



Genetics and genomics of biological stress responses as related to product quality and welfare

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Genetics and STRESS

- STRESS is the set of non specific responses to environmental challenges, with **behavioural** and **biological** components
- Stress has profound consequences on sustainability of animal breeding
 - Level of production (growth rate, feed efficiency)
 - Product quality (carcass composition, meat quality)
 - Resistance to diseases (immune system and inflammatory processes)
 - Welfare
- Stress is the result of an **interaction** between the animal and its environment
 - Individual variability (**genetic** and/or acquired)
 - ROBUSTNESS

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STRESS biology

- Hypothalamic-pituitary-adrenal (HPA) axis
→ glucocorticoid hormones (cortisol, corticosterone)
- Sympathetic nervous system → catecholamines (adrenaline et noradrenaline)
- Relationships with animal production
 - Catecholamines → meat pH (-)
 - Glucocorticoids → growth rate (-)
fatness (+)
newborn survival (+)
- Relationships with the immune system
- Relationships with behaviour

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Correlation between neuroendocrine measures, carcass composition and meat quality

	AD	NA	pH-AF
Cortisol	.42 ****	.15 *	.04
Adrenaline (AD)		.55 ****	.27 ****
Noradrenaline (NA)			.24 ****

- **Catecholamine** levels were positively correlated with meat pH measured 24 hours after slaughter. Indeed, sympathetic activation before slaughter increases muscle glycogenolysis and therefore reduces lactic acid production post-mortem and meat acidification


pH-AF = pH₂₄ *adductor femoris*

309 female and castrated male pigs from a F2 intercross between the Large White and Duroc breeds

Foury et al. Meat Science 69:703 (2005)

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Correlation between neuroendocrine measures, carcass composition and meat quality

	AD	NA	pH-AF	ADI	MBT
Cortisol	.42 ****	.15 *	.04	.24 ****	.23 ****
Adrenaline (AD)		.55 ****	.27 ****	.29 ****	.25 ****
Noradrenaline (NA)			.24 ****	.07	.07

- **Cortisol** levels were positively correlated with adiposity and back fat thickness. This correlation reflects the general metabolic effects of cortisol that favours the accretion of lipids in fat at the expense of proteins from muscle and other tissues


- The correlation between **adrenaline** and adiposity most probably results from its co-regulation with cortisol

pH-AF = pH₂₄ *adductor femoris*
ADI = loin weight / back fat weight
MBT = mean backfat thickness

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Correlation between neuroendocrine measures, carcass composition and meat quality

	AD	NA	pH-AF	ADI	MBT	IMF
Cortisol	.42 ****	.15 *	.04	.24 ****	.23 ****	.02
Adrenaline (AD)		.55 ****	.27 ****	.29 ****	.25 ****	.07
Noradrenaline (NA)			.24 ****	.07	.07	-.07


- No correlation was found between urine hormone levels and intramuscular fat content, showing that this metabolic compartment has a different regulation than other fat tissues

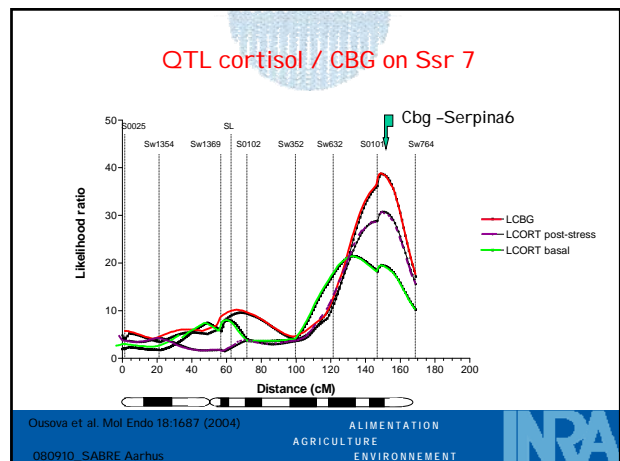
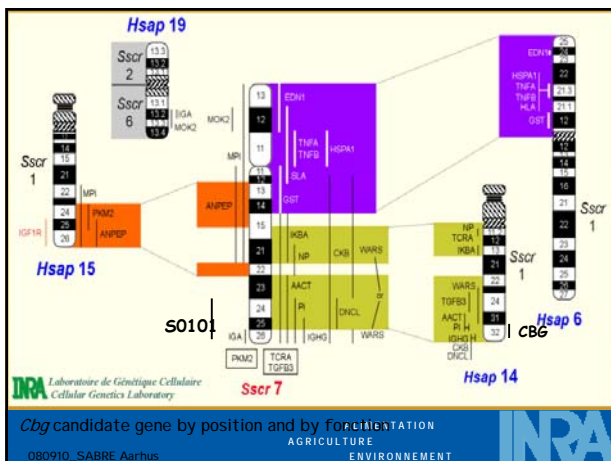
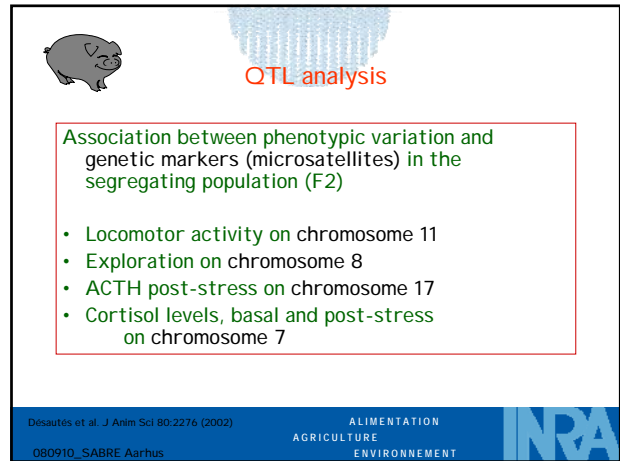
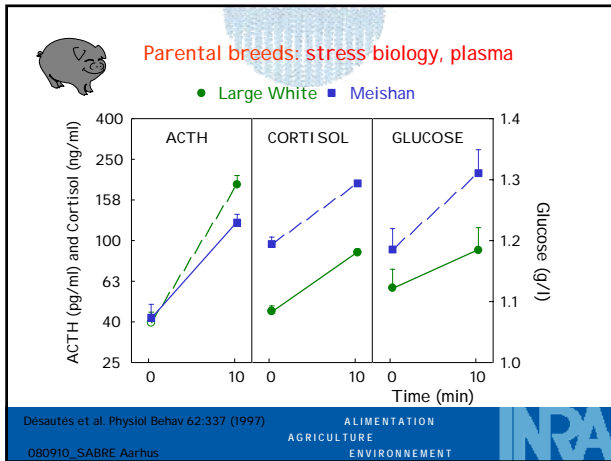
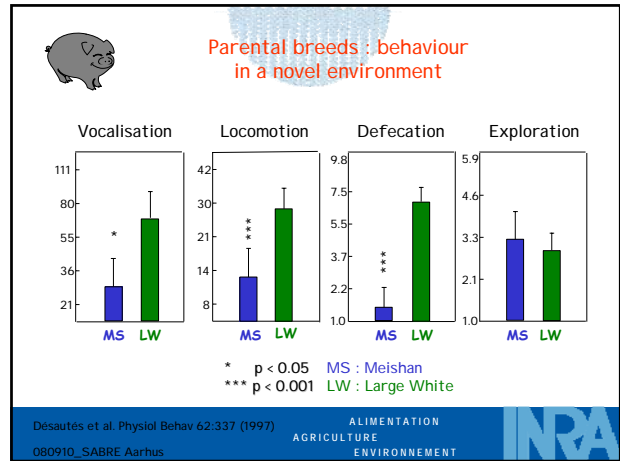
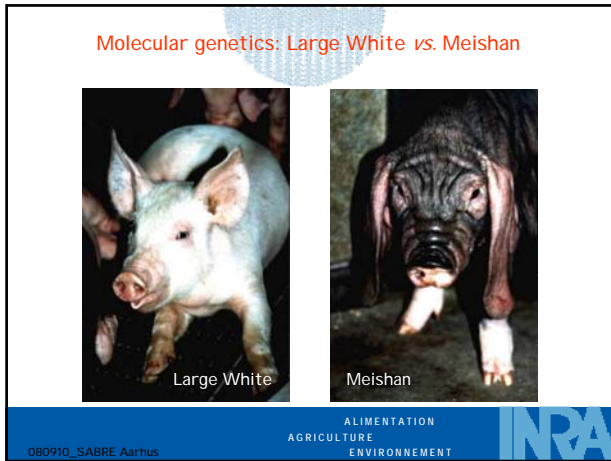
pH-AF = pH₂₄ *adductor femoris*
ADI = loin weight / back fat weight
MBT = mean backfat thickness
IMF = intramuscular fat %

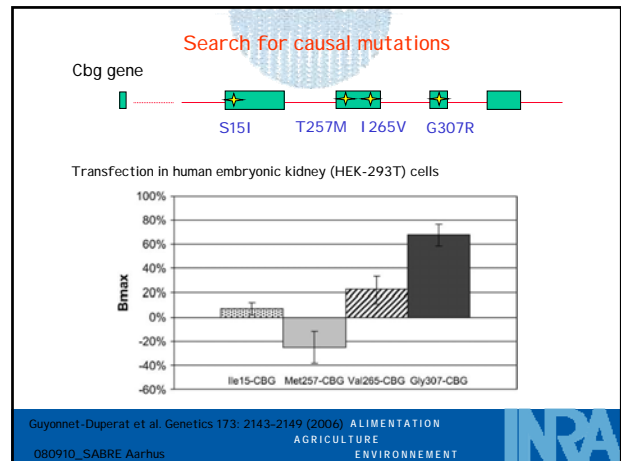
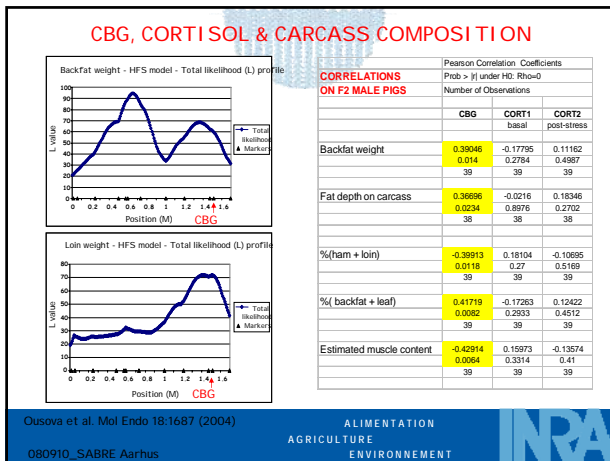
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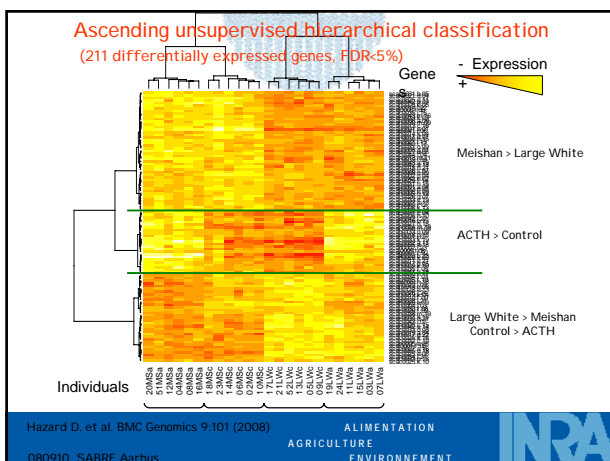
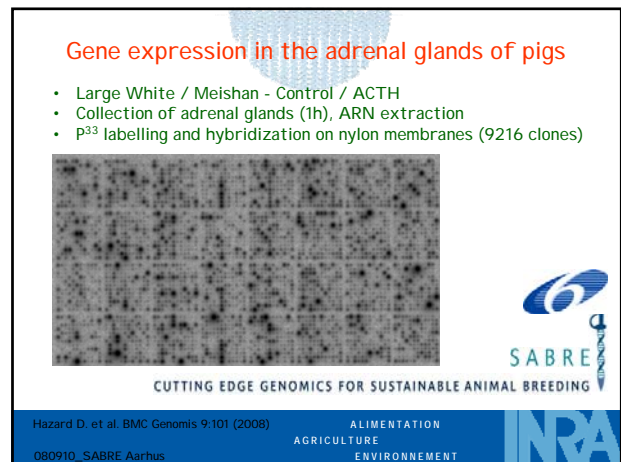




Sensitivity of the adrenal cortex to ACTH

- Is the main source of genetic variation in cortisol production
- Is an individual trait
 - Pigs - Hennessy *et al.* 1988
 - Humans 'Adrenal phenotype' Bertagna *et al.* 1994 ; Coste *et al.* 1994
- Is heritable
 - $h^2 = 0.26$ half-sib analysis in 357 litters from 24 boars (D.P. Hennessy)
 - Divergent selection
 - In chicken, response to ACTH (Edens et Siegel, 1975)
 - In trout, confinement stress (Pottinger et Carrick, 1999)
- We used molecular genomics to search for mechanisms responsible for genetic variation in adrenal cortex responses to ACTH

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Differentially expressed genes

- No difference
 - In the ACTH signaling pathway (i.e. ACTH receptor, G protein, Adenylate Cyclase, Protein Kinase A and MAPK ERK1, ERK2) except *Crem* (cAMP response element modulator) that activates genes involved in steroidogenesis
 - In steroidogenic enzymes (i.e. *Cyp11a1*, *Cyp17*, *3βhsd*, *Cyp21*, *Cyp11b*)
- Differentially expressed
 - Cholesterol transport (*Star*, *Ldlr*) and several kinases involved in phosphorylation of *STAR* (*Snf1IK*)
 - Tricarboxylic acid cycle (*Mdh2*, *Sdh* and *Suclg2*) involved in heme biosynthesis (*Alas1*)
 - Still to be characterized transcripts / genes

Hazard D. et al. BMC Genomics 9:101 (2008)
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