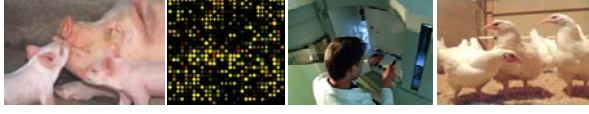



EADGENE **SABRE**
 CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING


EADGENE and SABRE Post-Analyses Workshop
 12-14th November 2008, Animal Sciences Group, Wageningen UR, Lelystad



QTL & Microarrays

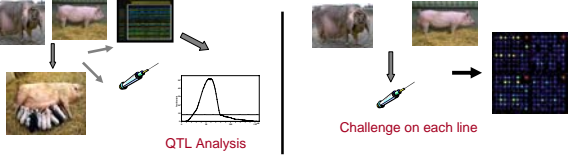


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Principle



- QTL study in experimental cross
- Expression study between founder lines
- Differentially expressed genes in QTL region

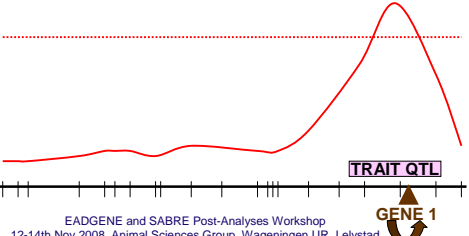



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QTL and Expression Information

- Differential expression between founder lines
- Gene maps to QTL region
- Cis-acting regulation of expression causes QTL effect?





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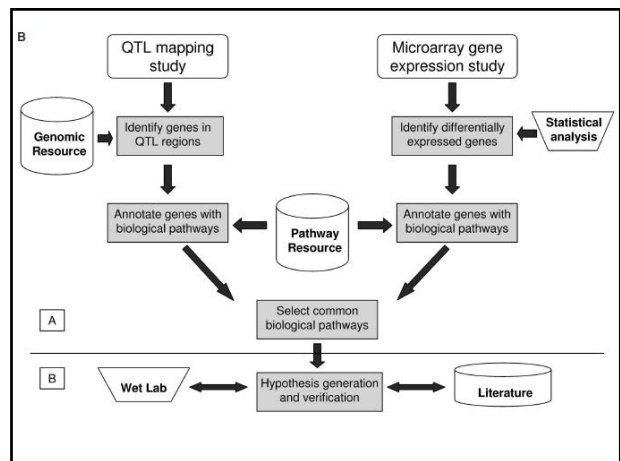
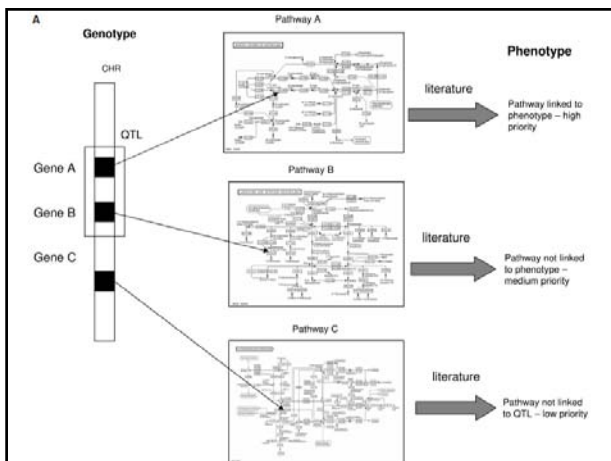
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Combining QTL and microarray Information

- Currently: ad-hoc comparison of QTL location with location of differentially expressed genes
- Hypothesis driven and often biased
- More formal approach proposed recently: Fisher et al, 2007. Nucleic Acids Research, vol 35(16), pages 5625-5633




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The data set

- **Data set 2: Pig adrenal sensitivity data provided by Pierre Mormede's group at INRA**
- **QTL:** J. Anim. Sci. 2002. 80:2276-2285
- **Gene expression:** Hazard D. et al. BMC Genomics 9:101 (2008)



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Session 5: QTL and microarrays, phenotypes

13:00 Introduction to QTL and microarray results - Dirk-Jan de Koning (University of Edinburgh)

13:10 In silico mapping of a few genes differentially expressed in pig adrenal glands as a function of sensitivity to ACTH - Vincent Jouffe, Pierre Mormede (INRA)

13:40 The missing link - QTLs and microarrays - Li Jiang, Lene Nagstrup Conley, Henrik Hornshøj, Bart Buitenhuis, Axel Skarman, Peter Sørensen, Jakob Hedegaard (University of Aarhus)

14:10 X marks the spot - but how deep is the treasure? - Suzanne Rowe (University of Edinburgh)

14:40 *Coffee break*

15:00 Predicting qualitative phenotypes from microarray data: the Eadgene pig data set - Christele Robert-Granié, Kim-Anh Lê Cao, Magali San Cristobal (INRA)

15:30 General discussion (chaired by DJ de Koning)

16:00 **Close. Buses to Lelystad train station**

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