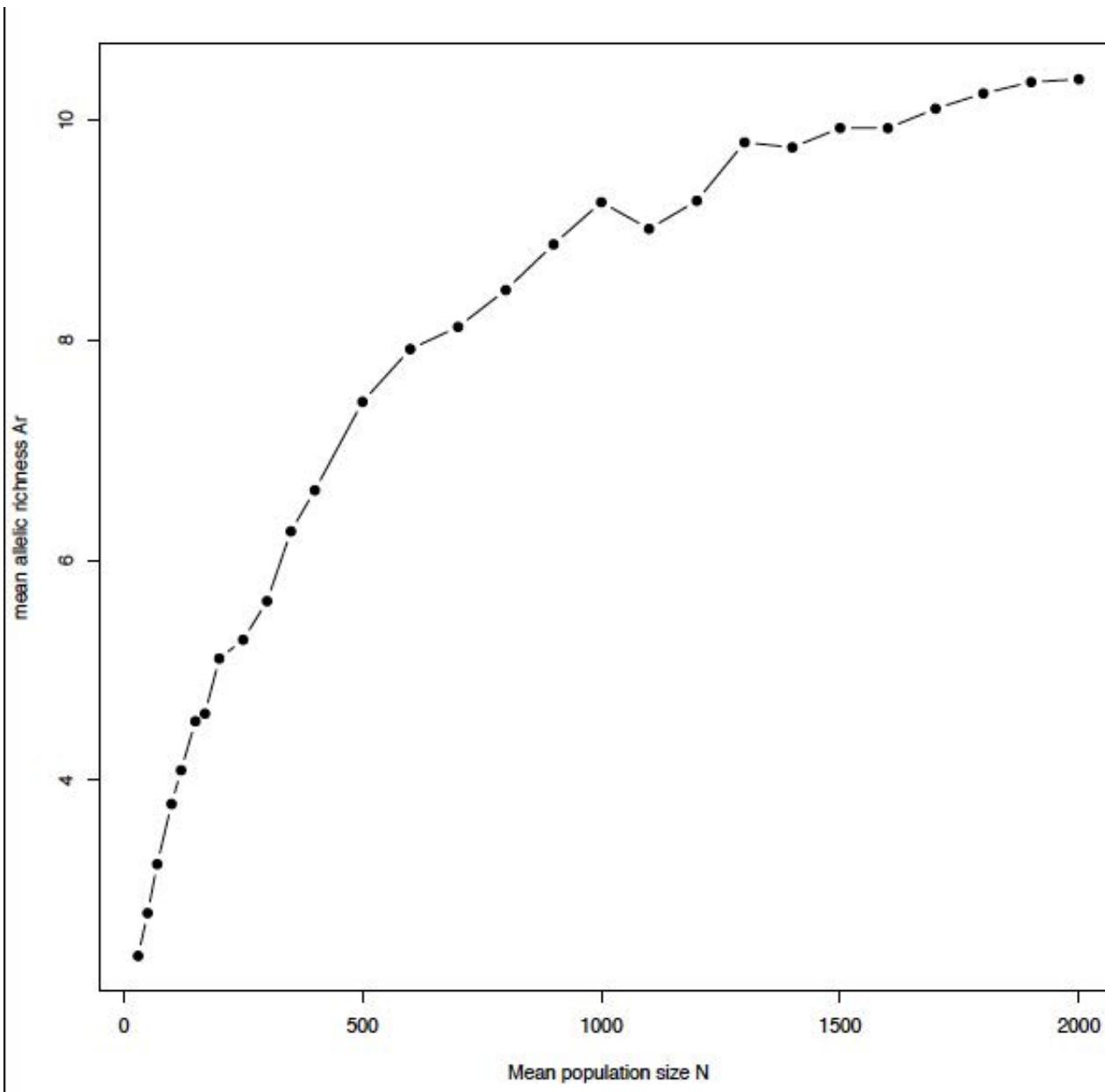


LES FINANCEURS



ET VOUS.

(III) INTRASPECIFIC DIVERSITY AND CONSERVATION PLANNING





**INTRASPECIFIC DIVERSITY VARIES SPATIALLY AND IT MATTERS FOR ECOLOGICAL PROCESSES.
HOW TO PRIORITIZE CONSERVATION AREAS FOR ID?**

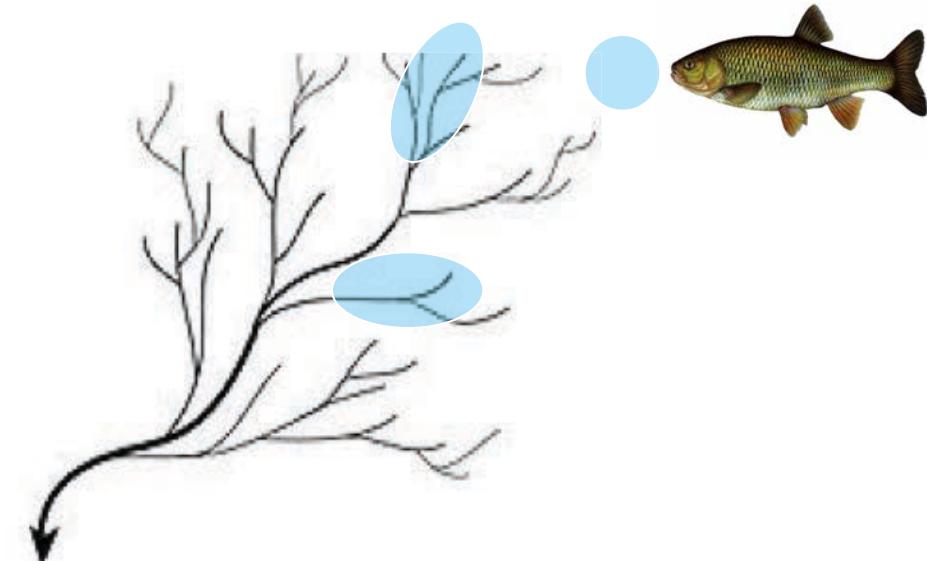




**INTRASPECIFIC DIVERSITY VARIES SPATIALLY AND IT MATTERS FOR ECOLOGICAL PROCESSES.
HOW TO PRIORITIZE CONSERVATION AREAS FOR ID?**



Ivan Paz-Vinas



WHICH PARTS OF THE NETWORK SHOULD WE TARGET TO CONSERVE INTRASPECIFIC DIVERSITY?



INTRASPECIFIC DIVERSITY VARIES SPATIALLY AND IT MATTERS FOR ECOLOGICAL PROCESSES.
HOW TO PRIORITIZE CONSERVATION AREAS FOR ID?



Ivan Paz-Vinas



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Ivan Paz-Vinas



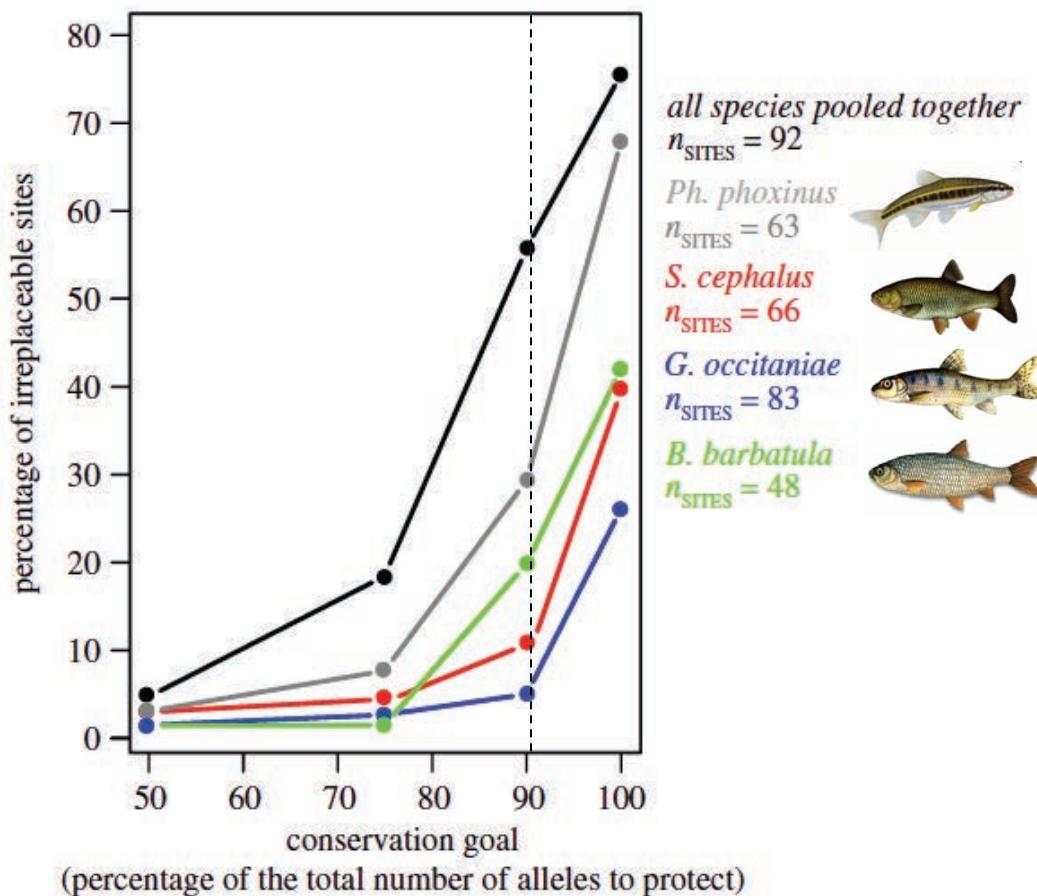
A multispecies conservation planning approach:

- 6 species sampled in 92 sites and typed for microsatellites
- Identifying the sites (*irreplaceable sites*) required to cover a certain amount of genetic diversity (*conservation target*)
- Mapping these sites and testing for congruencies among species

WHICH PARTS OF THE NETWORK SHOULD WE TARGET TO CONSERVE INTRASPECIFIC DIVERSITY?



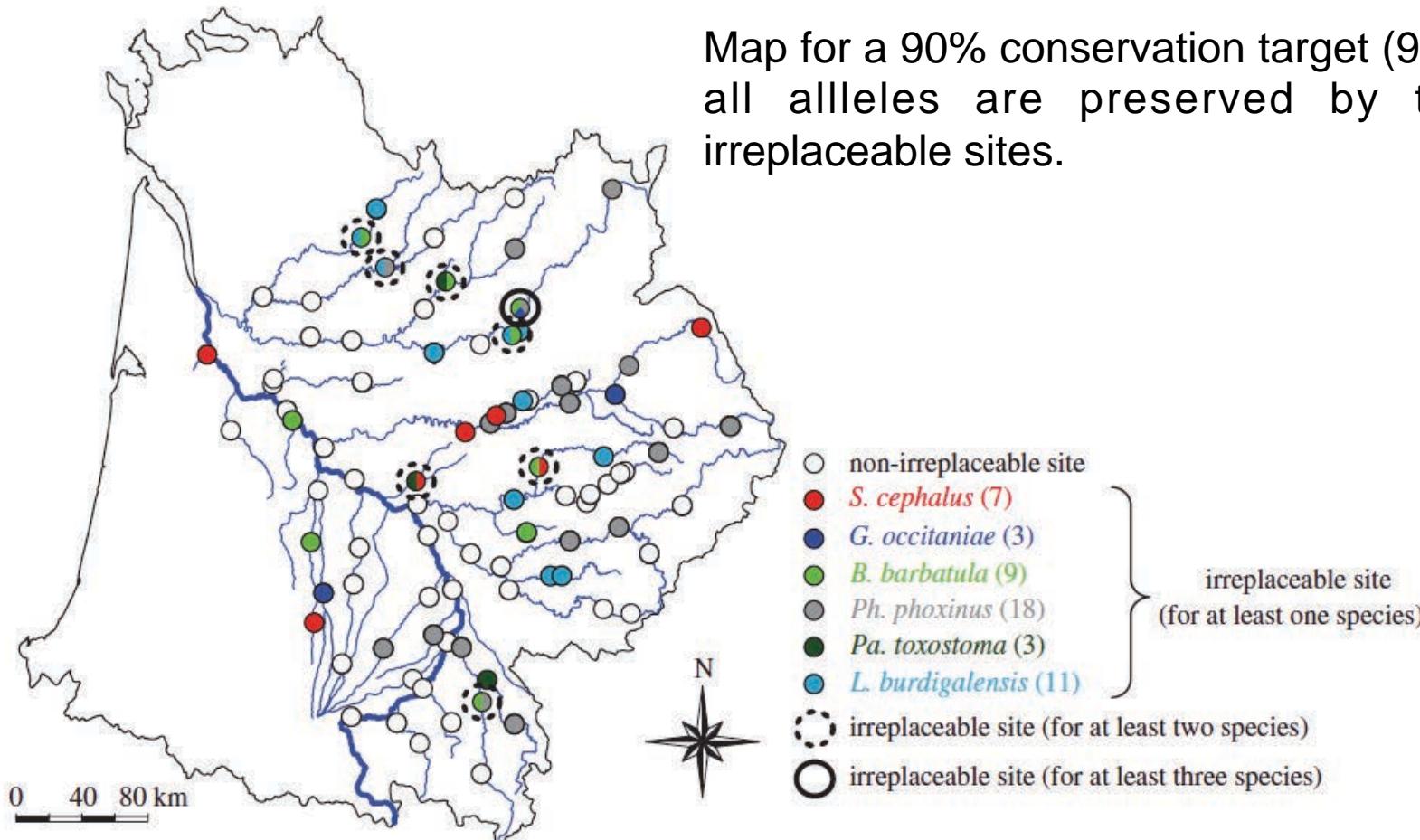
CONSERVATION PLANNING: IDENTIFYING PRIORITY ZONES FOR ID



THE NUMBER OF IRREPLACEABLE SITES VARY ACCORDING TO THE CONSERVATION TARGET AND THE SPECIES



CONSERVATION PLANNING: IDENTIFYING PRIORITY ZONES FOR ID



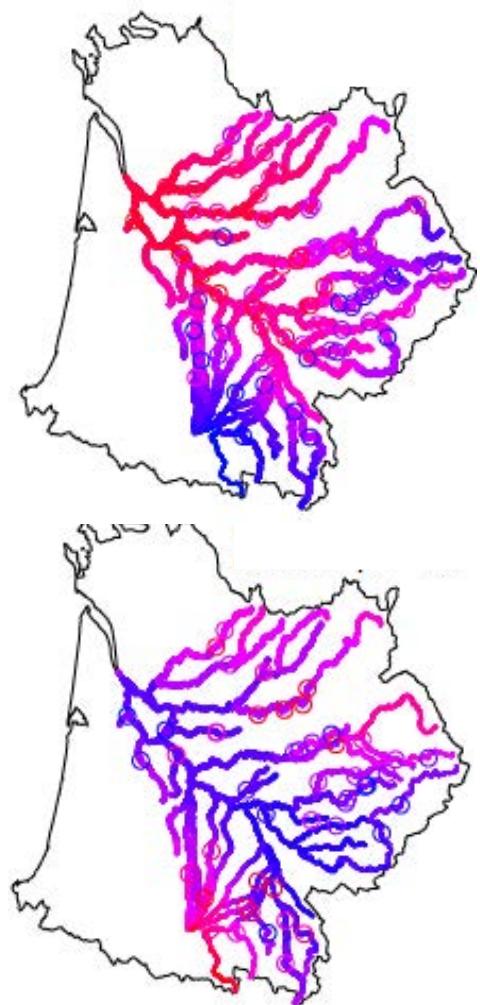
MOST IRREPLACEABLE SITES ARE SPECIES-SPECIFIC. HARD TO CONSERVE ID FOR A POOL OF SPECIES



ALLELIC RICHNESS



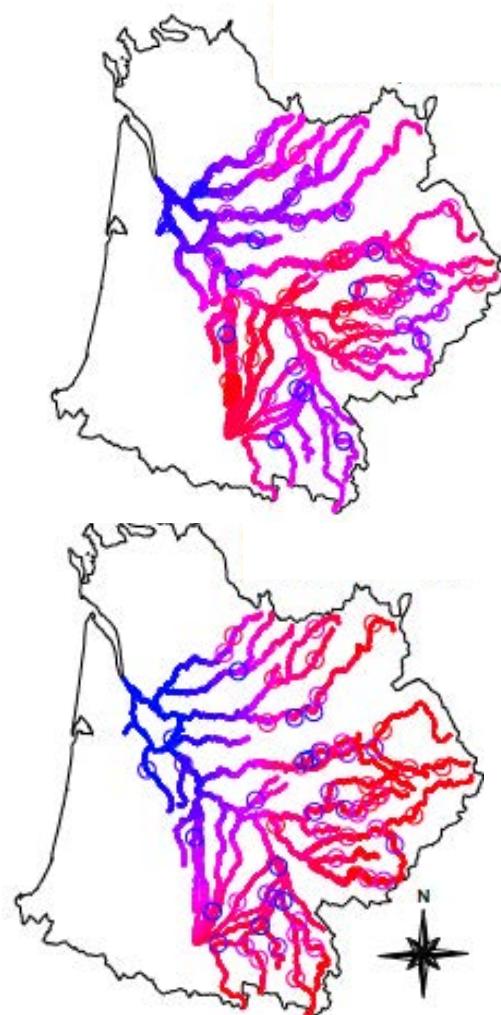
CHUB



GENETIC UNIQUENESS (D_{jost})



LOACH



**SPATIAL PATTERNS OF GENETIC DIVERSITY ARE NOT CONGRUENT
AMONG SPECIES**

Molecular level: Gene expression profile & biological functions involved

D

- 10/177 regulation of interleukin-1 production *
- 39/782 regulation of defense response *
- 9/327 positive regulation of I-kappaB kinase/NF-kappaB signaling
- 14/470 regulation of I-kappaB kinase/NF-kappaB signaling
- 43/1286 proteolysis *
- 20/579 innate immune response *
- 69/1271 defense response *
- 1/83 regulation of viral release from host cell
- 10/137 humoral immune response
- 49/1091 immune response *
- 26/463 defense response to other organism *
- 64/1408 multi-organism process *
- 58/977 response to biotic stimulus *
- 20/262 response to bacterium *
- 33/621 response to other organism *
- 2/75 interferon-gamma-mediated signaling pathway
- 12/380 myeloid cell activation involved in immune response
- 30/860 immune effector process *
- 3/110 antigen processing and presentation of exogenous antigen
- 11/182 embryonic organ morphogenesis
- 24/671 animal organ morphogenesis
- 8/158 skeletal system morphogenesis
- 25/634 embryonal morphogenesis
- 4/46 negative regulation of embryonic development
- 44/996 cellular component morphogenesis *
- 6/49 endodermal cell differentiation
- 34/387 extracellular matrix organization *
- 6/59 cAMP metabolic process
- 3/36 cyclic nucleotide catabolic process
- 11/483 RNA splicing
- 22/998 RNA processing *
- 13/734 mRNA metabolic process
- 3/73 RNA secondary structure unwinding
- 2/56 maturation of SSU-rRNA
- 5/250 rRNA metabolic process
- 14/522 ncRNA metabolic process
- 11/375 ncRNA processing *
- 7/133 RNA modification
- 2/239 ribonucleoprotein complex subunit organization
- 1/71 ribonucleoprotein complex biogenesis

- 19/572 G-protein coupled receptor signaling pathway
- 0/11 positive regulation of heart rate by epinephrine-norepinephrine
- 0/28 adrenergic receptor signaling pathway
- 0/14 G-protein coupled receptor signaling pathway involved in heart process
- 4/78 positive regulation of blood circulation
- 3/33 cyclic nucleotide catabolic process
- 48/1058 cellular response to oxygen-containing compound *
- 76/1906 cellular response to chemical stimulus *
- 48/970 cellular response to endogenous stimulus *
- 35/639 cellular response to nitrogen compound *
- 58/1258 response to nitrogen compound *
- 2/47 regulation of endocrine process
- 28/643 regulation of system process *
- 25/582 growth *
- 39/1142 positive regulation of immune system process *
- 58/1665 regulation of immune system process *
- 39/1052 regulation of immune response *
- 22/673 regulation of cell activation *
- 31/889 regulation of cytokine production *
- 5/186 B cell activation
- 2/111 B cell differentiation
- 17/378 cellular response to cytokine stimulus
- 26/564 response to cytokine
- 63/1910 regulation of programmed cell death *
- 6/47 hyaluronan metabolic process
- 2/43 negative regulation of epithelial cell differentiation
- 44/1944 negative regulation of biosynthetic process *
- 33/1235 positive regulation of transcription from RNA polymerase II promoter
- 43/1810 positive regulation of RNA metabolic process
- 1/73 regulation of mRNA catabolic process
- 40/856 ion homeostasis
- 4/118 iron ion homeostasis
- 3/20 bone trabecula formation
- 1/13 sequestering of TGFbeta in extracellular matrix
- 11/735 mitotic cell cycle process
- 19/582 cell division
- 9/408 microtubule-based movement
- 4/101 cilium movement
- 2/50 axonemal dynein complex assembly
- 2/34 cilium or flagellum-dependent cell motility
- 10/342 cilium organization
- 36/250 transposition, DNA-mediated
- 72/808 DNA recombination *
- 54/429 transposition

- 19/586 pattern specification process *
- 11/341 regionalization *
- 32/1213 anatomical structure formation involved in morphogenesis *
- 19/680 animal organ morphogenesis
- 29/967 system development *
- 30/901 cell development *
- 4/201 blood vessel development
- 27/760 cell part morphogenesis *
- 38/1090 cellular component morphogenesis *
- 21/443 neuron projection morphogenesis *
- 56/1323 cell projection organization *
- 43/1483 regulation of cell development *
- 13/414 regulation of cellular response to growth factor stimulus *
- 26/648 regulation of system process
- 84/1513 system process *
- 36/957 cellular response to endogenous stimulus *
- 33/749 positive regulation of immune response
- 41/1140 positive regulation of immune system process
- 60/1659 regulation of immune system process *
- 25/567 activation of immune response
- 46/1050 regulation of immune response *
- 9/228 antigen receptor-mediated signaling pathway
- 17/453 positive regulation of cell activation
- 21/669 regulation of cell activation
- 11/88 complement activation
- 30/885 immune effector process *
- 12/107 protein activation cascade
- 13/158 humoral immune response
- 48/1133 immune response *
- 28/602 innate immune response *
- 51/1284 defense response *
- 13/597 DNA repair *
- 6/378 ncRNA processing
- 10/1018 RNA processing
- 8/529 ncRNA metabolic process *
- 5/251 rRNA metabolic process
- 3/203 tRNA metabolic process *
- 8/399 peptide metabolic process
- 2/282 peptide biosynthetic process
- 13/594 cellular amide metabolic process
- 4/376 amide biosynthetic process



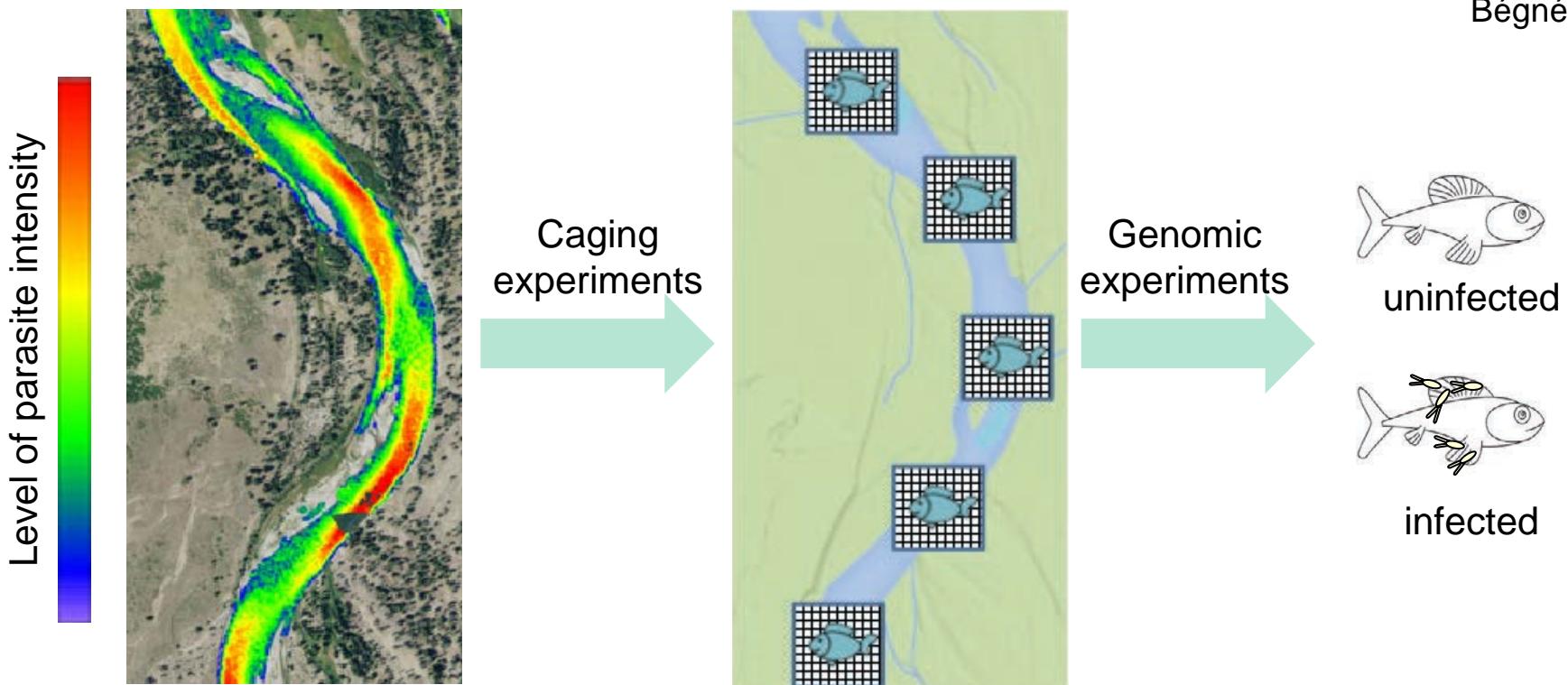


THE ENVIRONMENTAL AND GENOMIC BASES OF RESISTANCE



Eglantine
Mathieu-
Bégné

Meetic: How can an ugly larvae meet a lovely host in a desert?



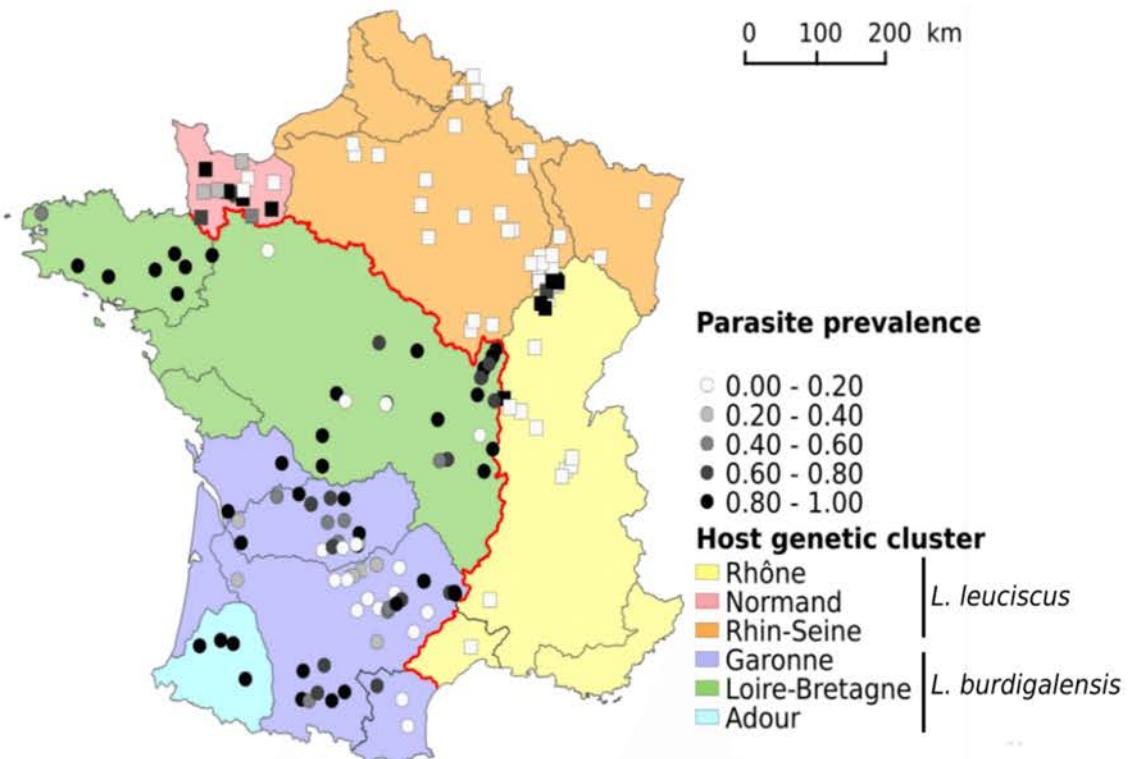
RESOLVING THE “NEEDLE IN A HAYSTACK” PARADOX



THE ENVIRONMENTAL AND GENOMIC BASES OF RESISTANCE



Eglantine
Mathieu-
Bégné



Environmental niche limitations
vs. host resistance in uninfected
areas?
→ Combining niche modeling
and genomic analyses

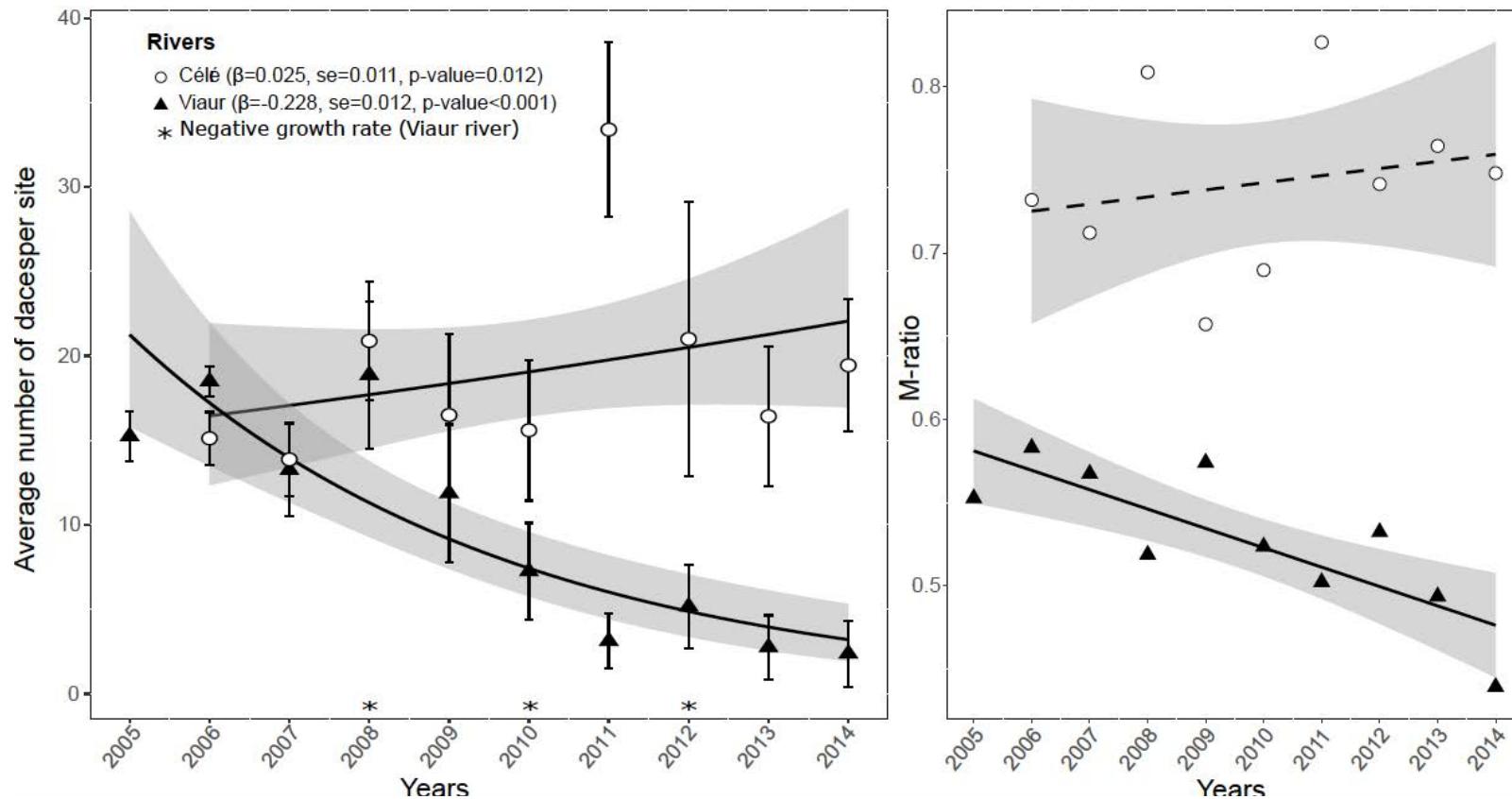
UNDERSTANDING THE DRIVERS OF RESISTANCE AT LARGE SPATIAL SCALE



LONG-TERM CONSEQUENCES



Eglantine
Mathieu-
Bégné

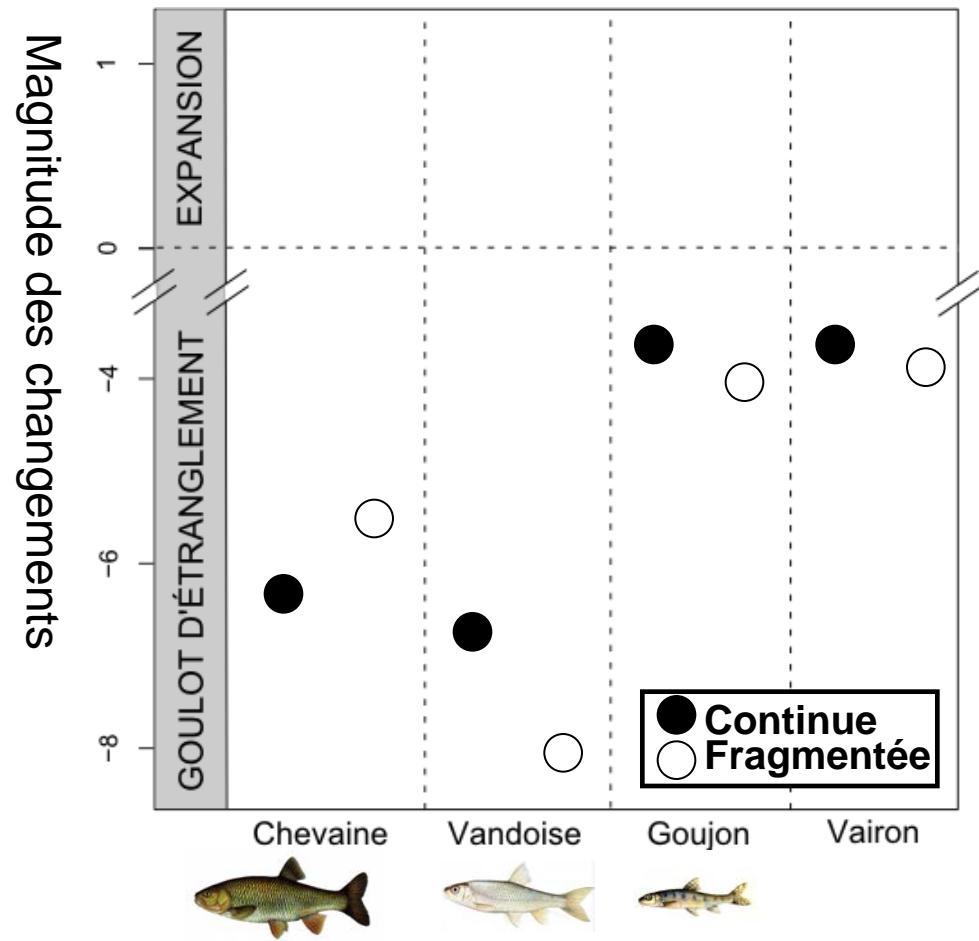


TEMPORAL DYNAMICS OF NEUTRAL AND NON-NEUTRAL
GENETIC DIVERSITY IN HOST POPULATIONS

DYNAMIQUE DÉMOGRAPHIQUE DES POPULATIONS :

=> Restriction (goulot d'étranglement) attendue en cas de perte d'habitat

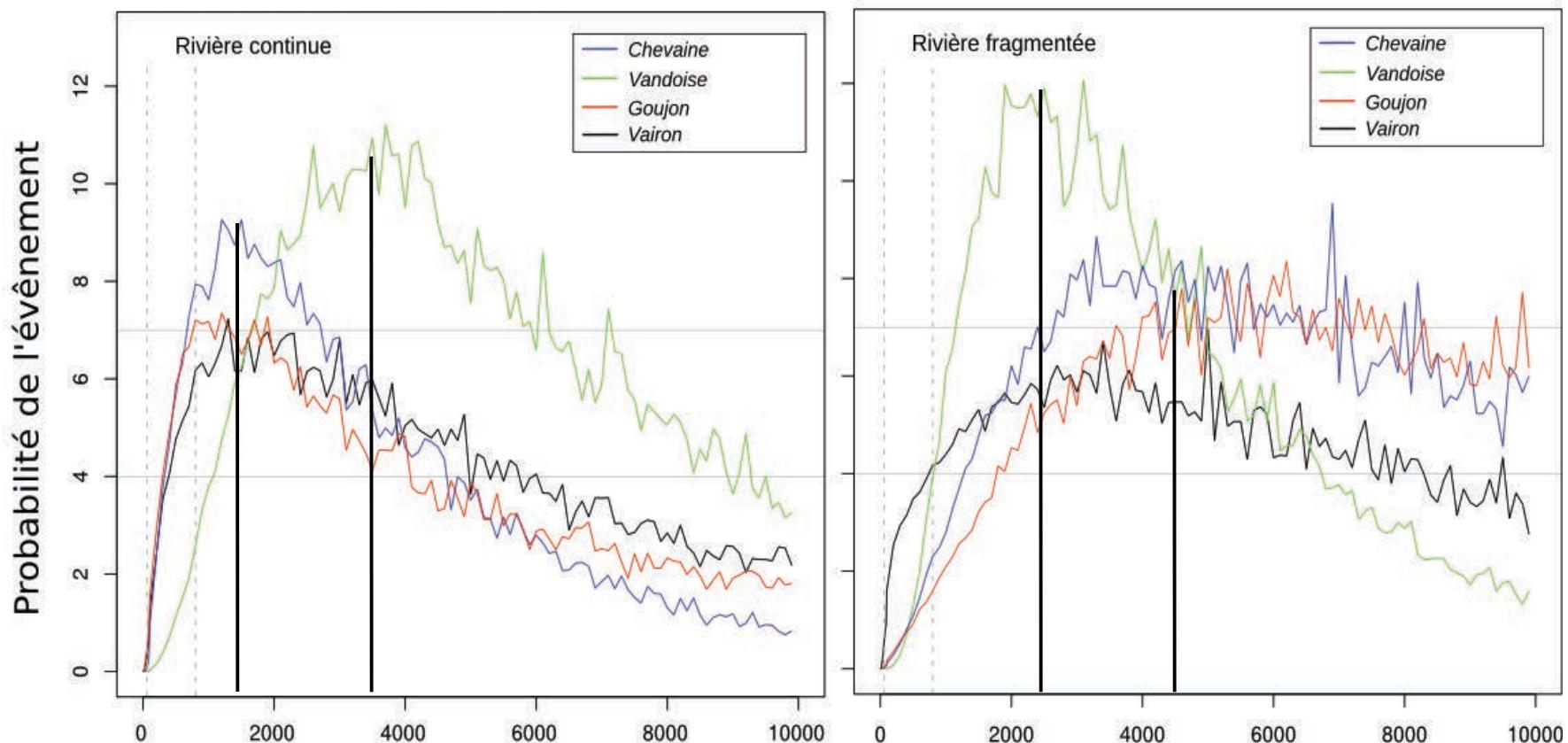
Deux rivières (Viaur et Célé) - Dix stations / rivière



DIFFÉRENCE ENTRE TAILLE DE LA POP ANCESTRALE ET TAILLE DE LA POP ACTUELLE

FORTS GOULOTS
D'ÉTRANGLEMENT POUR TOUTES
LES ESPÈCES DANS LES DEUX
RIVIÈRES

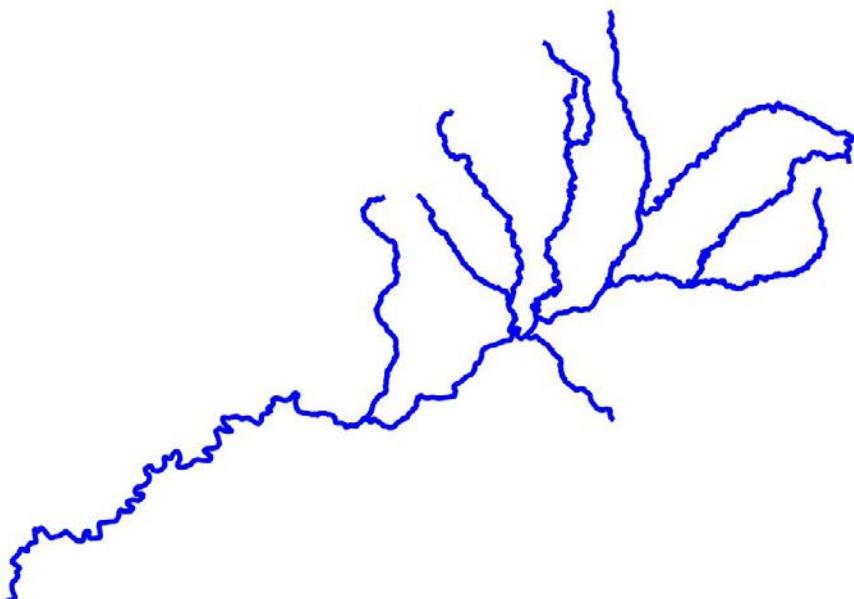
DYNAMIQUE DÉMOGRAPHIQUE DES POPULATIONS :



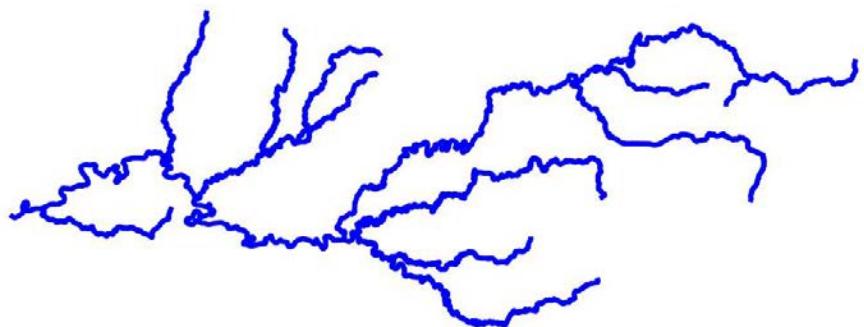
LA FRAGMENTATION NE SEMBLE PAS ÊTRE À L'ORIGINE DES GOULOTS D'ÉTRANGLEMENT DANS LE VIAUR ET LE CÉLÉ

DEUX RÉSEAUX HYDROGRAPHIQUES :

LE CÉLÉ



LE VIAUR



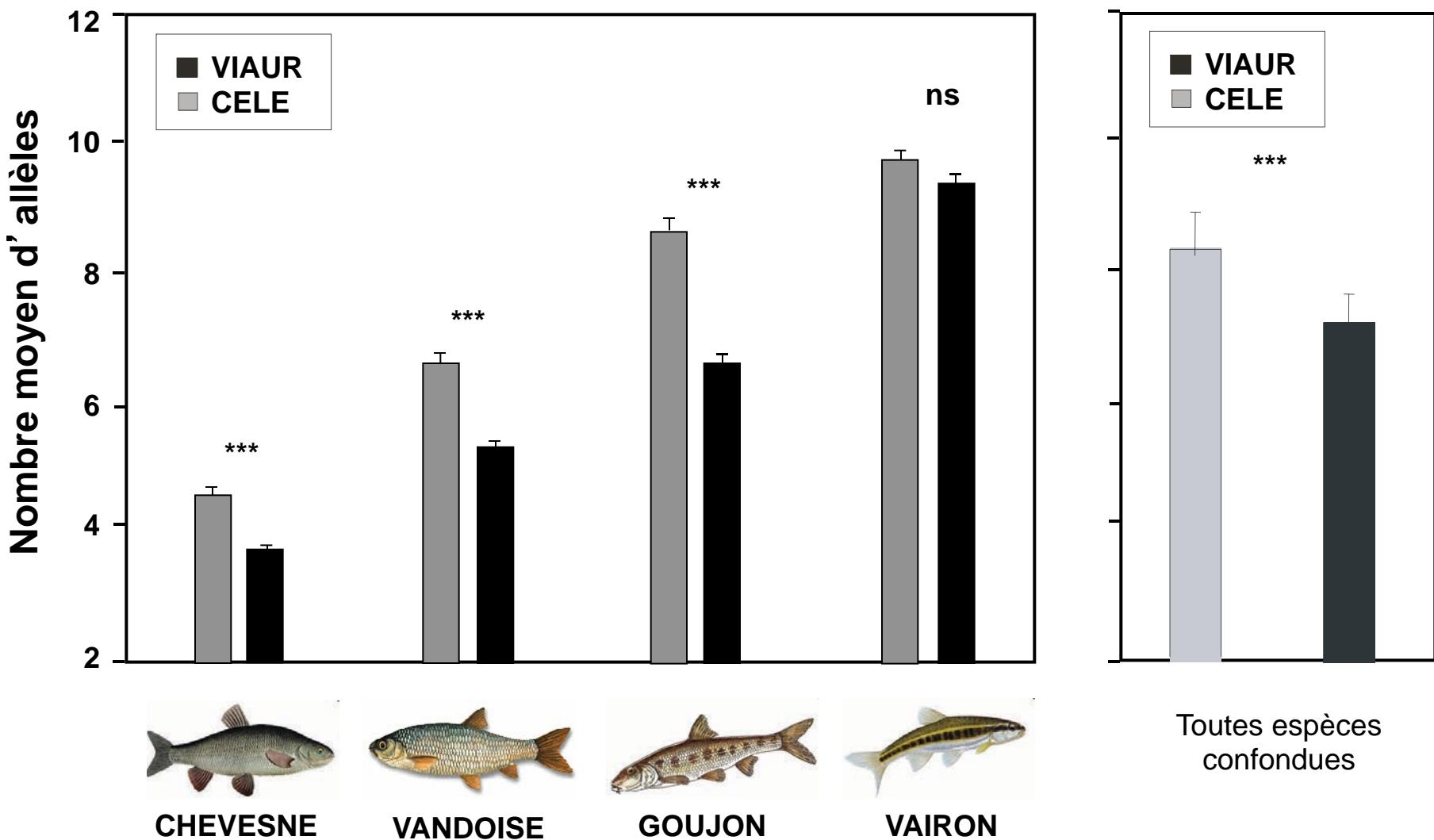
“Faiblement fragmentée”

(~15 chaussées, passes à poissons)

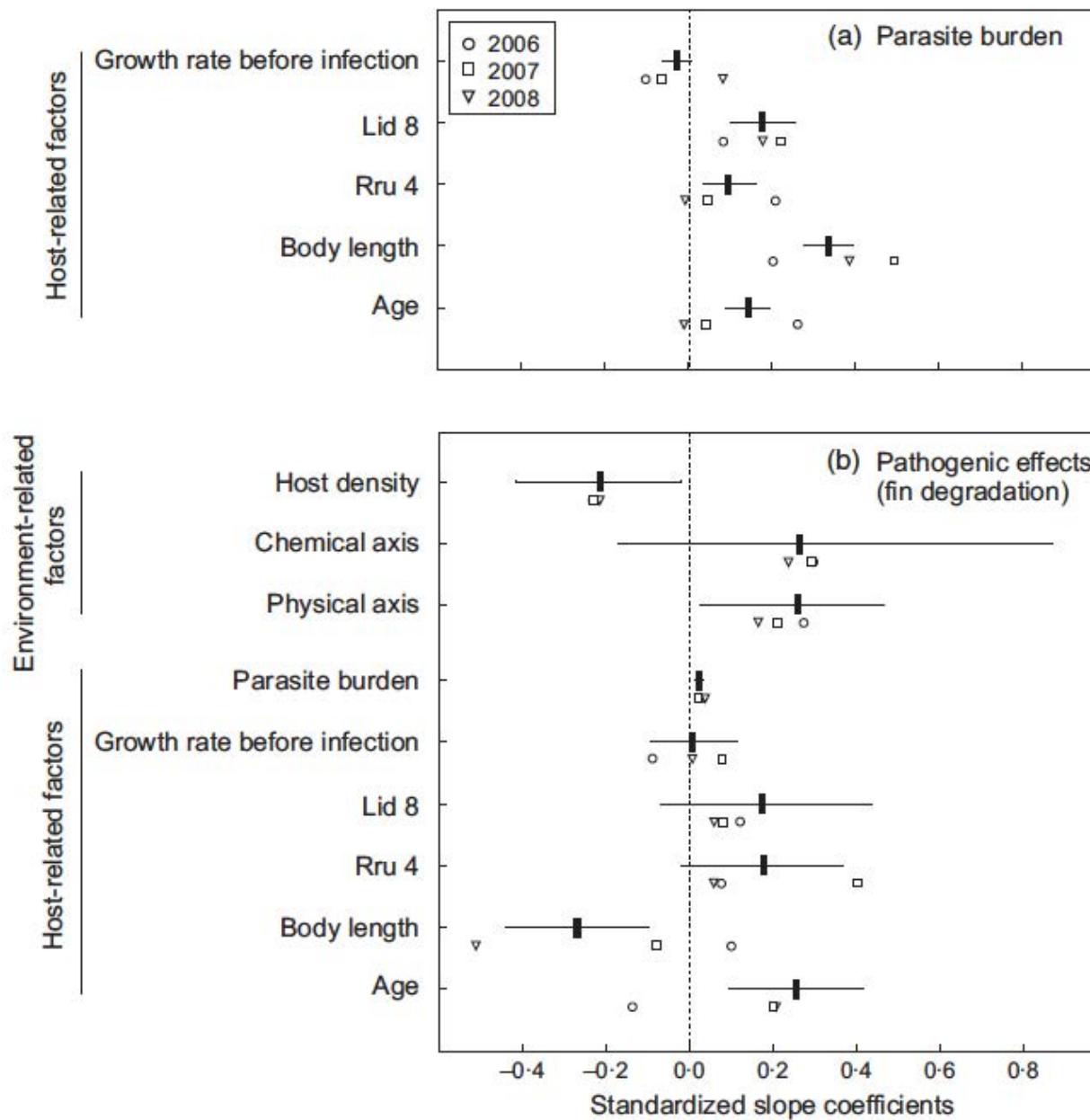
“Fortement fragmentée”

(~50 chaussées, 2 barrages hydro)

“FORTEMENT FRAGMENTÉ” = DIVERSITÉ PLUS FAIBLE

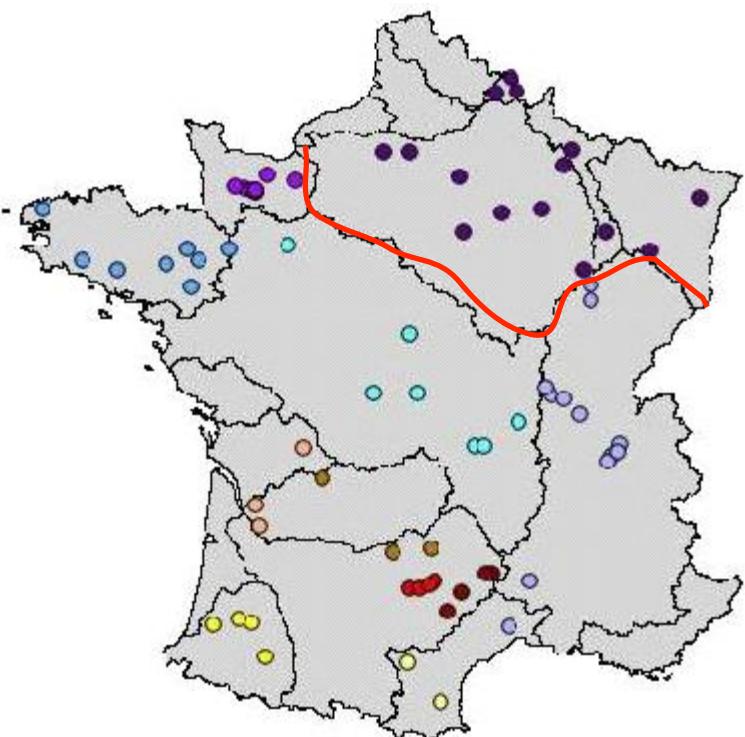


(III) RÉSISTANCE ET TOLÉRANCE

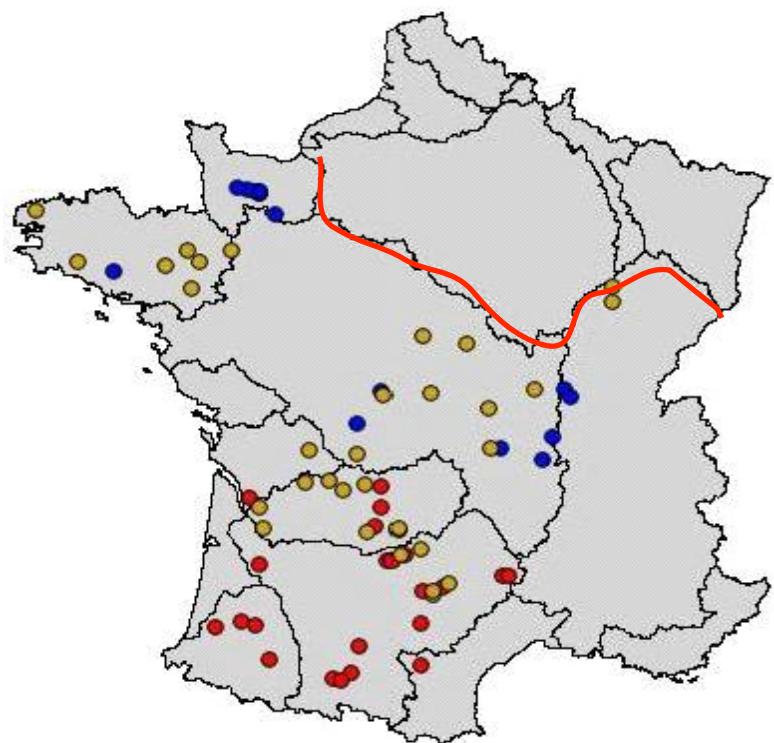


STRUCTURE GÉNÉTIQUE HÔTE ET PARASITE (MICROSATELLITES)

HOST



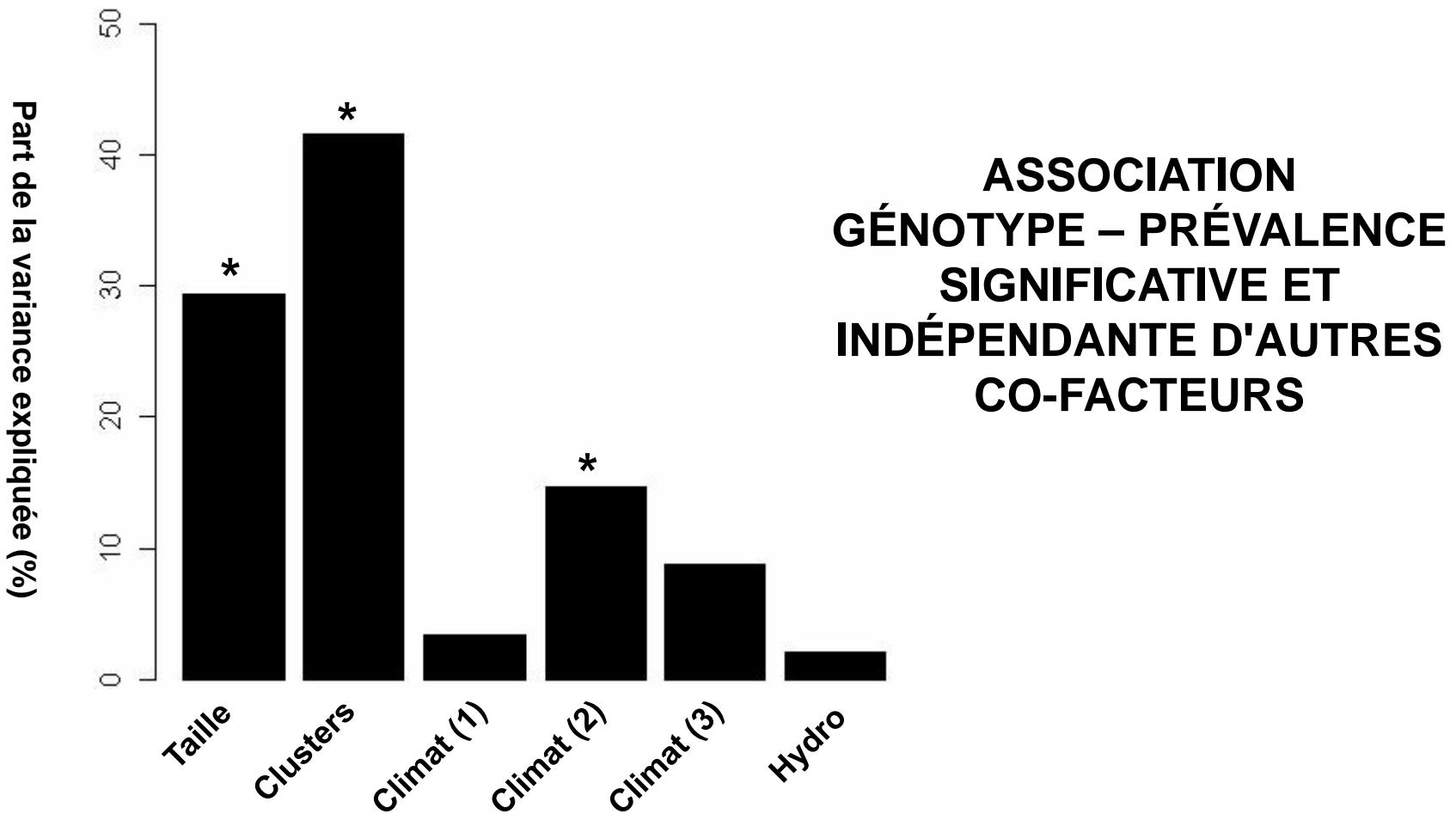
PARASITE



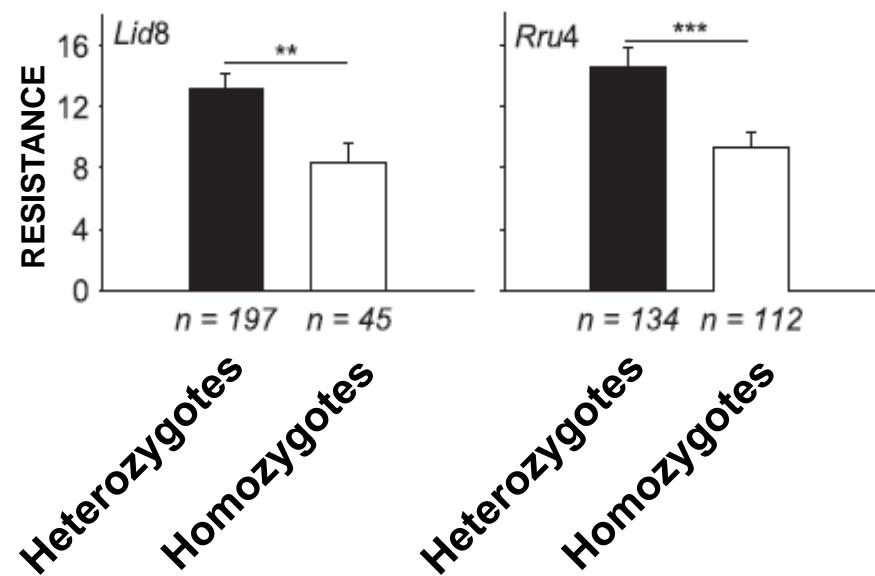
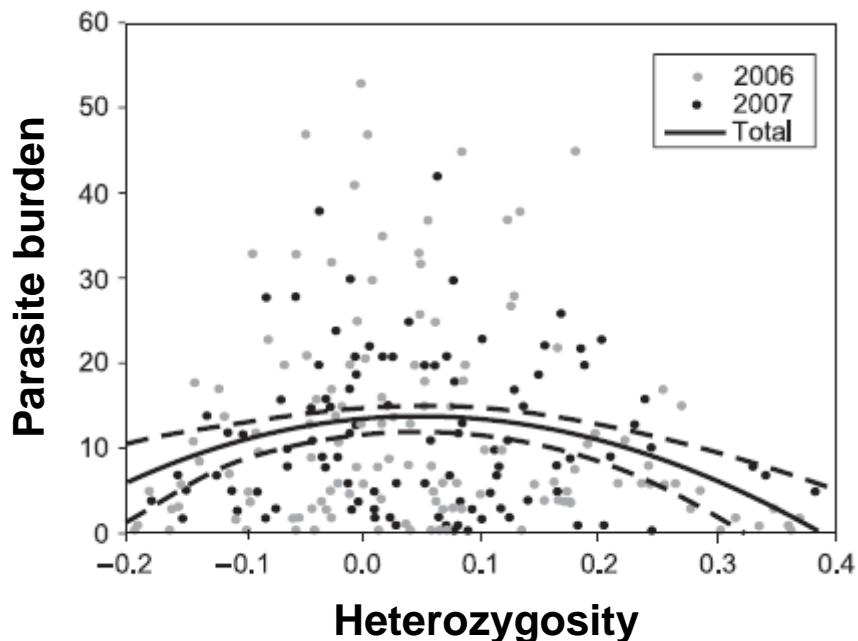
ASSOCIATION GÉNOTYPE – PRÉVALENCE?

PARTITIONEMENT DE LA VARIANCE

(PRÉVALENCE~TAILLE+CLUSTER GÉNÉTIQUE+HYDROMORPHO+CLIMAT)



DÉTERMINISMES ENVIRONNEMENTAUX ET GÉNÉTIQUES



**RELATIONS SIGNIFICATIVE ENTRE DIVERSITÉ
GÉNÉTIQUE (MICROSAT), TOLÉRANCE ET RÉSISTANCE**

ET LA RECHERCHE APPLIQUÉE ?

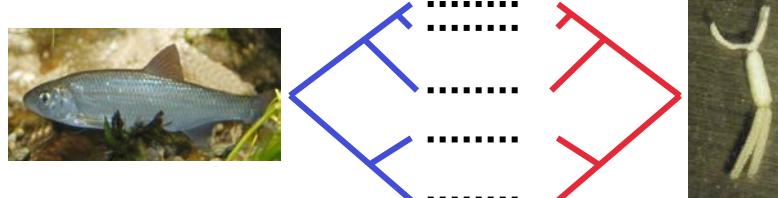
=> CAPACITÉ DE COLONISATION



(1) Filtre environnemental

- => Facteurs abiotiques (T°C, courant, oxygénation)
- => Facteurs biotiques (densité de l' hôte)

(2) Capacité de dispersion



(3) Adaptation locale

- => Expérimentation en mésocosmes



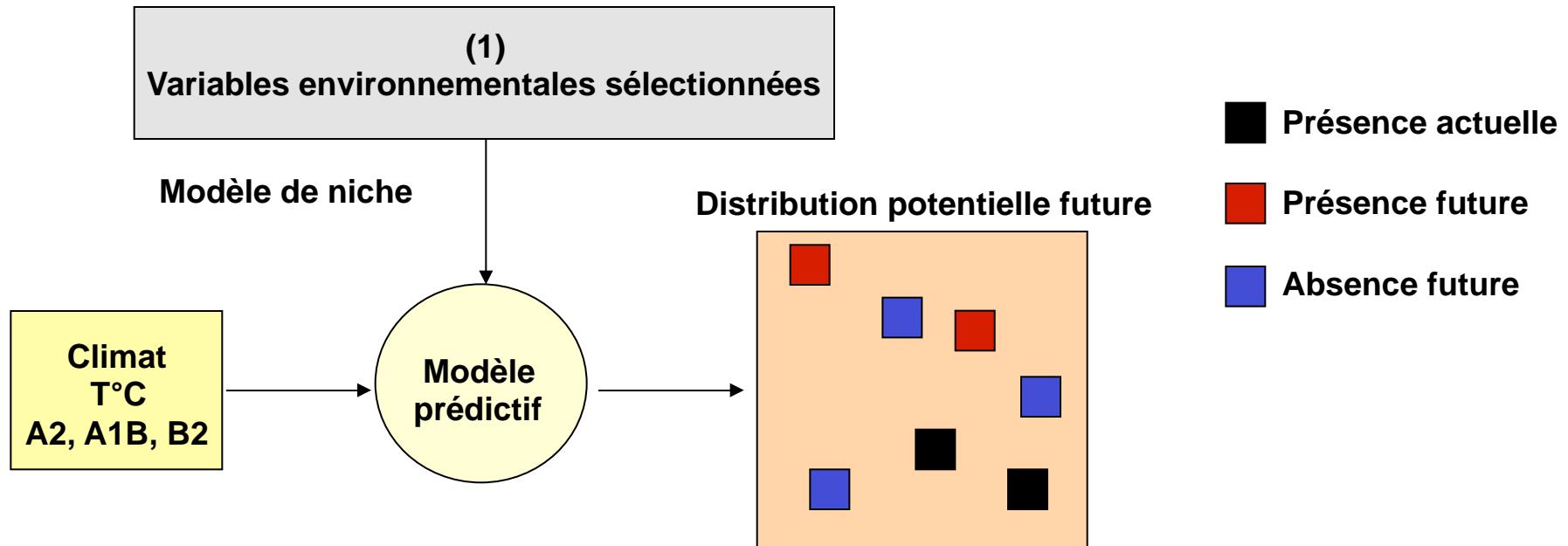
(4) Capacité de transfert d'hôtes

- => Etude descriptive comparative
- => Etude fitness parasite



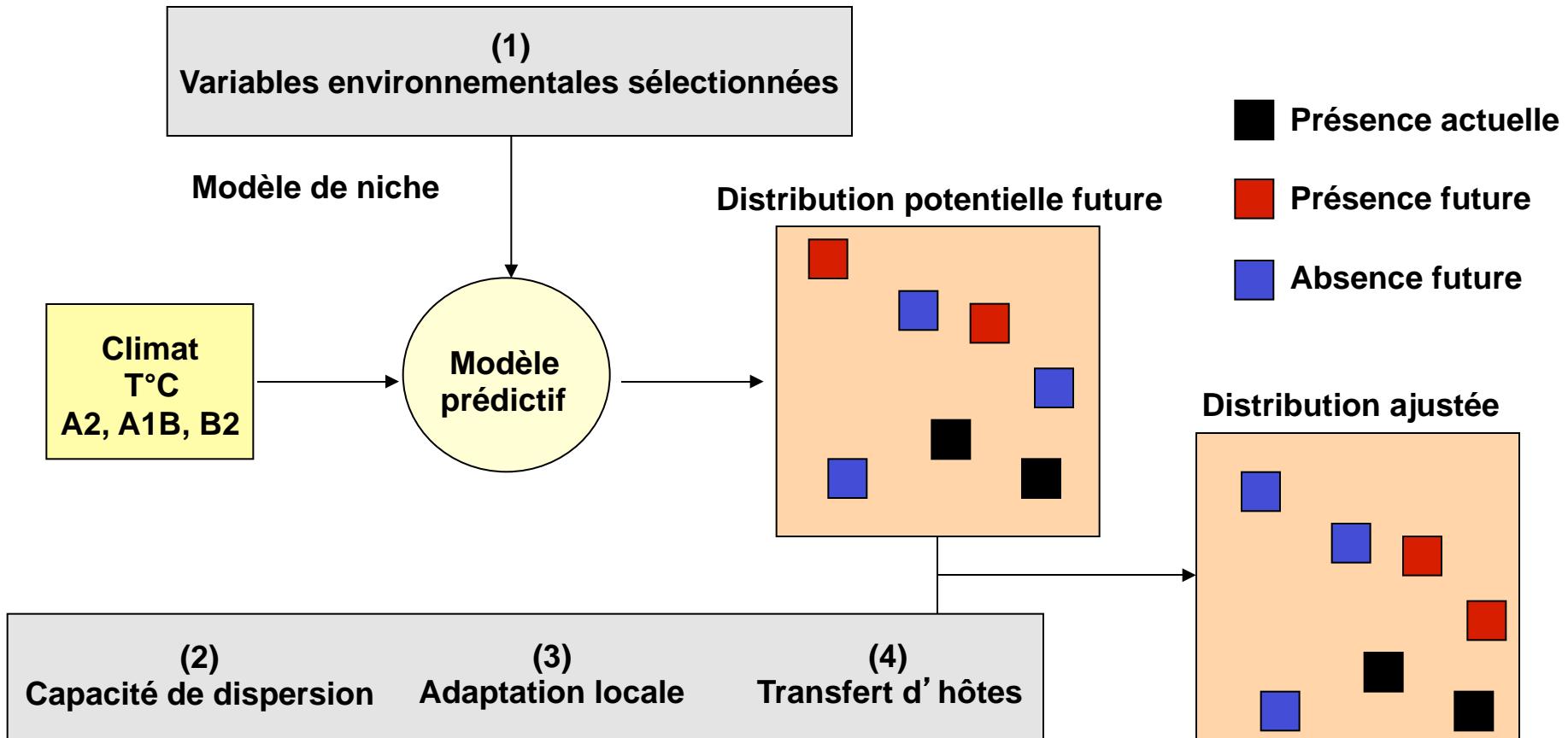
ET LA RECHERCHE APPLIQUÉE ?

=> PRÉDIRE DISTRIBUTION FUTURE



ET LA RECHERCHE APPLIQUÉE ?

=> PRÉDIRE DISTRIBUTION FUTURE



⇒ Carte de distribution future : outil de gestion
⇒ Modèles prédictifs plus réalistes

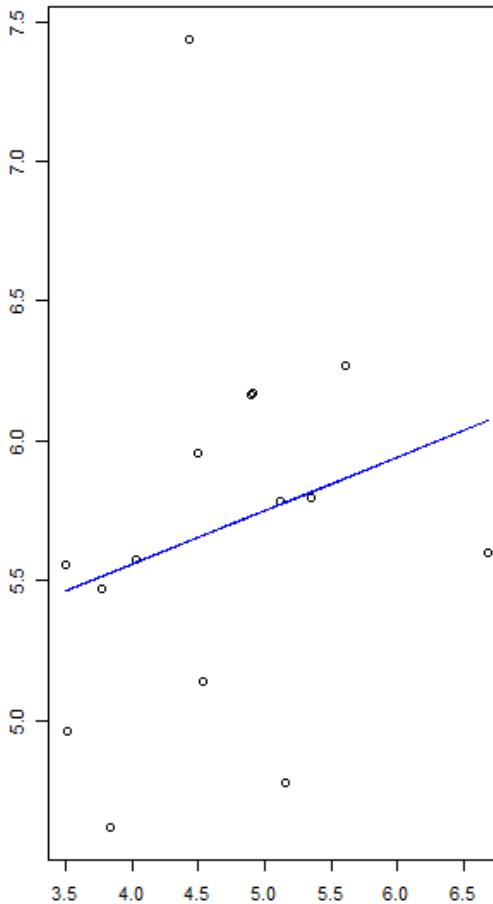
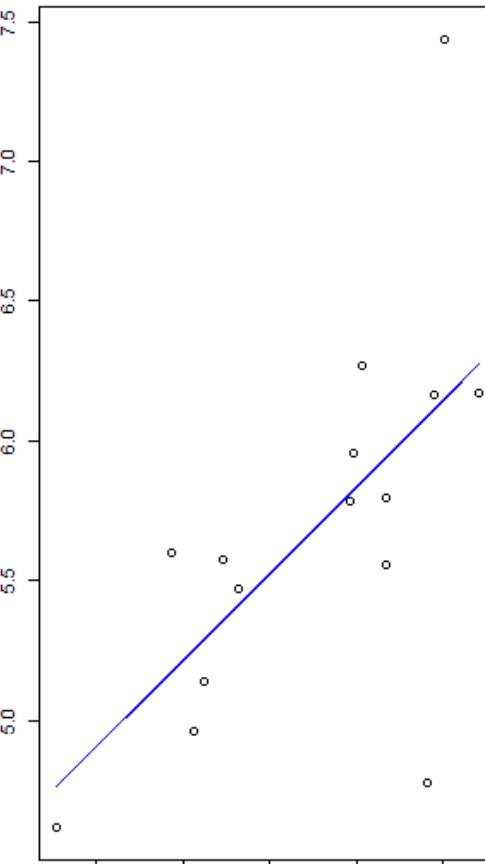
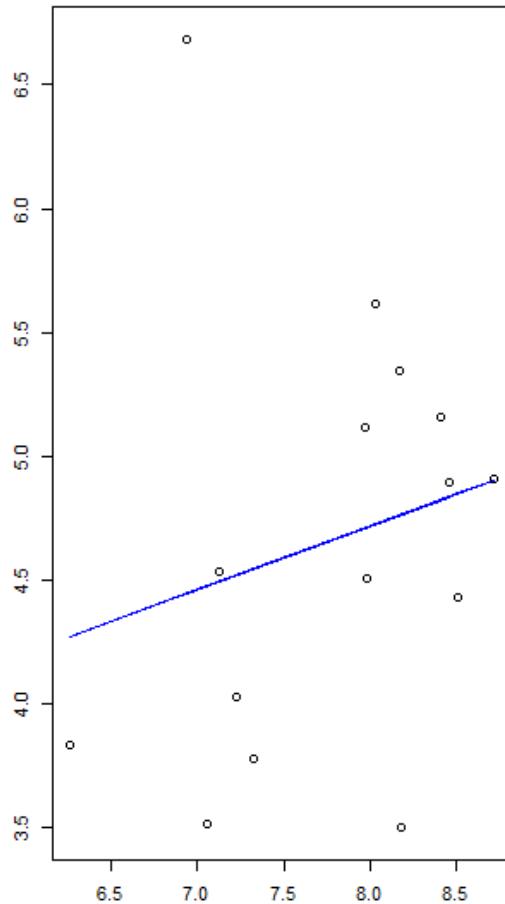
III - PREMIERS RÉSULTATS

Chevaine vs

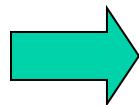
Vandoise vs

Vandoise vs

Richesse allélique



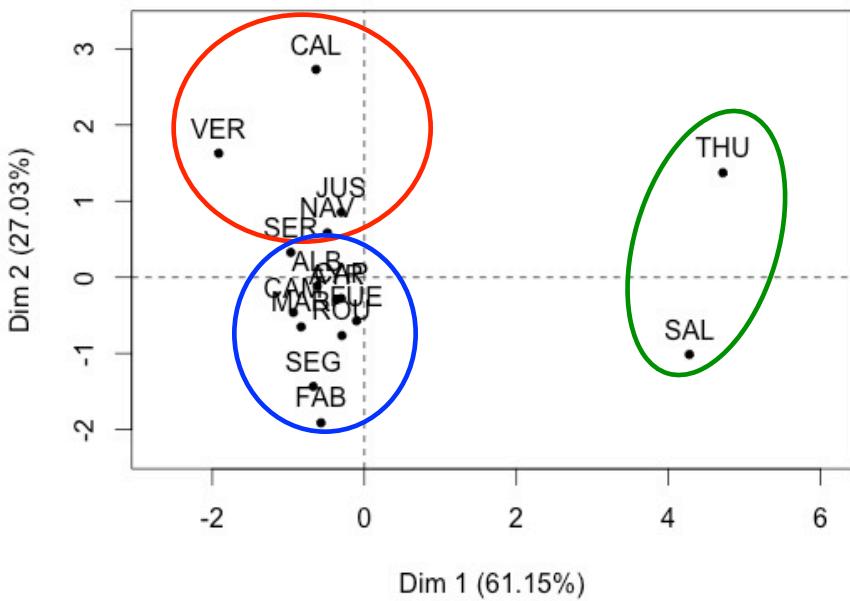
Richesse allélique



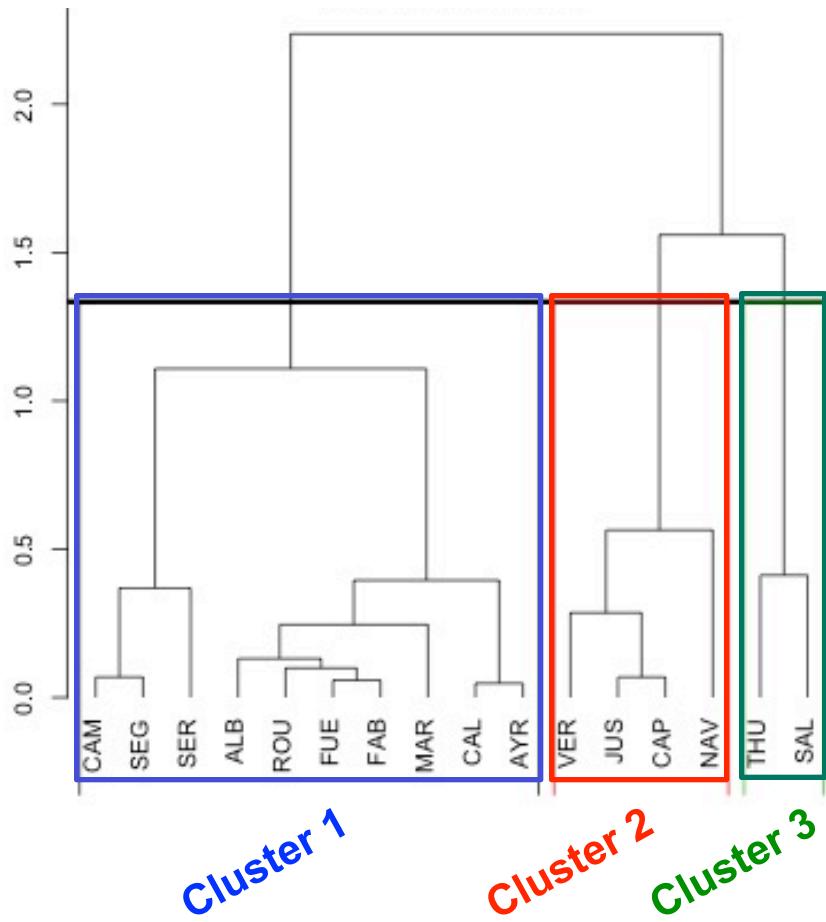
Congruence pour la vandoise et le goujon

VIAUR

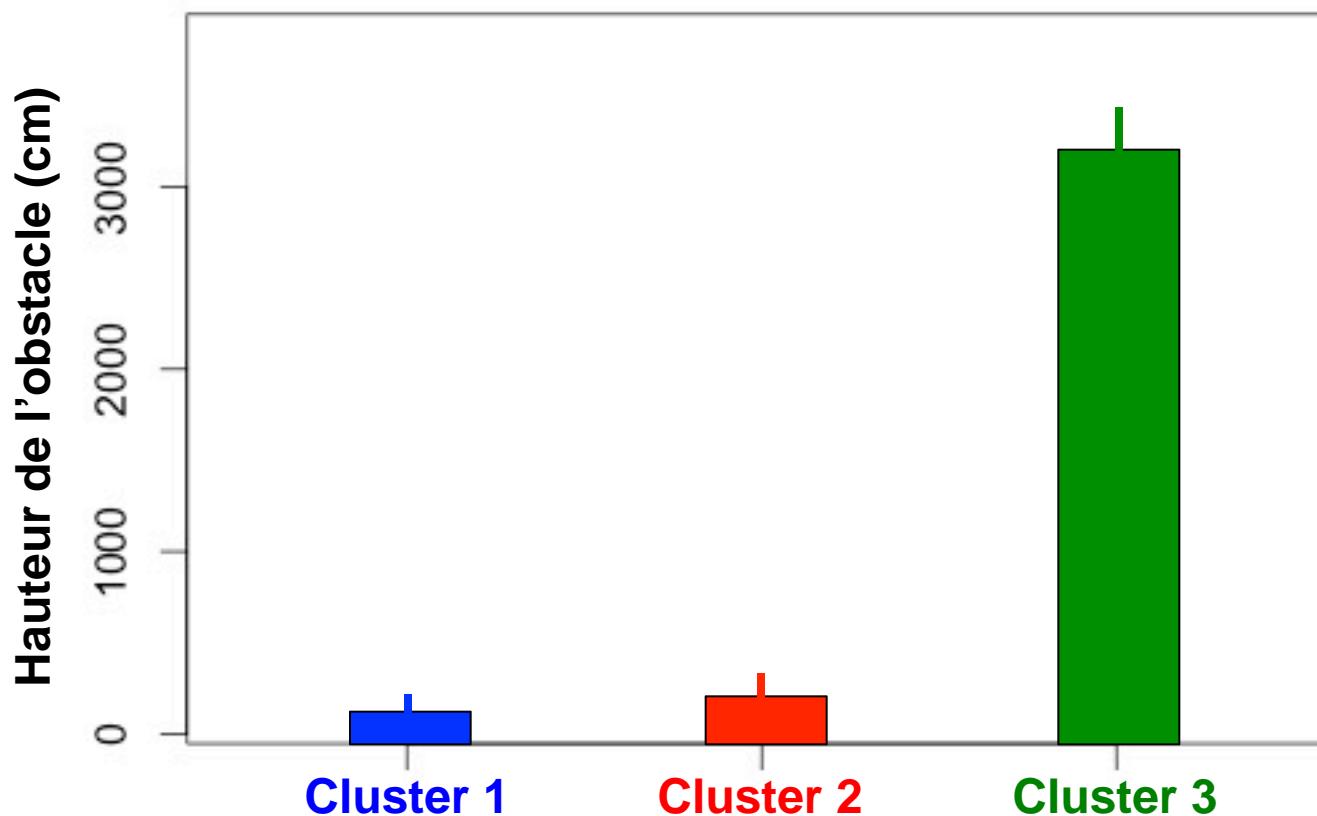
ACP SUR INDICES DE CONNECTIVITÉ



CLUSTERING



VIAUR



⇒ Pas d'effets de distance à la source, pente, tirant d'eau
⇒ Importance de la hauteur de l'obstacle
(barrages hydroélectriques)