

Diversité de l'espèce *Flavobacterium psychrophilum*



Les principaux acteurs



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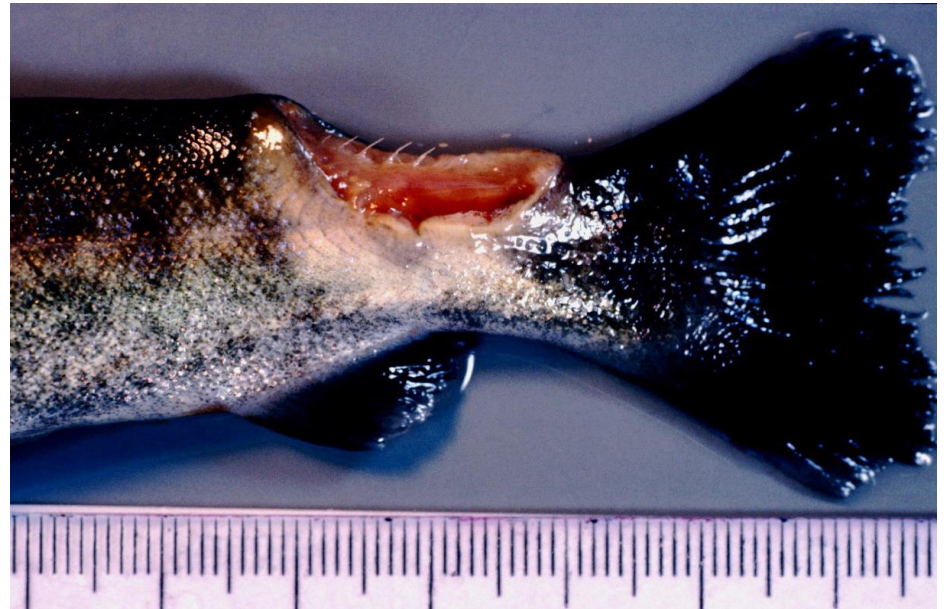
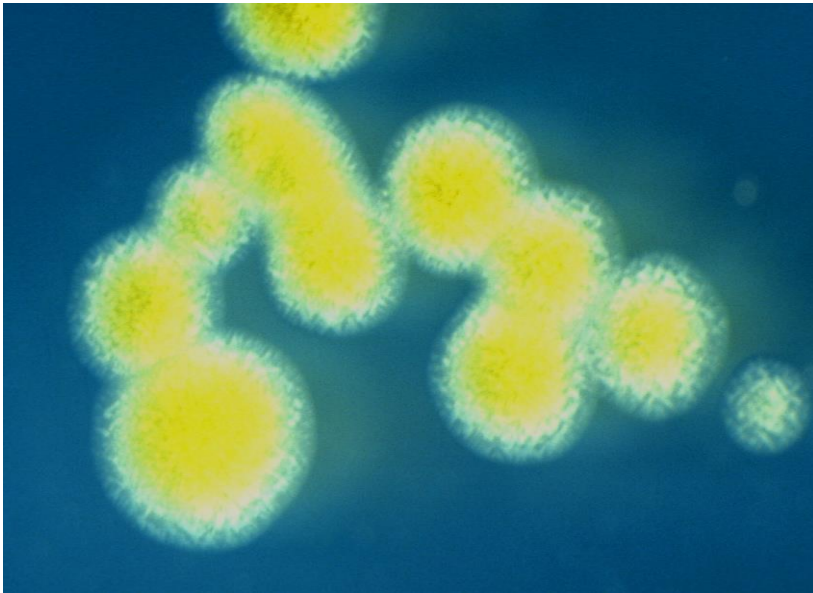
J-F Bernardet

INRA, Unité Malage



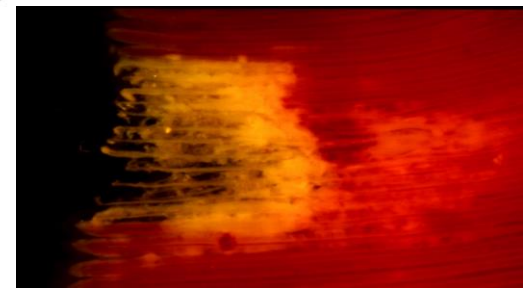
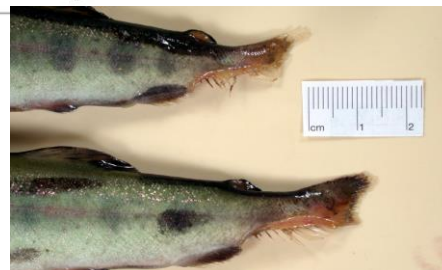
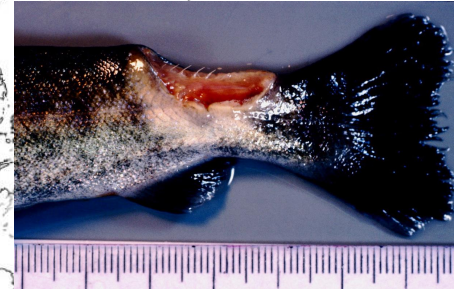
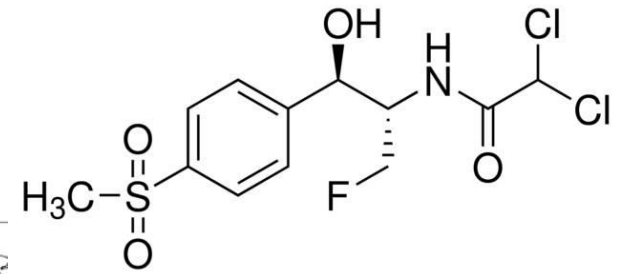
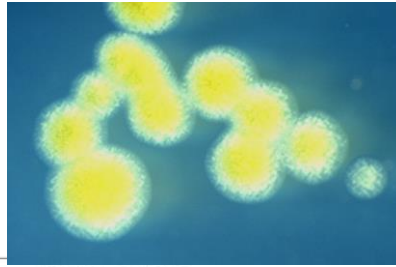
P. Nicolas

Notre objet d'étude



Flavobacterium psychrophilum

Un problème majeur pour la salmoniculture

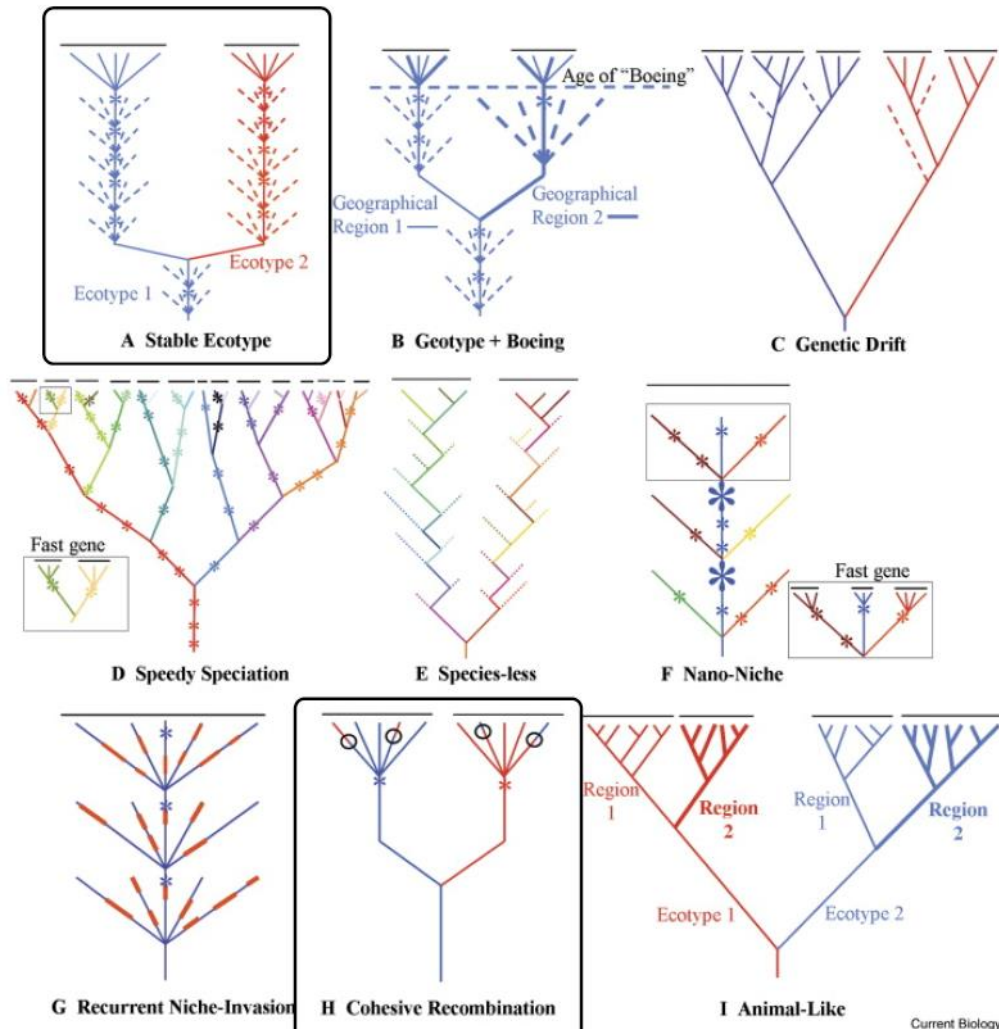


Tous pareils, tous différents



Quel scénario évolutif ?

Quelle structure de population ?



[Cohan and Perry, 2007]

Current Biology

Questions clefs

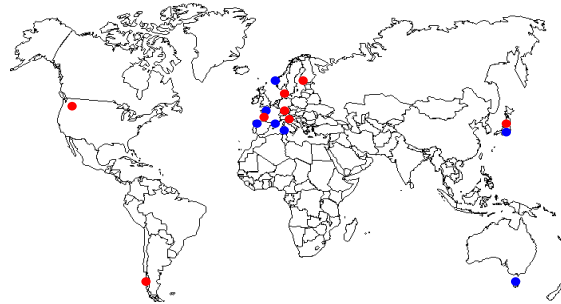


Comment on y répond

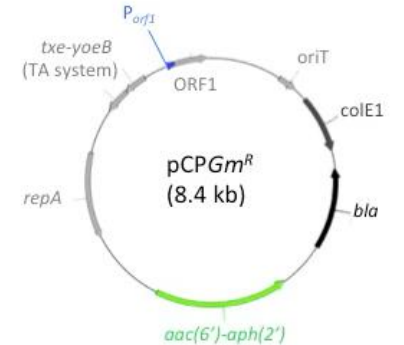
Microbiologie



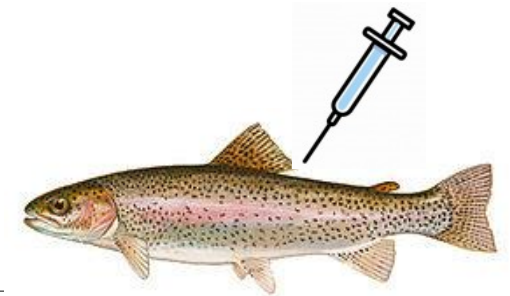
Echantillonnage



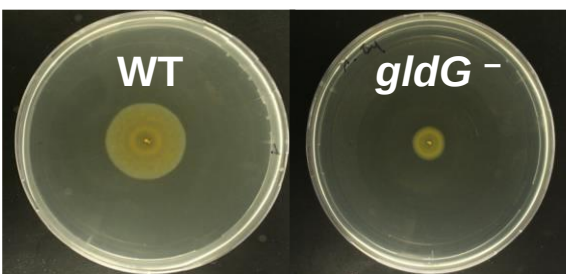
Génétique



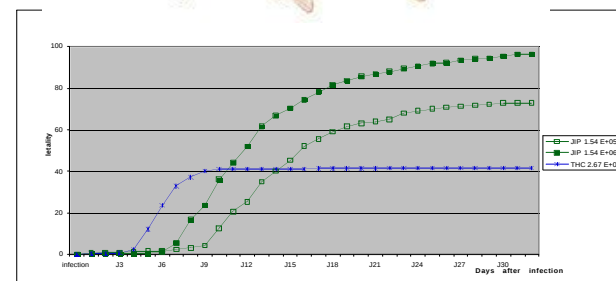
Phénotypes *in vivo*

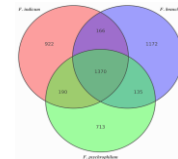
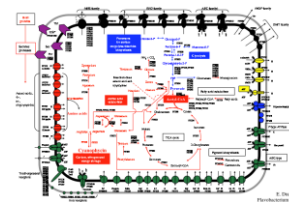
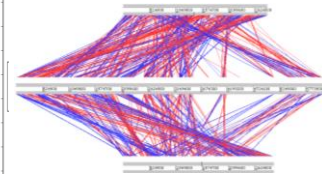
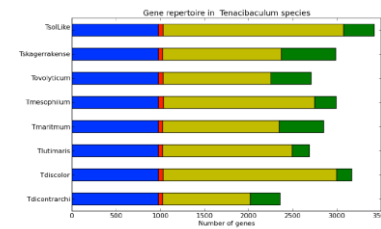
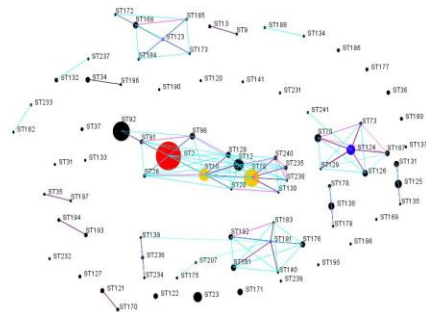


Phénotypes *in vitro*



-omics



[illegible]

génomés

Approche MLST

Fujiwara-Nagata et al. *Veterinary Research* 2013, **44**:34
<http://www.veterinaryresearch.org/content/44/1/34>



VETERINARY RESEARCH

RESEARCH

Open Access



Population structure of the fish pathogen *Flavobacterium psychrophilum* at whole-country and model river levels in Japan

Erina Fujiwara-Nagata^{1,2*}, Céline Chantry-Darmon^{2,3}, Jean-François Bernardet², Mitsuru Eguchi¹, Eric Duchaud^{2†} and Pierre Nicolas^{3†}

Multilocus Sequence Typing Identifies Epidemic Clones of *Flavobacterium psychrophilum* in Nordic Countries

Hanne Nilsen,^a Krister Sundell,^b Eric Duchaud,^c Pierre Nicolas,^d Inger Dalsgaard,^e Lone Madsen,^e Anna Aspán,^f Eva Jansson,^f Duncan J. Colquhoun,^a Tom Wiklund^b

Norwegian Veterinary Institute, Bergen, Norway^a; Åbo Akademi University, Turku, Finland^b; INRA, Virologie et Immunologie Moléculaires, UR892, Jouy-en-Josas, France^c; INRA, Mathématique Informatique et Génome, UR1077, Jouy-en-Josas, France^d; National Veterinary Institute, Technical University of Denmark, Frederiksberg, Denmark^e; National Veterinary Institute, Section of Fish, Uppsala, Sweden^f



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Introduction, expansion and coexistence of epidemic *Flavobacterium psychrophilum* lineages in Chilean fish farms

Ruben Avendaño-Herrera^{a,b,*}, Armel Houel^c, Rute Irgang^a, Jean-François Bernardet^c, Marcos Godoy^{d,e,f}, Pierre Nicolas^{e,f,1}, Eric Duchaud^{c,1}



Genetic diversity of *Flavobacterium psychrophilum* isolated from rainbow trout in France: Predominance of a clonal complex

C. Siekoul-Nguedia^{a,b}, G. Blanc^b, E. Duchaud^c, S. Calvez^{a,b,*}

^aINRA, UMR1300 Biologie, Épidémiologie et Analyse de Risque en santé animale, BP 40706, F-44307 Nantes, France

^bLUNAM Université, Oniris, Ecole nationale vétérinaire, agroalimentaire et de l'alimentation Nantes-Atlantique, UMR BioEPAR, F-44307 Nantes, France

^cINRA, UR892 Virologie et Immunologie Moléculaires, F-78350 Jouy-en-Josas, France

AMERICAN SOCIETY FOR MICROBIOLOGY Applied and Environmental Microbiology



Genetic Diversity of *Flavobacterium psychrophilum* Isolates from Three *Oncorhynchus* spp. in the United States, as Revealed by Multilocus Sequence Typing

Danielle Van Vliet,^a Gregory D. Wiens,^b Thomas P. Loch,^c Pierre Nicolas,^d Mohamed Faisal^{a,c}

Department of Fisheries and Wildlife, College of Agriculture and Natural Resources, Michigan State University, East Lansing, Michigan, USA^a; National Center for Cool and Cold Water Aquaculture, United States Department of Agriculture, Agricultural Research Service, Kearneysville, West Virginia, USA^b; Department of Pathobiology and Diagnostic Investigation, College of Veterinary Medicine, Michigan State University, East Lansing, Michigan, USA^c; MaIAGE, INRA, Université Paris-Saclay, Jouy-en-Josas, France^d

Molecular epidemiology of *Flavobacterium psychrophilum* from Swiss fish farms

Nicole Strepparava^{1,*}, Pierre Nicolas², Thomas Wahl³, Helmut Segner³, Orlando Petrini¹

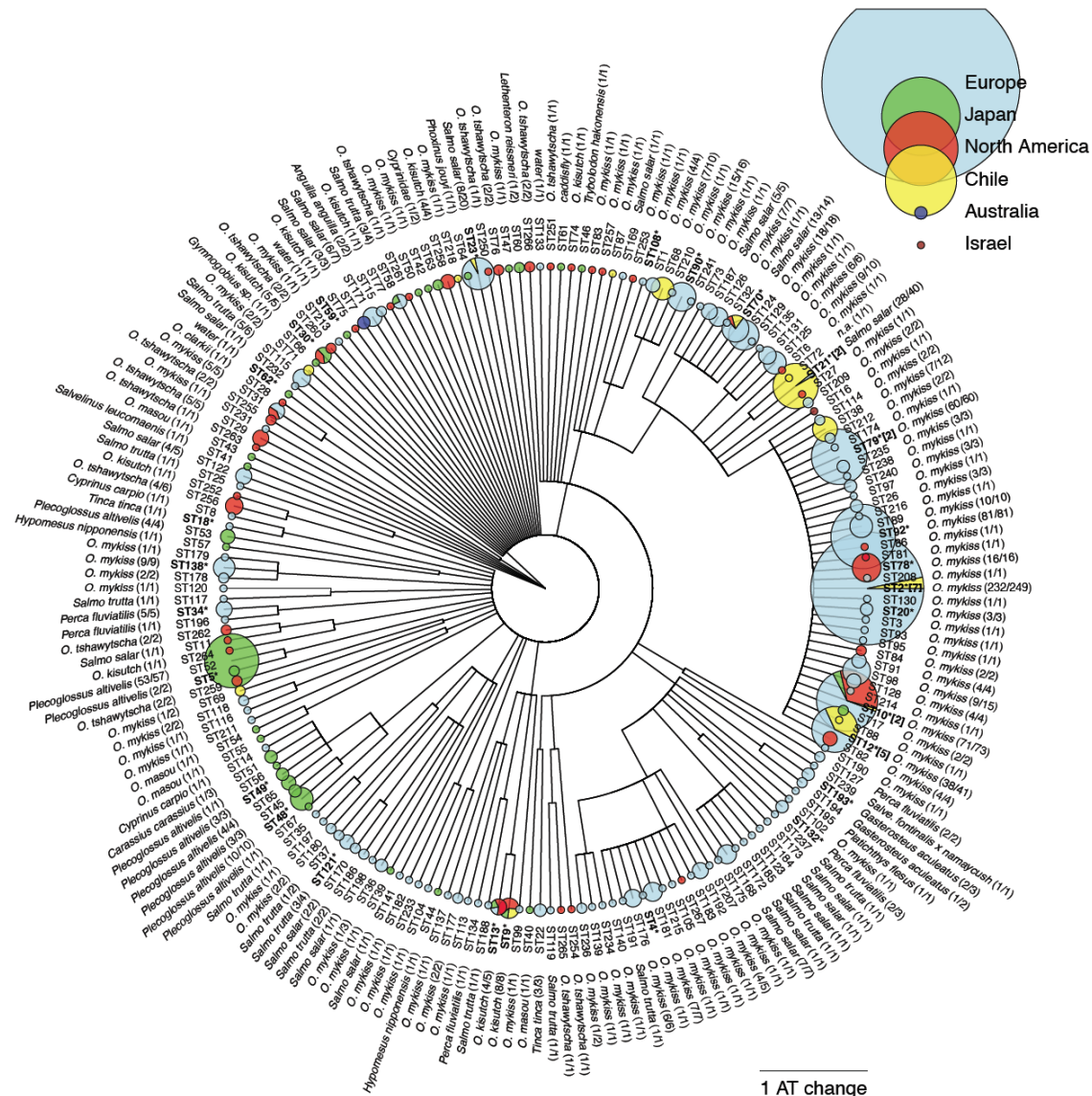
¹Cantonal Institute of Microbiology, Via Mirasole 22a, 6500 Bellinzona, Switzerland

²Institut National de la Recherche Agronomique (INRA), UR1077 Mathématique Informatique et Génome, 78350 Jouy-en-Josas, France

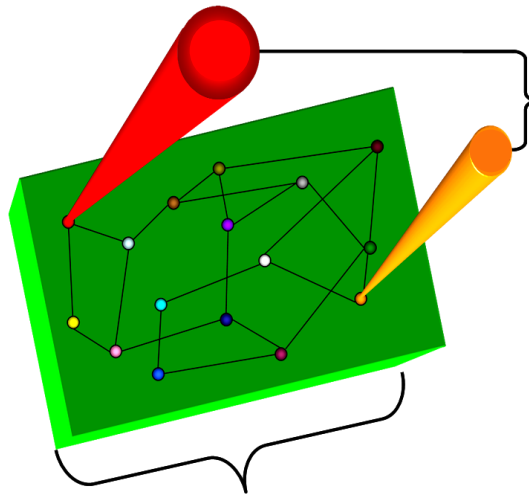
³Centre for Fish and Wildlife Health (FTWI), University of Bern, 3012 Bern, Switzerland

MLST web database

1097 isolats, 194 génotypes (ST)



Premières conclusions



Populations clonales en pisciculture

Population épidémique à génotypes dominants:

- Associé au poisson hôte.
- Mêmes génotypes dans différents pays.
- Sur un « fond » d'isolats probablement moins virulents.
- Co-infections.

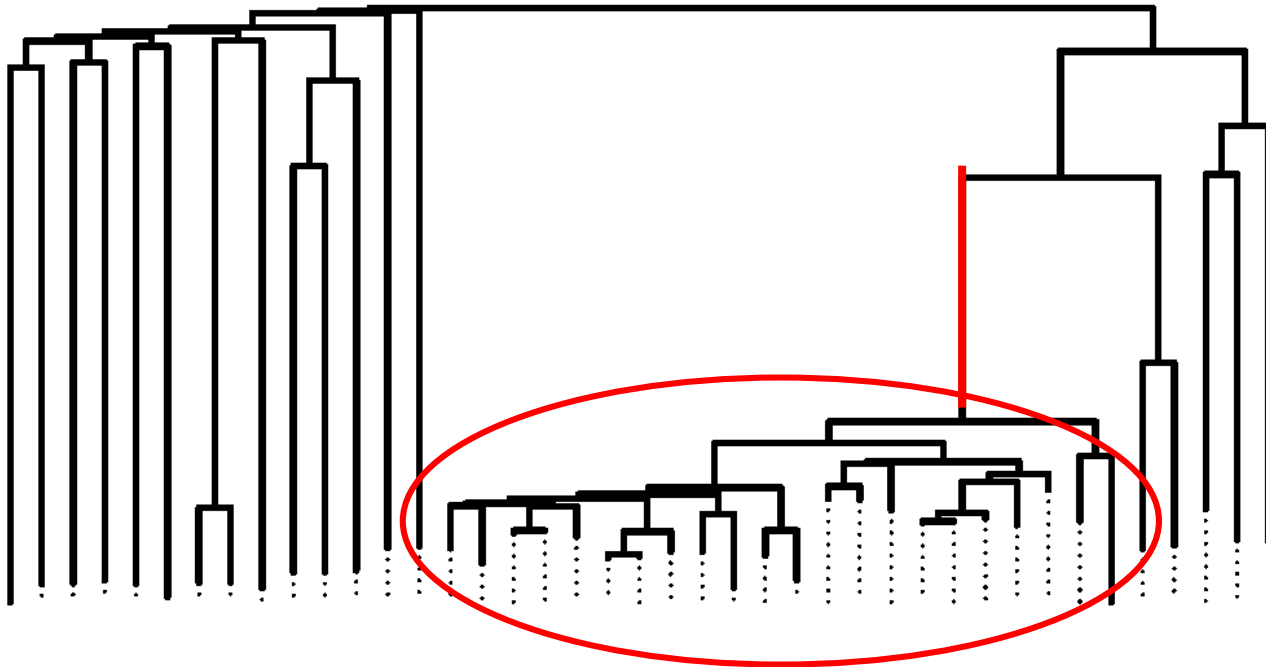
Population issue de
l'environnement
panmictique

Diffusion intercontinentale liée aux mouvements de poissons

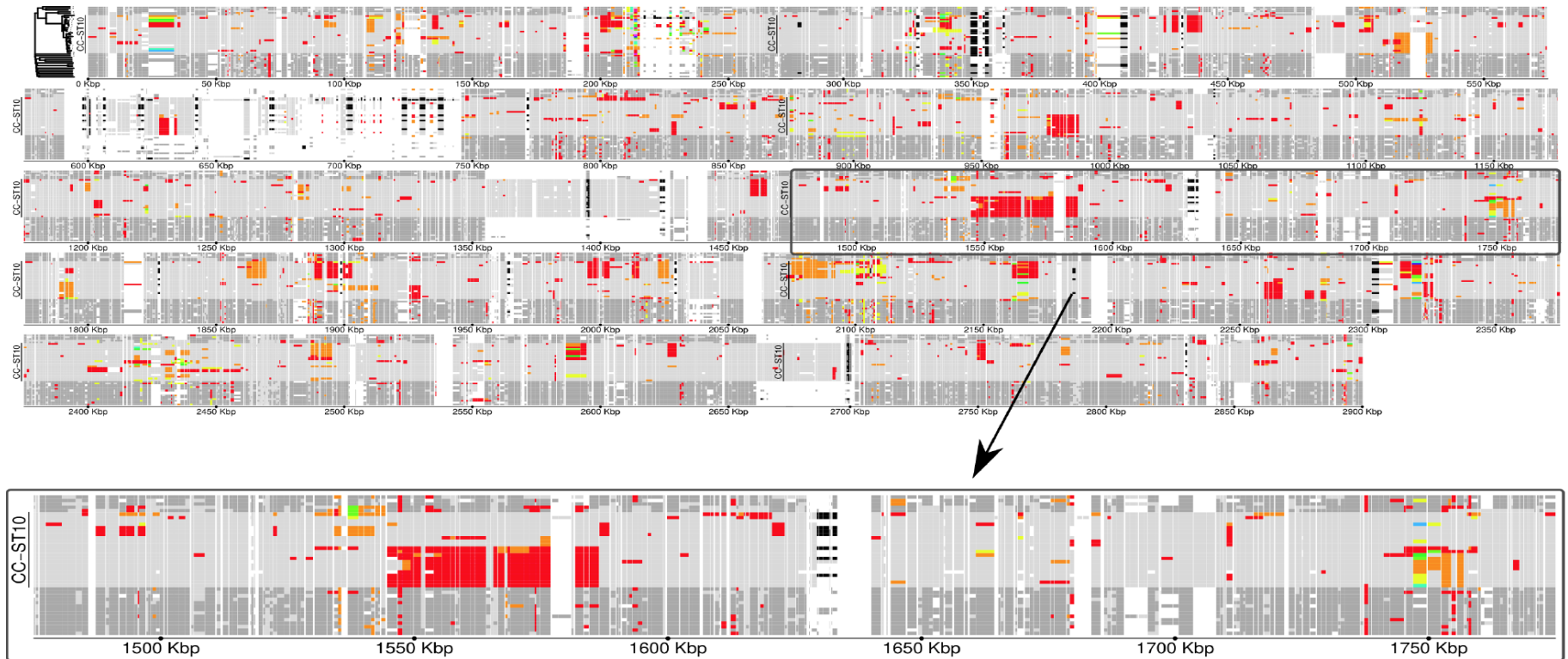
Approche génomes complets

50 isolats séquencés et comparés :

- Echantillonnage représentant une diversité maximale dans l'espèce.
- Permettant un focus particulier sur le complexe clonal (CC-ST10) infectant les fermes de truites arc-en-ciel (22 isolats).



Scénarios évolutifs

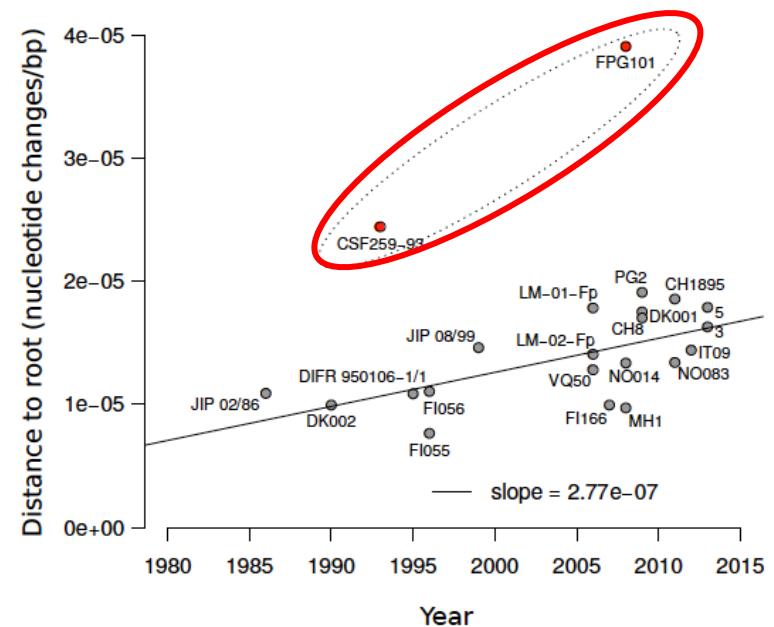
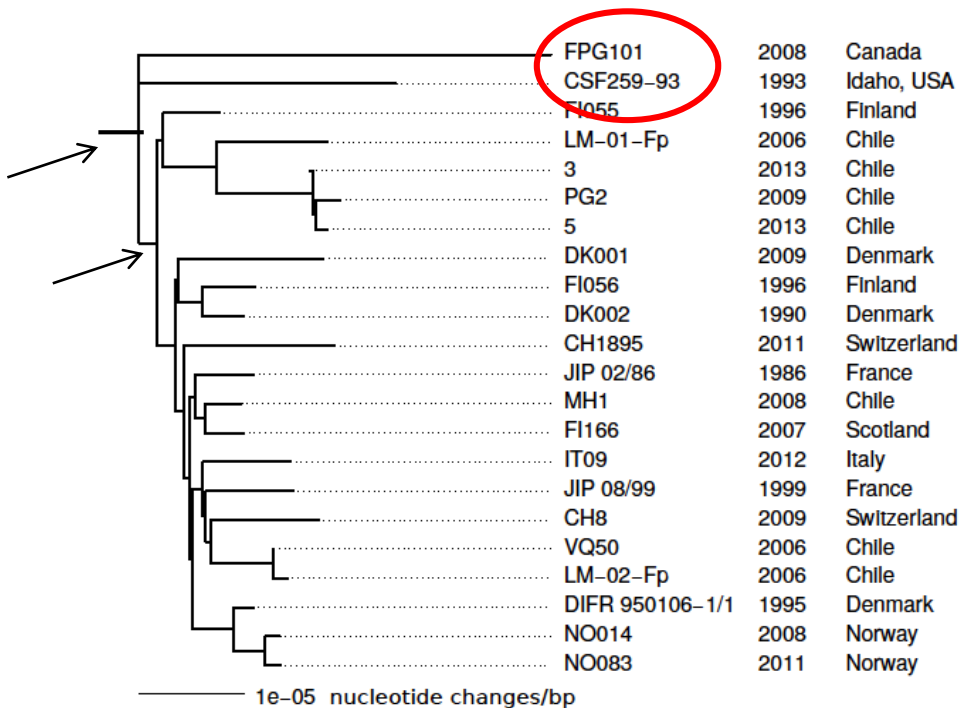


Diversité génomique limitée (core génome, 3 SNP/Gène)

Recombinaison/mutation ~ 13

Taille moyenne des segments recombinaisonnés ~ 4.0Kbp

Histoire du CC-ST10

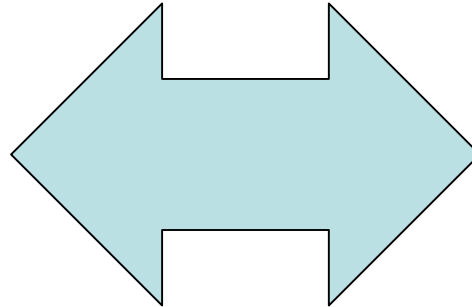
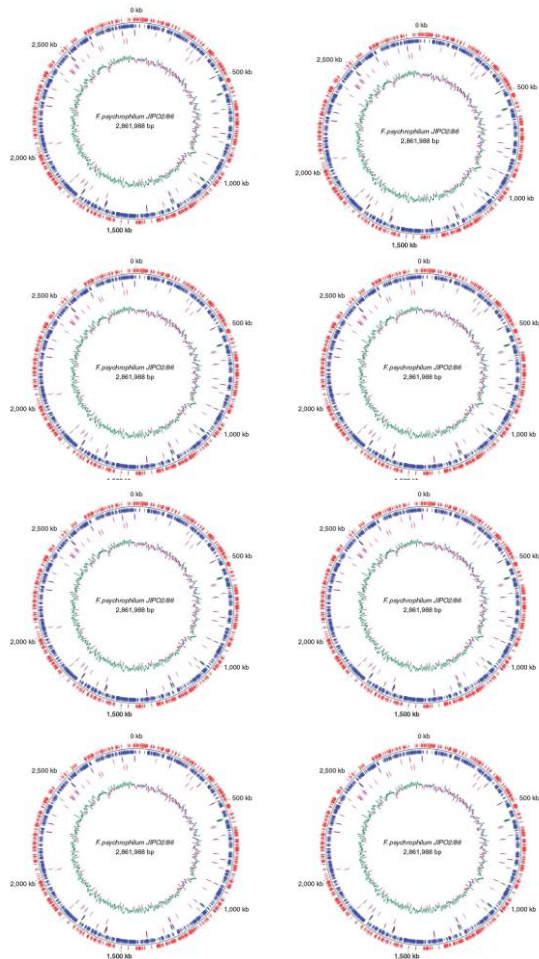


~ 1900 pour le CC-ST10

~ 1950 pour le groupe d'isolats échantillonnés à l'extérieur de l'Amérique du Nord.

Échelle de temps correspondant au développement de l'élevage de la truite arc-en-ciel d'abord en Amérique du Nord, puis dans le reste du monde.

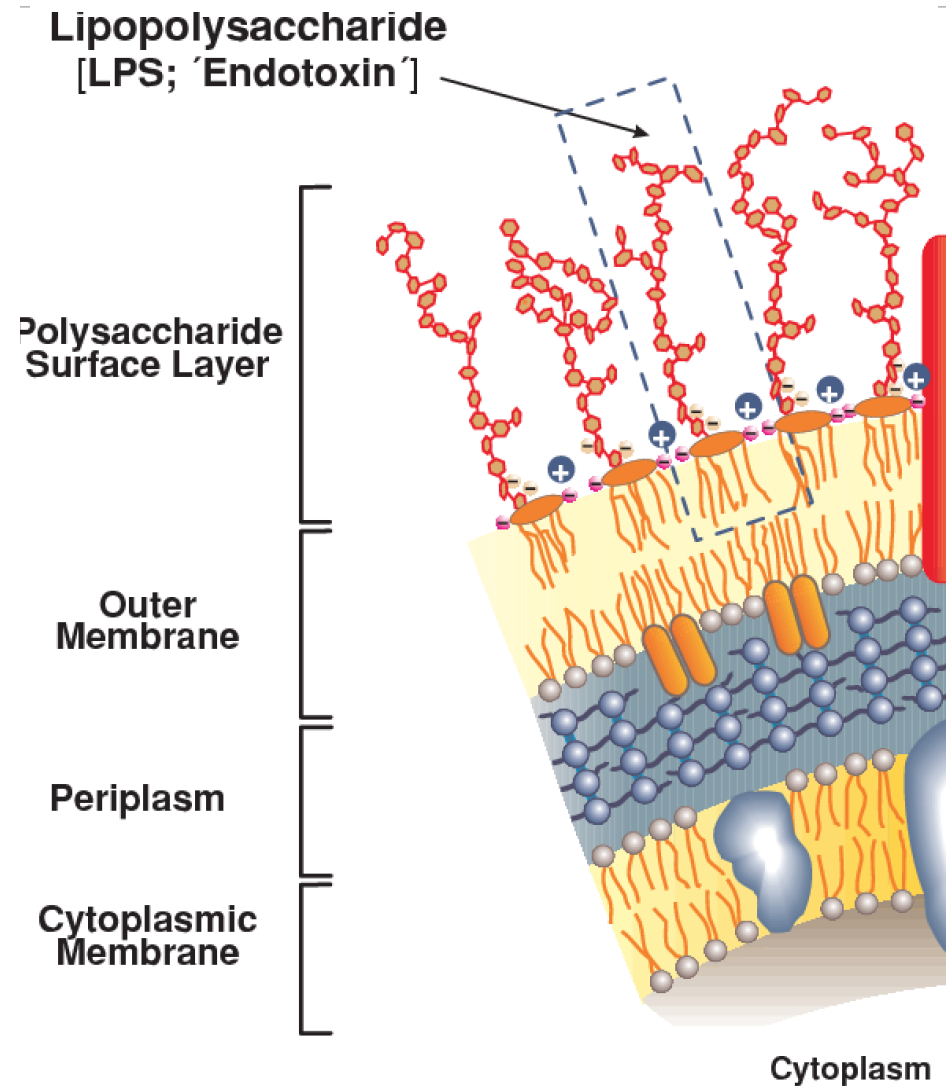
Études d'association pangénomique...



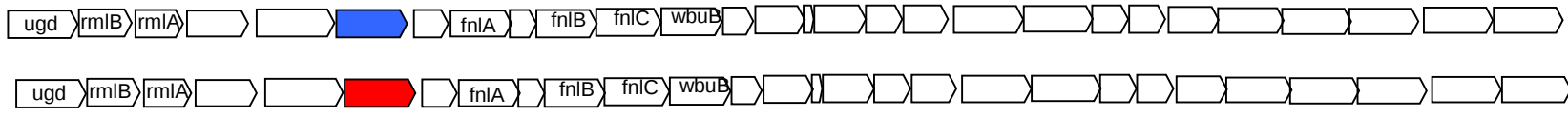
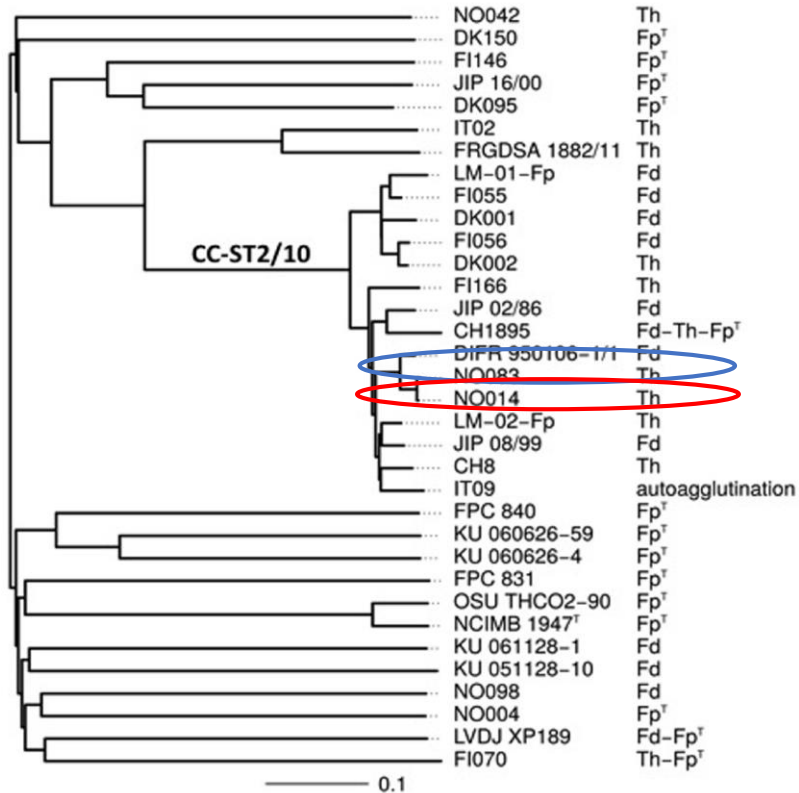
Mais les gènes sont nombreux et les phénotypes parfois complexes...



Les sérotypes...



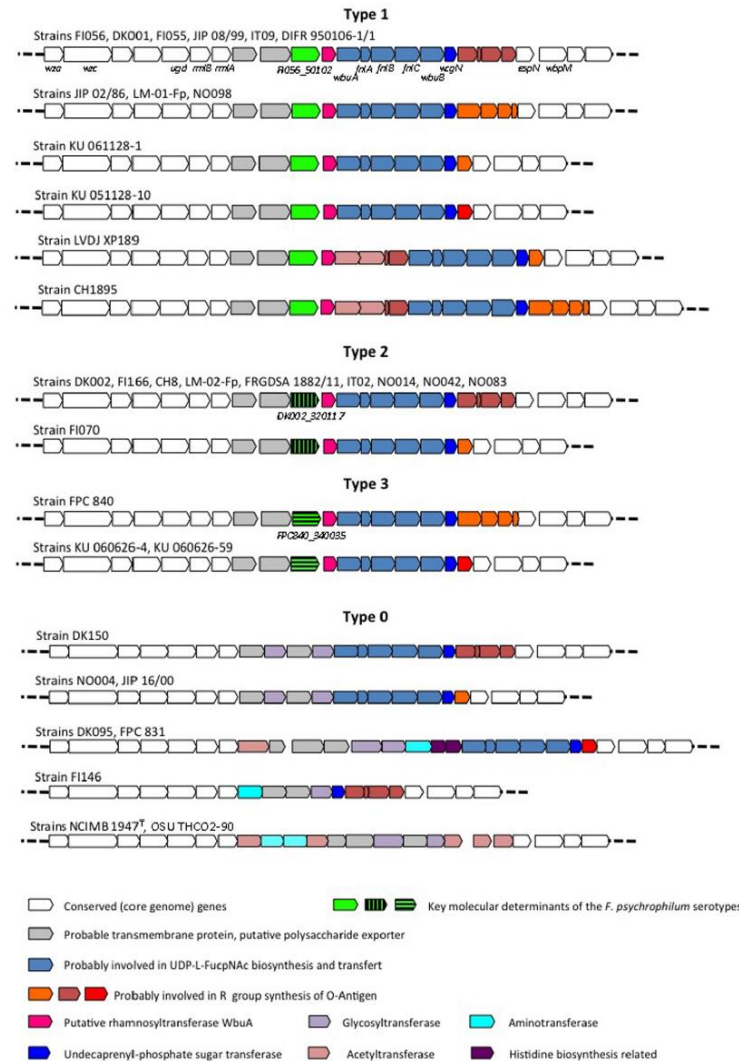
Le « maître gène » du sérotype



Th

Fd

Loci et gènes impliqués dans la biosynthèse du LPS



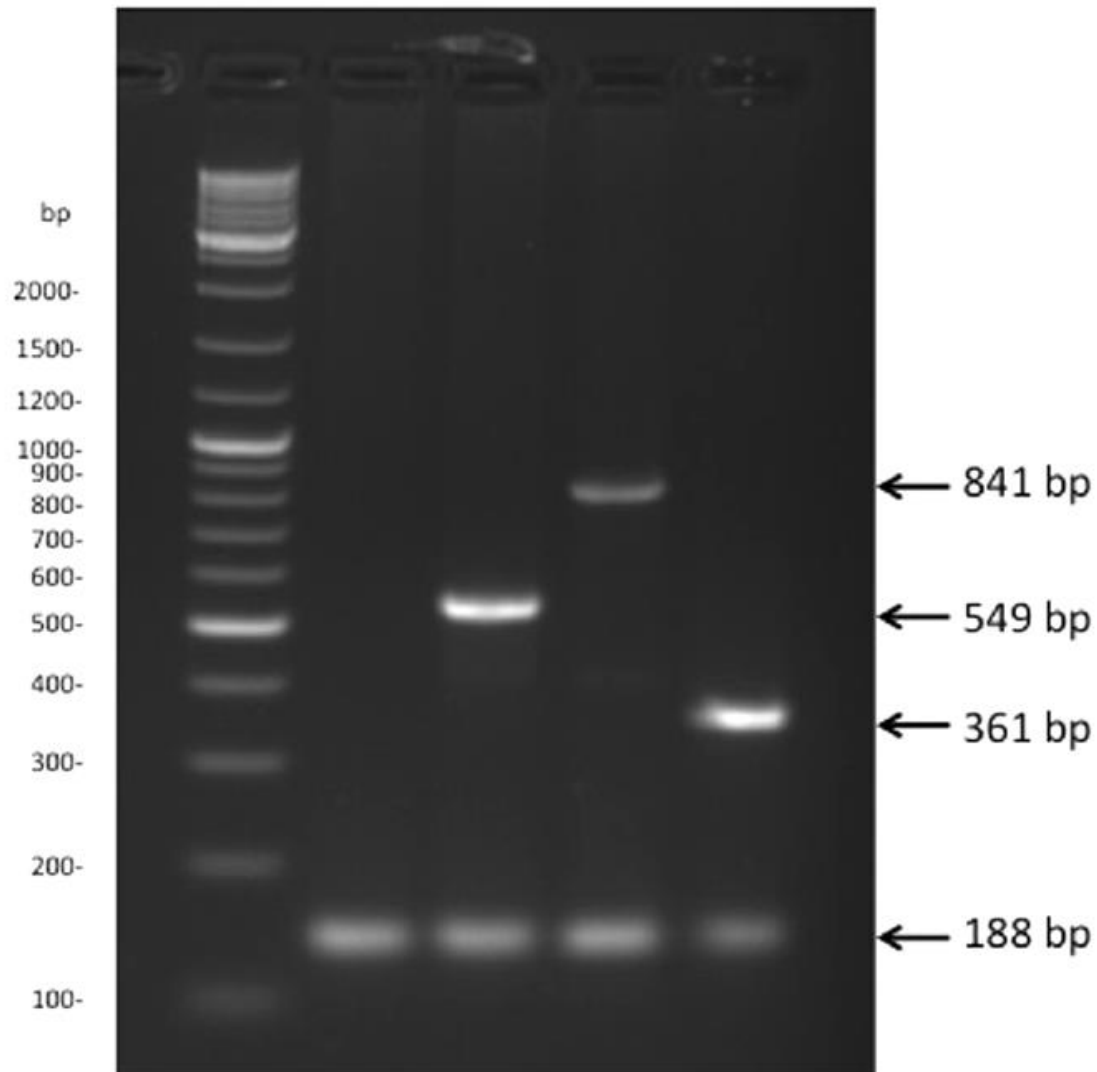
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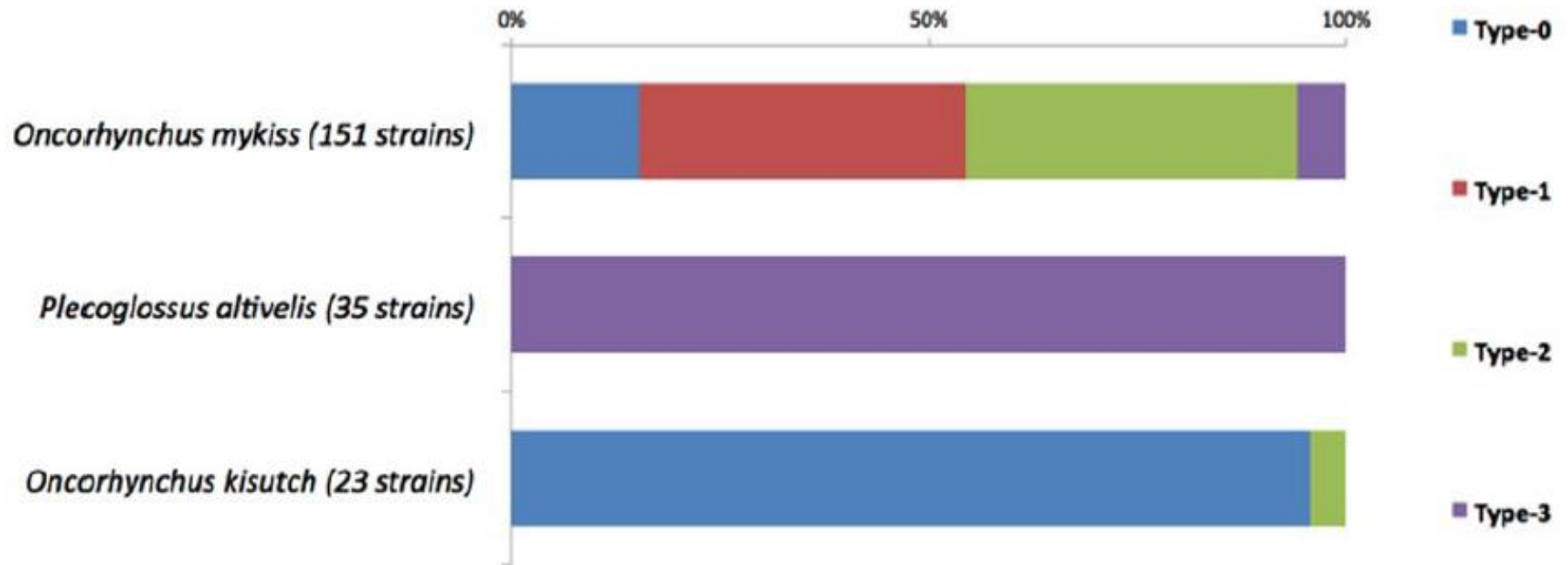
Fp(T)

Les données génomiques suggèrent l'existence d'au moins 17 sérotypes différents !

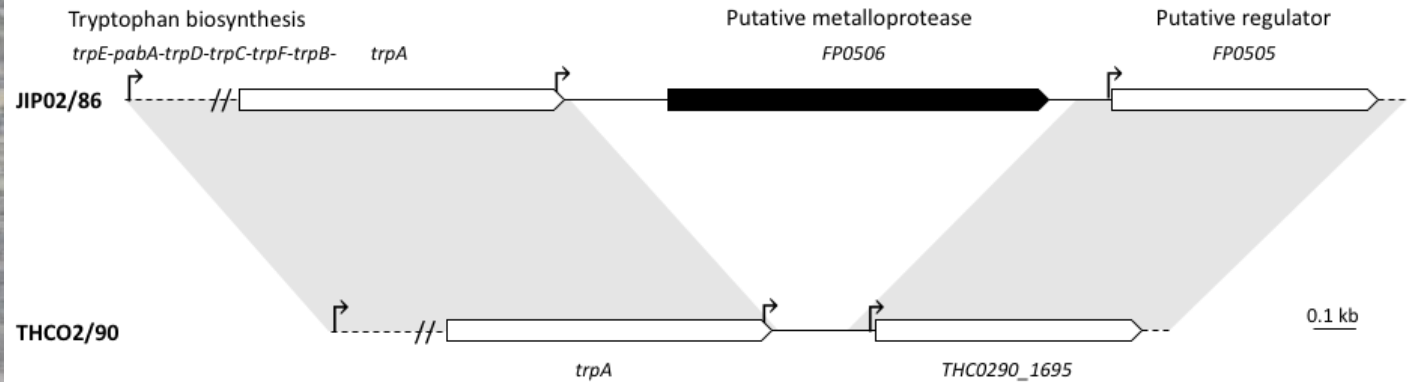
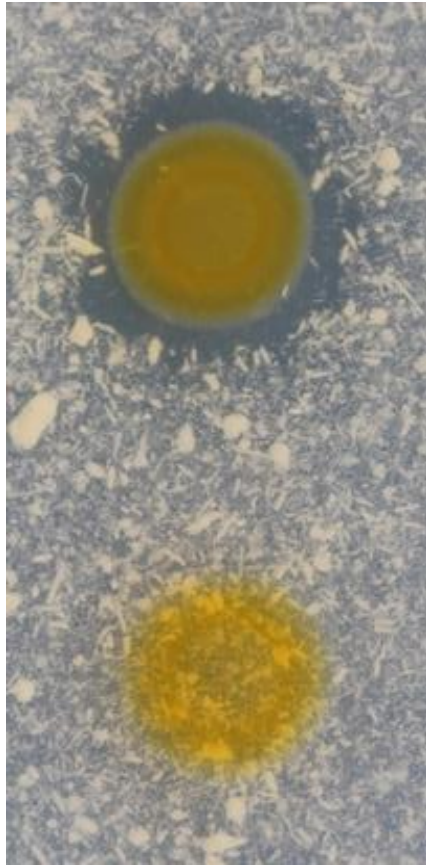
Kit de mPCR – 4 types majeurs identifiables



Association entre sérotypes et poissons hôte



Identification d'un facteur de virulence

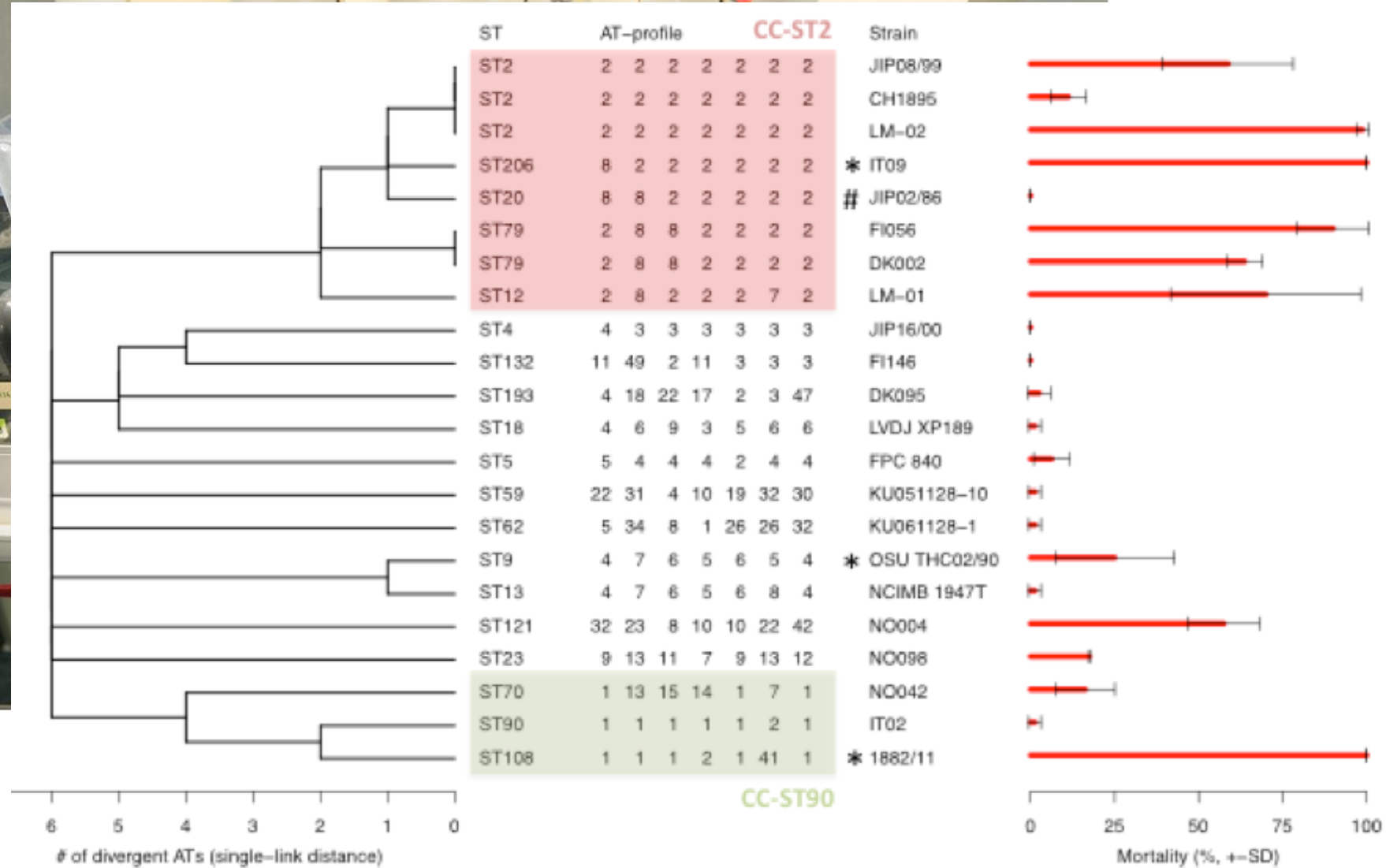


Virulence et génomes



Challenge par bain (coll. IERP, GenAqua)

Virulence et génomes



Conclusions

Les études d'associations pangénomiques sont des outils puissants pour identifier des traits moléculaires d'intérêt et expliquant des caractéristiques phénotypiques jusqu'à présent non résolues !

Remerciements

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INRA IERP (D. Rigaudeau)

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Switzerland: N. Strepparava, T. Wahli.

USA: G. Wiens, M. McBride.

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Récits complets dans :

Rochat et al., 2017. **Genomic Characterization of *Flavobacterium psychrophilum* Serotypes and Development of a Multiplex PCR-Based Serotyping Scheme.**

Front. Microbiol., 2017, 8:1752

Duchaud et al., 2018. **Genomic Diversity and Evolution of the Fish Pathogen *Flavobacterium psychrophilum*.**

Front. Microbiol., 2018, 9, e138.

Rochat et al., 2019. **Identification of a novel elastin-degrading enzyme from the fish pathogen *Flavobacterium psychrophilum*.**

Appl Environ Microbiol. 2019, 6:85