

EADGENE European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety

Genomics for Animal Health: Outlook for the Future
13- 14th October 2009, Muséum National d'Histoire Naturelle, Paris, France

**WP10.1 Technology Transfer
Poultry project**

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Projects and People involved

Two subprojects

- QTL detection for chicken production and resistance to disease traits
- Search for SNP markers associated with resistance to Salmonella

Board members

Academics	Breeders
Stephen Bishop ROSLIN INSTITUTE	Yves Jégo HUBBARD
Mari Smits WUR	Albert Paszek COBB-VANTRESS
Martien Groenen WUR	Gerard Albers HENDRIX GENETICS
Hervé Chapuis SYSAAF	Kellie Watson AVIAGEN
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QTL detection for chicken production and resistance to disease traits

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Why ?

Eimeria tenella

loss of weight
feed efficiency
death

7 different *Eimeria*

drugs
live vaccines

Each year: 800 million dollars

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Objectives

- How many QTLs are involved in resistance to coccidiosis and what are their effects ?
 - QTL detection
- Selection for coccidiosis resistance is interesting but what would be its effects on production traits (growth, meat quality, body composition) ?
 - Identification of QTL affecting the different traits and comparison of locations + transfer in commercial lines
- What is the epistasis extent for all these traits in chicken ? Would it affect the selection efficiency?
 - Modeling and testing epistasis

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Biological material

Identification of QTLs is much easier in experimental designs

=> Detection in experimental designs and transfer in commercial lines

Coccidiosis and growth (6 traits) Fayoumi x White Leghorn	Growth, body composition and meat quality (26 traits) Fat line x Lean line
↓	↓
6 F1 sires	5 F1 sires
↓	↓
860 F2 animals	650 F2 animals
	6 BC sires
	↓
	650 animals

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Genotyping

- Illumina Goldenpath technology : 1536 SNP
- SNP selection using MarkerSet[†] tool with different constraints:
 - covering all the available genome
 - Using chromosomal recombination rate variations information
 - Getting markers within a defined maximal interval
 - maximizing the informativity
 - Using F1 animals genotypes

[†] Demeure O. and Lecerf F. BMC Res. Notes. 2008 Mar 26;1:9.

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Genotyping

- Removing all mendelian errors
 - MendelSoft[†] was used
 - 76 (3226 SNP) and 117 (2220 SNP) animals modified for coccidiosis and fat/lean respectively
- Genetic map
 - No consensus genetic map for SNPs
 - Crimap not adapted to such amount of data
- Creation of a virtual map based on physical map and microsatellites locations
 - Future: use of Carthage^{*}

[†] De Givry et al. JCLP-05 workshop on Constraint Based Methods for Bioinformatics. 2005. page 9p., Sitges, Spain
^{*} De Givry et al. Bioinformatics. 2005. 21(8): 1703-1704

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QTL analyses – Additivity hypothesis

- Why using QTLmap[†] ?
 - It can analyse mixtures of half-sibs and full-sibs together
 - QTLmap allows multi-QTL and multi-traits analyses but also the use of discrete traits
- A large part of the problem is to handle hundreds of markers on one linkage group. QTLmap had to be adapted
 - Two points have been modified *:
 - Parents haplotypes computation
 - Transmission probabilities computation

[†] Elsen et al. EAAP 2009. Barcelona, Spain. Page 603 ; <https://qgp.jouy.inra.fr/>
^{*} Elsen et al. GSE. 2009. In press.

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QTL univariate analyses – QTLs distribution

5 QTLs with P<0.1 and 13 with P<0.05

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QTL univariate analyses – QTLs distribution

42 QTLs with P<0.1 and 49 with P<0.05

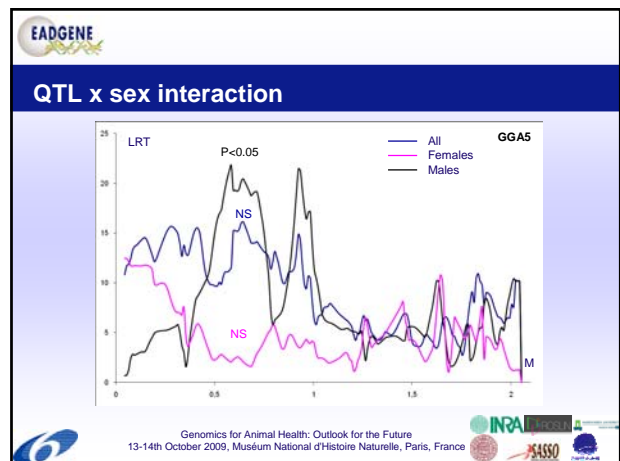
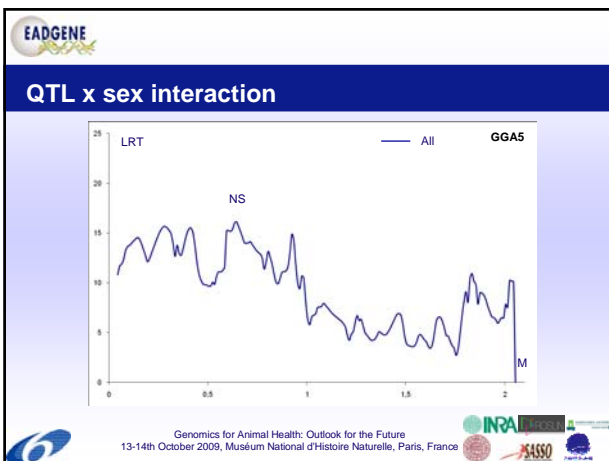
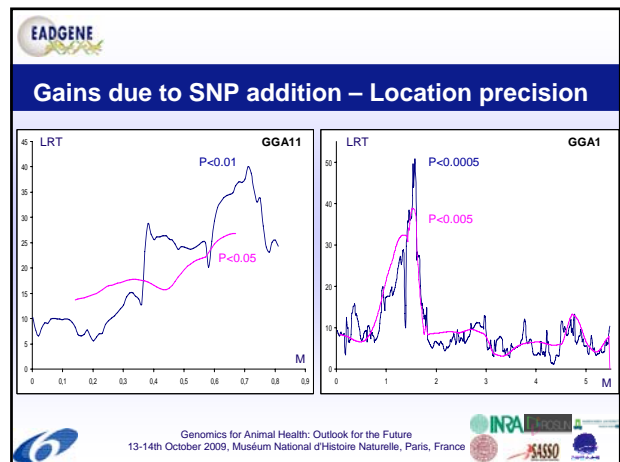
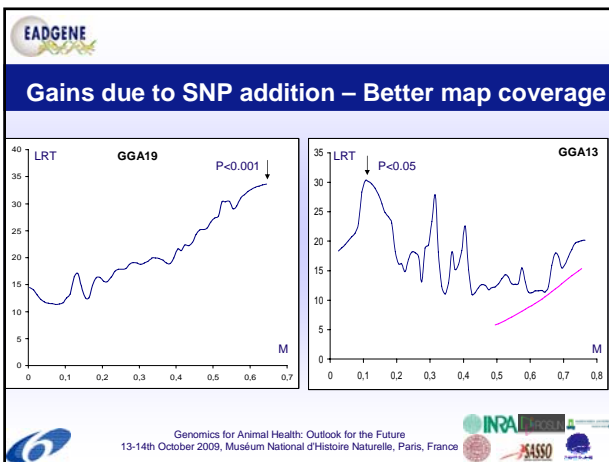
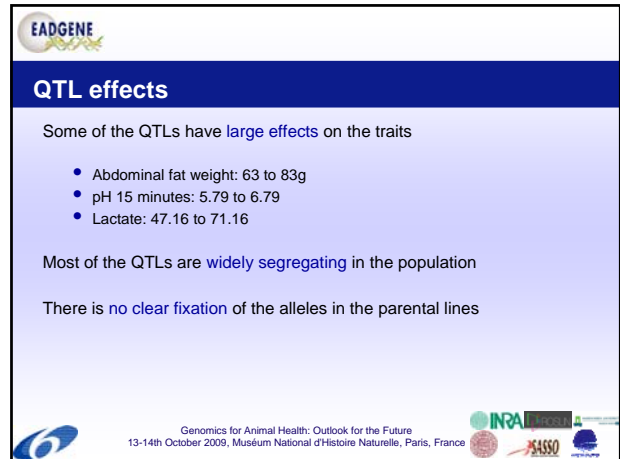
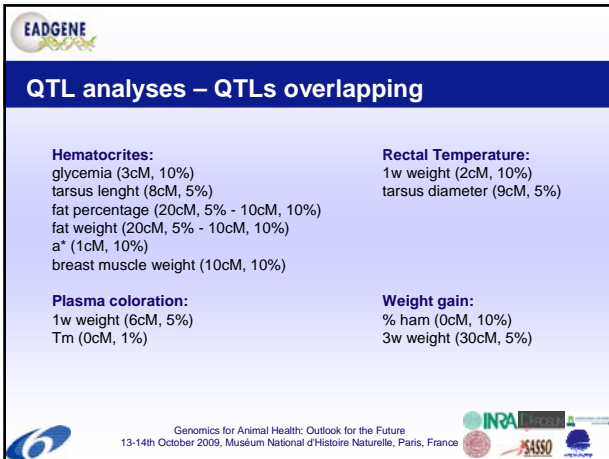
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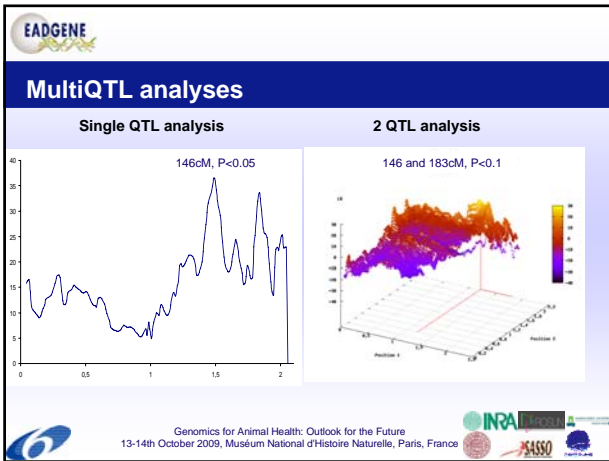
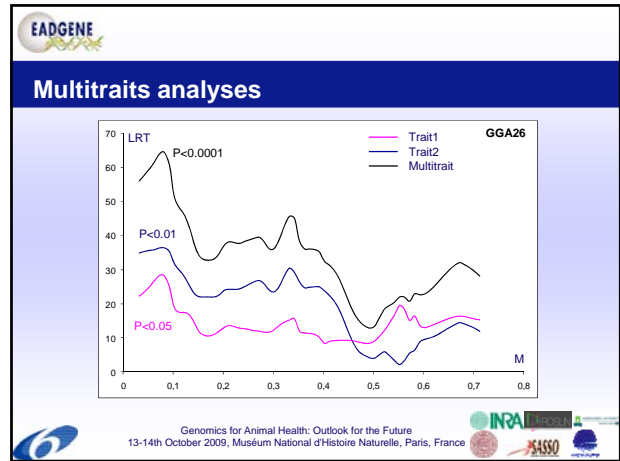
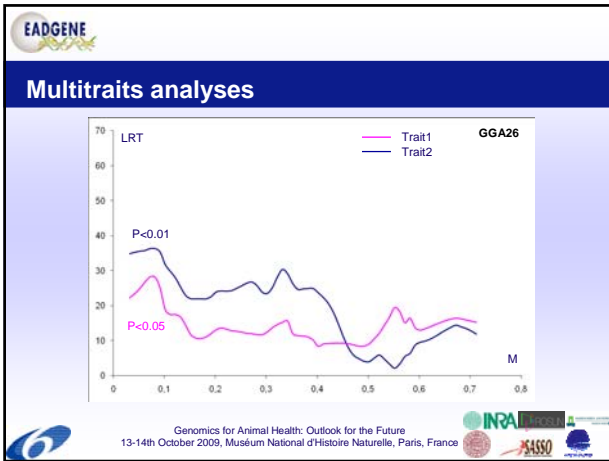
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QTL univariate analyses – QTLs distribution

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- ### Epistasis analyses
- Different models already exists. All of them use the hypothesis of fixed QTL alleles in founder lines
 - We need to define a new strategy for our outbred lines
 - Different meeting/talks have occurred between European partners and the model will be defined depending on single QTL results
 - Nicola Bacciu, a post-doc funded by the INRA arrived in December 2008 to work full time on this project until December 2010
 - He spent 3 weeks (25th May – 13th June) in Uppsala (O. Carlborg lab) to test the DIRECT algorithm and other softwares for analyzing epistasis (EADGENE short-term stay funding)

- ### Transfer to commercial lines
- **Coccidiosis susceptibility and growth measurements:**
SASSO design: 560 animals from 20 sires
Animals raised and tested in Ploufragan (AFSSA) ("Label" lines)
 - **Growth, body composition and meat quality:**
SASSO design: 1000 animals from 10 sires
Animals raised and phenotyped in Nouzilly (INRA)
 - All will be genotyped using 384 SNPs in QTL regions detected in experimental designs
 - QTL analysis (additivity or epistasis hypothesis) will be performed (early 2010)

- ### Partners
- | | | | |
|--|-------------|-----------------------------|-------------------------|
| | | | |
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W. Wei | |