

Genome mapping in shellfish aquaculture species

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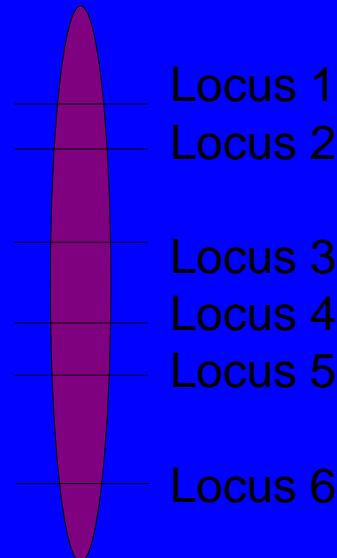
**Ifremer, Genetics and Pathology laboratory,
La Tremblade, France**



**Workshop “From genomics to applications in European temperate
and Mediterranean Aquaculture: Basis and prospects”
7-8th February, 2008**

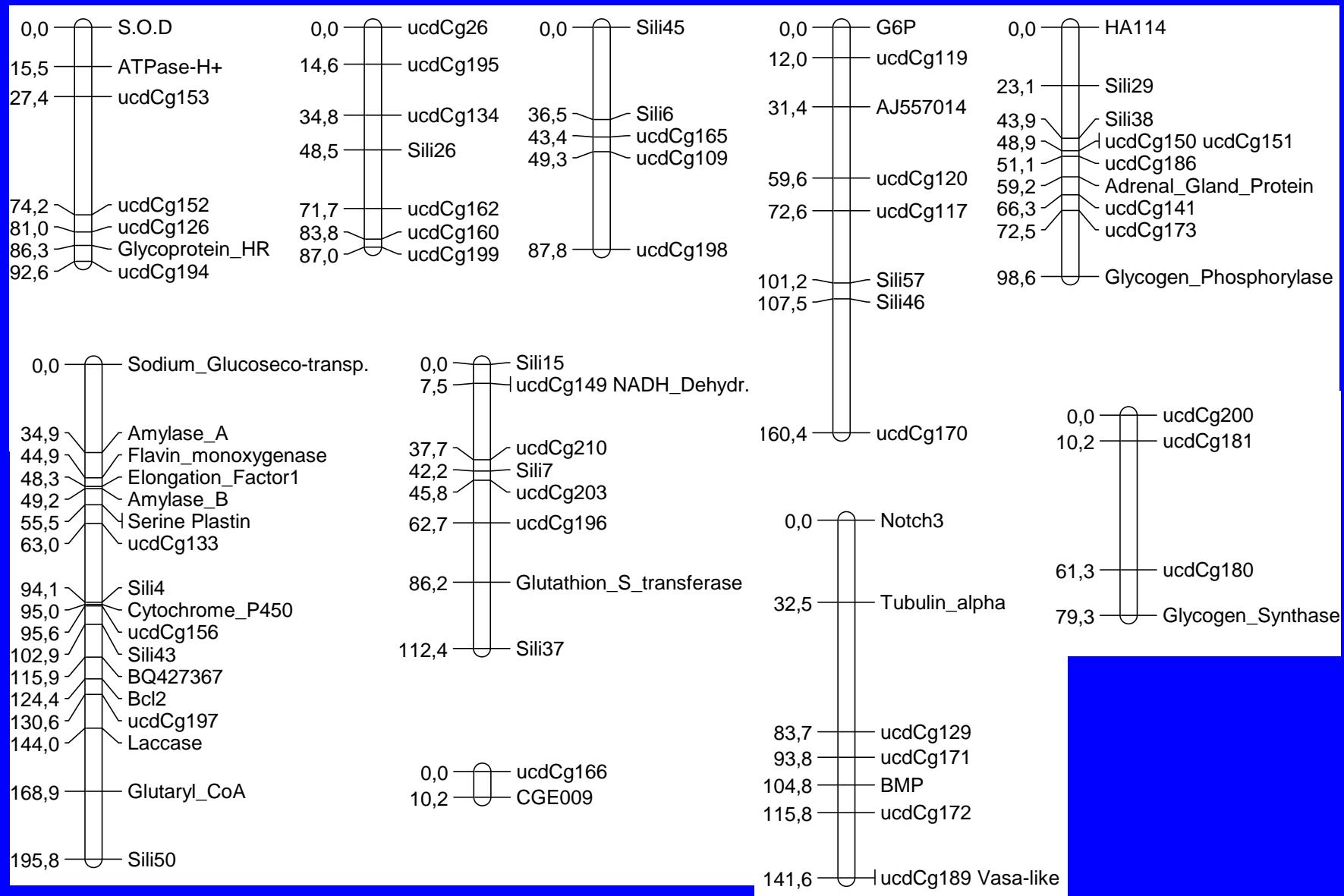
What does a genetic map show ?

- The ordering of marker loci on chromosomes
- The relative distances between them



Chromosome 1 = Linkage group 1

What does a genetic map show ?



How do we construct such maps ?

- Based on the estimation of the recombination frequency between two loci
- as this frequency is linked to the distance between the two loci:
The further apart on a chromosome two loci are,
The greater the probability is that one or more cross-overs will occur while gametes are produced
(chiasmata in prophase of meiosis I)



Old principle (Morgan, 1911) but lack of markers
N chromosomes = N linkage groups (LG)

A concrete example

$\begin{array}{c} \begin{array}{ccc} A & B & C \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \\ \times \\ \begin{array}{ccc} A & B & C \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \end{array}$	Homozygous for the 3 markers	
$\begin{array}{c} \begin{array}{ccc} A & B & C \\ \hline \end{array} \\ \times \\ \begin{array}{ccc} a & b & c \\ \hline \end{array} \end{array}$	Heterozygous for the 3 markers	
$\begin{array}{c} \begin{array}{ccc} A & B & C \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \\ \times \\ \begin{array}{ccc} a & b & c \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \end{array}$	F1 gametes	Number of progeny
$\begin{array}{c} \begin{array}{ccc} A & B & C \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \\ \times \\ \begin{array}{ccc} a & b & c \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \end{array}$ $\begin{array}{c} \begin{array}{ccc} A & B & C \\ \hline \end{array} \\ \times \\ \begin{array}{ccc} a & b & c \\ \hline \end{array} \end{array}$ $\begin{array}{c} \begin{array}{ccc} A & B & C \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \\ \times \\ \begin{array}{ccc} a & b & c \\ \hline \end{array} \quad \begin{array}{ccc} a & b & c \\ \hline \end{array} \end{array}$	ABC (p) abc (p) ABC (r II) abC (r II) Abc (r I) aBC (r I) AbC (r I+II) aBc (r I+II)	103 120 51 49 14 7 24 32 Total 400

From frequency (r) to distances (D)

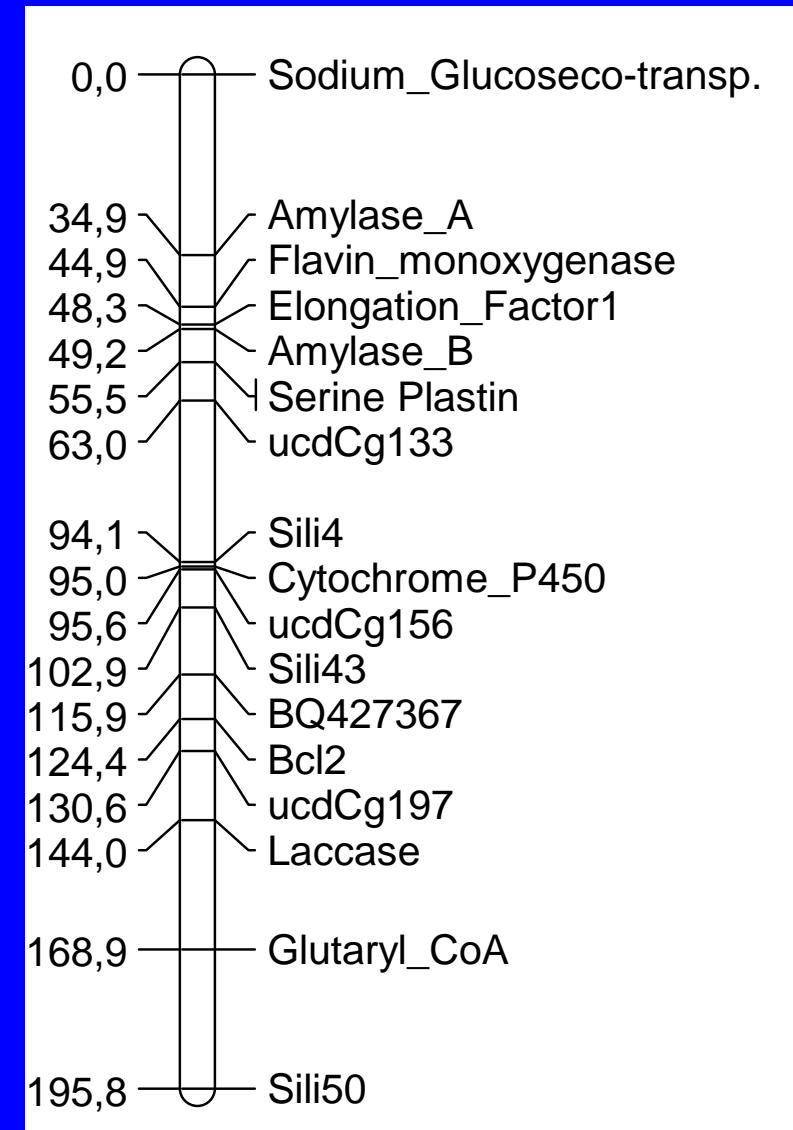
Several functions exist:

For example

$$D = \ln [(1 + 2r) / (1 - 2r)]$$

D is in cM : distance separating
two loci between which the
number of crossing over is
expected to be 0.01

Physical link but statistical
estimation





What do we need ?

- Polymorphic markers (microsatellites, AFLPs, RFLPs,...)
- Offspring allowing the analysis of alleles segregation
(specific cross design)
- Software (Linkage, Mapmaker, Joinmap, Crimap,...)

Genetic maps in shelfish

Prawns and Shrimps:

<i>Penaeus japonicus</i>	Moore et al, 1999 Li et al., 2003	AFLPs AFLPs
<i>Penaeus monodon</i>	Wilson et al., 2002	AFLPs
<i>Penaeus chinensis</i>	Li et al., 2006	AFLPs
<i>Penaeus vannamei</i>	Perez et al., 2004 Zhang et al., 2006	AFLPs AFLPs, microsatellites
<i>Marsupenaeus japonicus</i>	Lyons et al., 2007	AFLPs

Abalones:

<i>Haliotis discus</i>	Liu et al., 2006	AFLPs, RAPDs, microsatellites
<i>Haliotis rubra</i>	Li et al., 2007 Baranski et al., 2007	AFLPs microsatellites

Genetic maps in shellfish

Urchins:

Strongylocentrotus

Zhou et al., 2006

AFLPs

Scallops:

Chlamys farreri

Whang et al., 2004

AFLPs

Li et al., 2005

AFLPs

Wang et al., 2005

AFLPs

Argopecten irradians

Wang et al., 2007

AFLPs, microsatellites

Genetic maps in shellfish

Oysters:

Crassostrea virginica

Yu and Guo, 2003

AFLPs, microsatellites,
ESTs

Crassostrea gigas

Hubert & Hedgecock, 2004

microsatellites
AFLPs

Li and Guo, 2004

Sauvage et al. to be submitted



Microsatellites Markers

- 46 from Hubert & Hedgecock (2004)
- 3 from Yu & Li (2007)

In silico SSR derived form ESTs

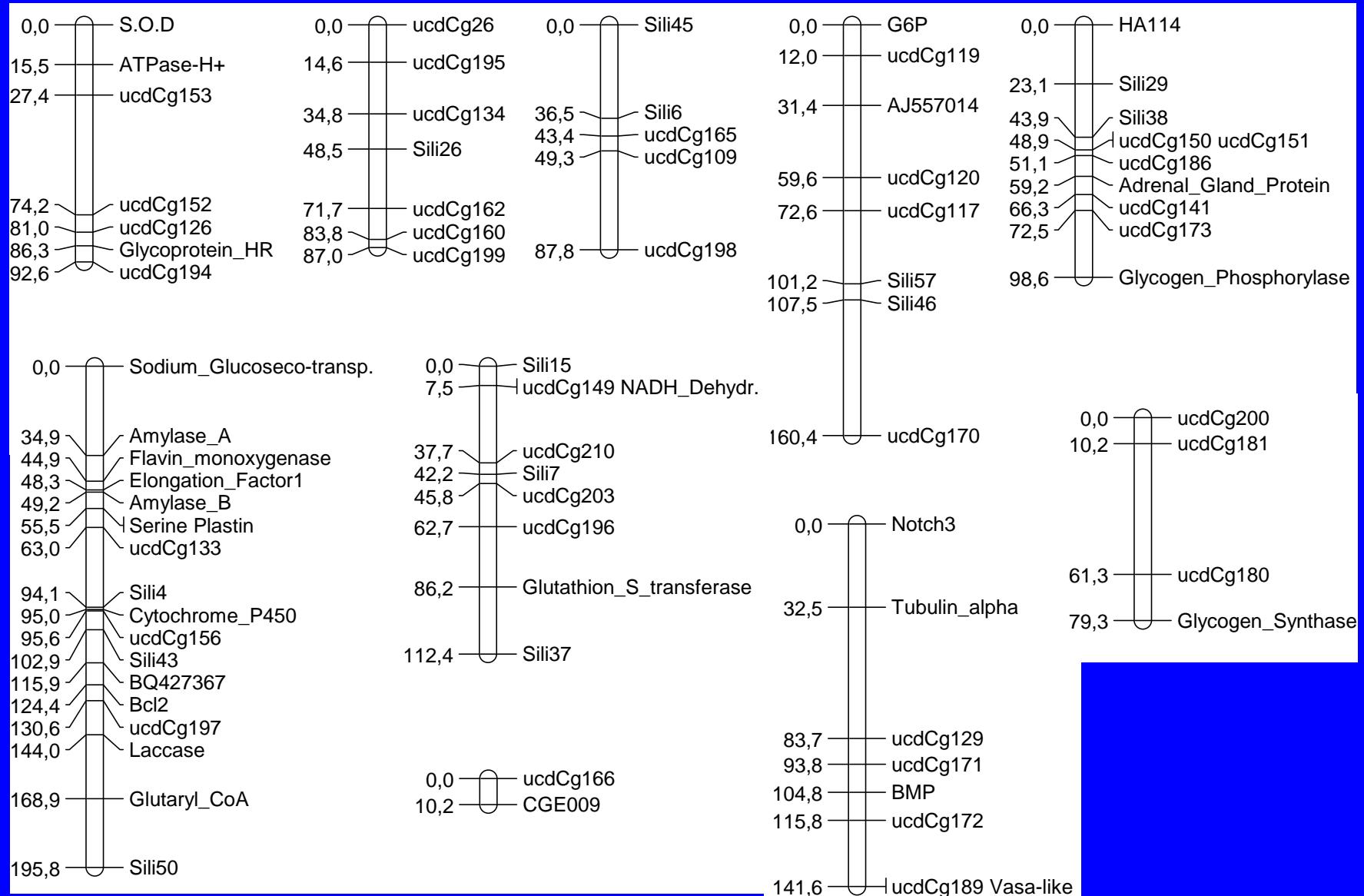
- 18 from Sauvage et al. (2008, submitted)

SNP markers

- 47 from Sauvage et al. (2007)

Genetic map in the cupped oyster *C. gigas*

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Consensus Map :

10 LG / Length 1218cM / 82 Markers / average spacing of 13.5 cM/ Coverage=93%

Genetic maps in shellfish

Oysters:

Ostrea edulis

Lallias et al., 2007

AFLPs, microsatellites,

doi:10.1111/j.1365-2052.2007.01647.x

A first-generation genetic linkage map of the European flat oyster
Ostrea edulis (L.) based on AFLP and microsatellite markers

D. Lallias^{*†}, A. R. Beaumont[†], C. S. Haley[‡], P. Boudry*, S. Heurtebise* and S. Lapègue*

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Mussels:

Mytilus edulis

Lallias et al., 2007

AFLPs

doi:10.1111/j.1365-2052.2007.01611.x

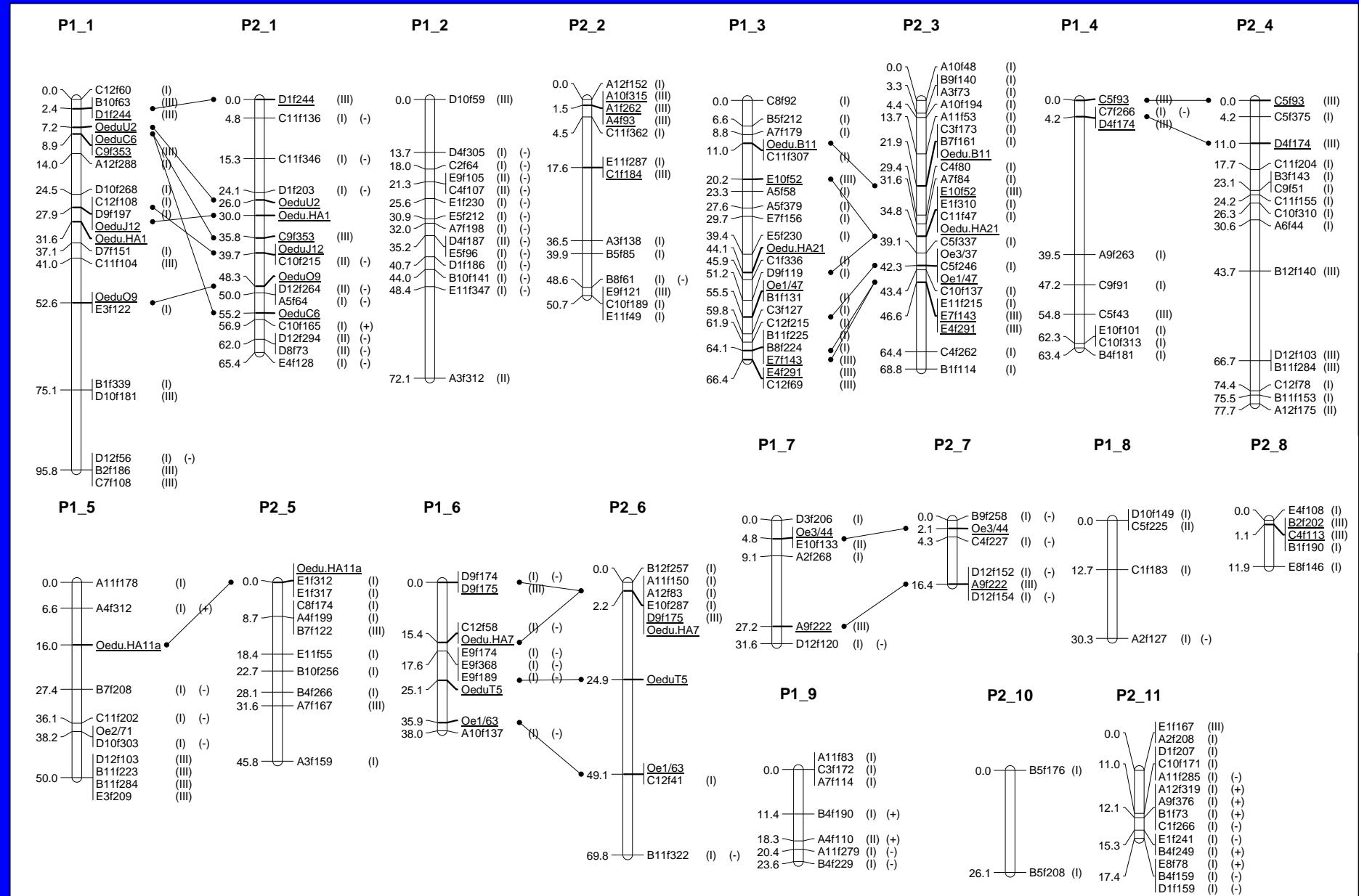
AFLP-based genetic linkage maps of the blue mussel
(*Mytilus edulis*)

D. Lallias^{*†}, S. Lapègue*, C. Hecquet*, P. Boudry* and A. R. Beaumont[†]

*Ifremer, Laboratoire Génétique et Pathologie, Ronce-les-bains, 17390 La Tremblade, France. [†]School of Ocean Sciences, College of Natural Sciences, University of Wales, Bangor, Menai Bridge, Gwynedd LL59 5AB, UK

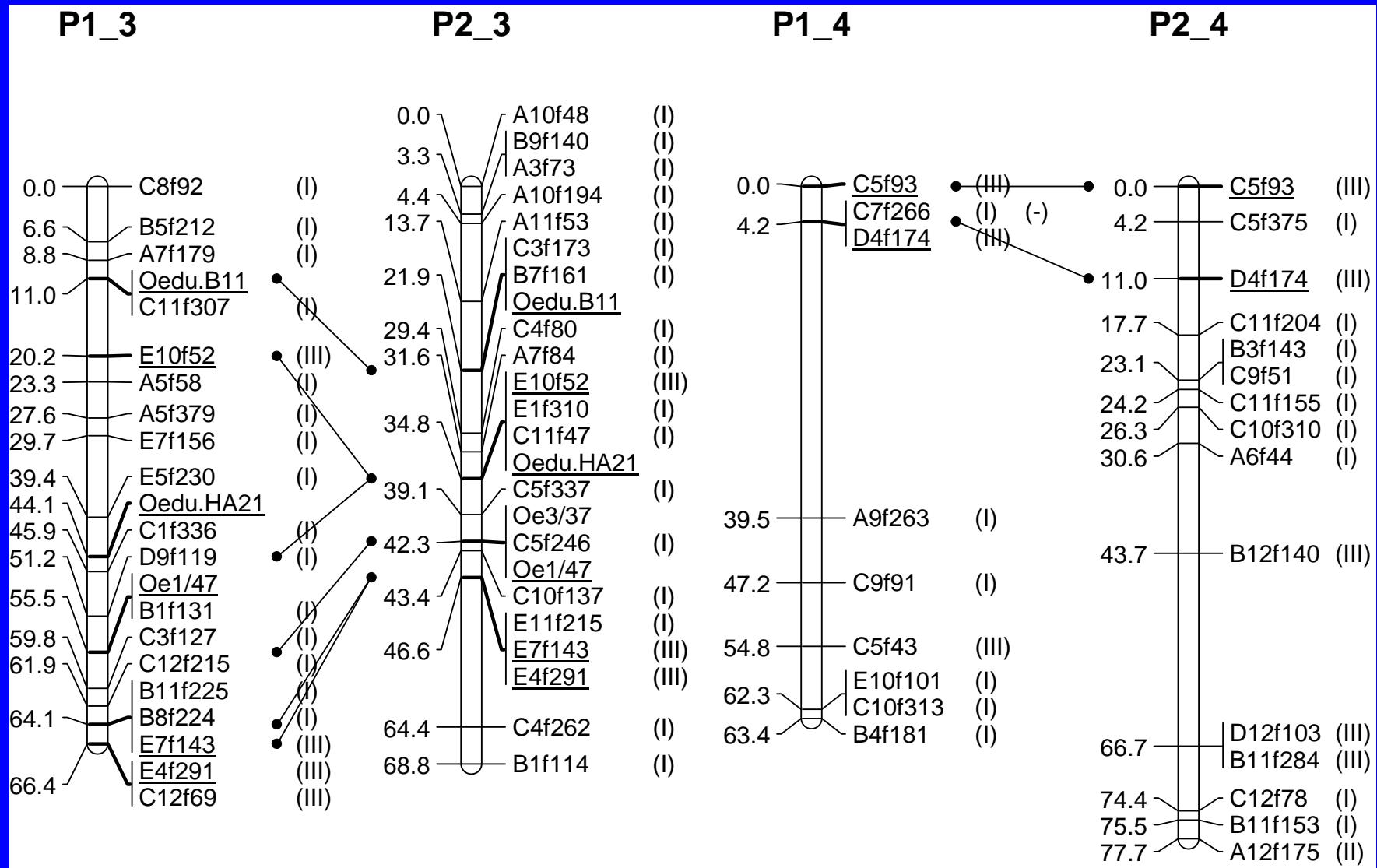
Genetic map in the European flat oyster *Ostrea edulis*

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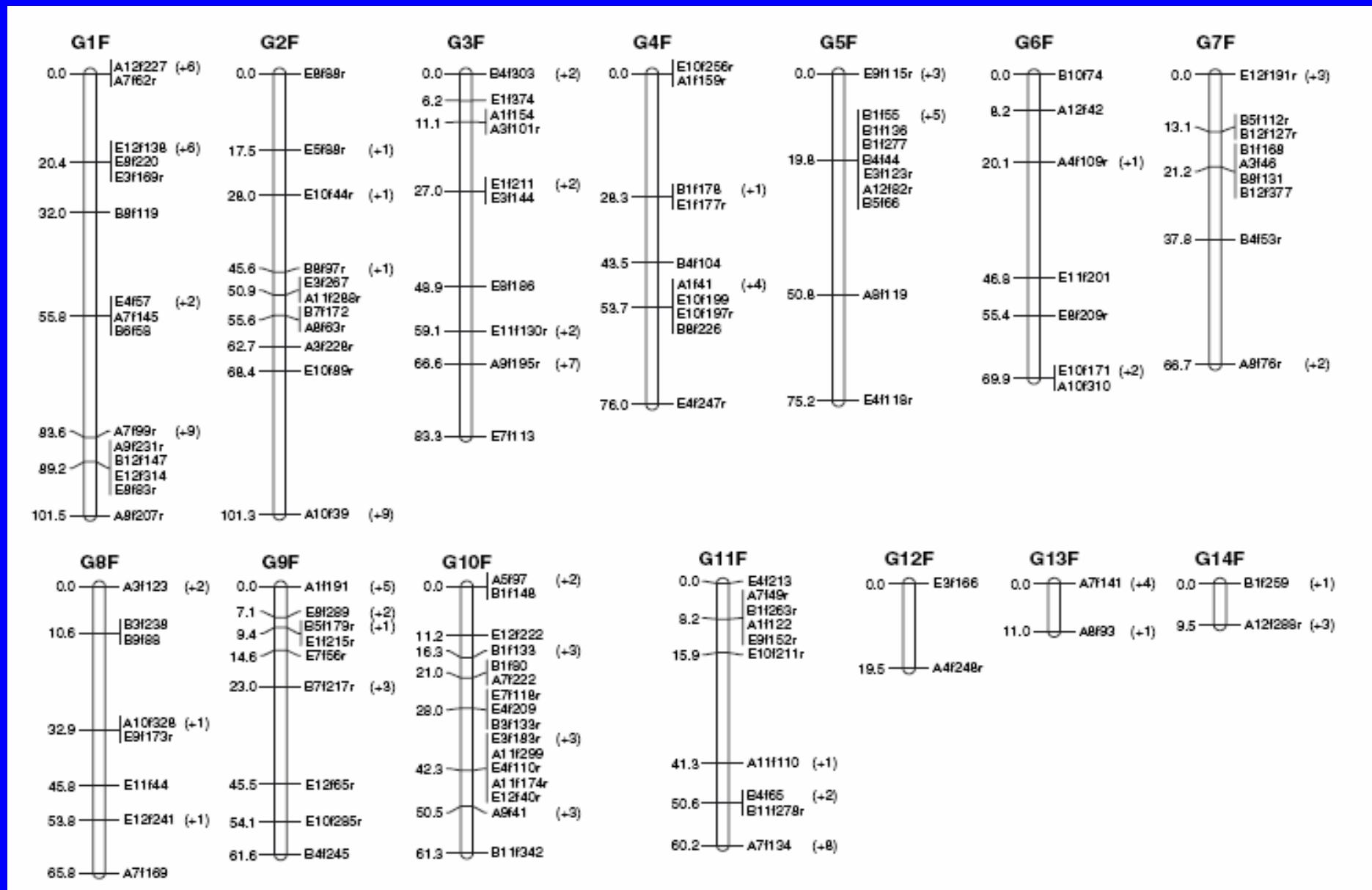


Genetic map in the European flat oyster *Ostrea edulis*

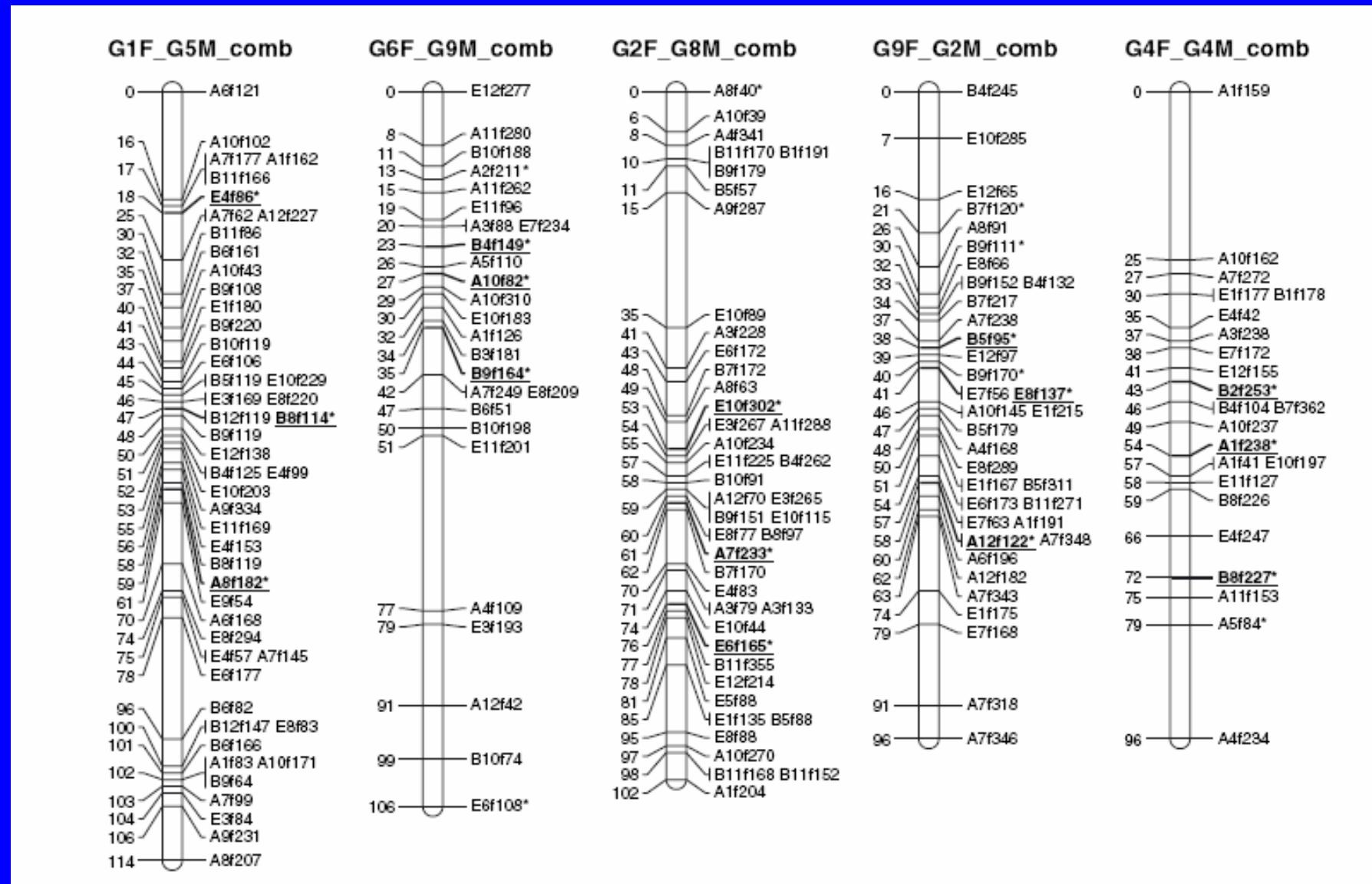
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Genetic map in the blue mussel *Mytilus edulis*



Genetic map in the blue mussel *Mytilus edulis*



General features of genetic maps

- Preliminary maps ...
- ...But already useful to look for links between markers and phenotypes (QTLs)
- Segregation distortion
- Clustering of markers (AFLPs)
- Sex specific differences in recombination rates
- Need of more codominant markers for a better coverage

Future in genome mapping

- High numbers of EST sequences
22323 hits for ESTs in *C. gigas* (06/02/08)

Development of new markers:
in silico microsatellites
SNPs

- High Troughput genotyping technics
- Link between a marker and a candidate gene
SNPs and ESTs
- Developement for the use for QTL mapping, and MAS