Session 8

GENOMIC PROFILING DURING MYOGENESIS OF FŒTAL CLONES

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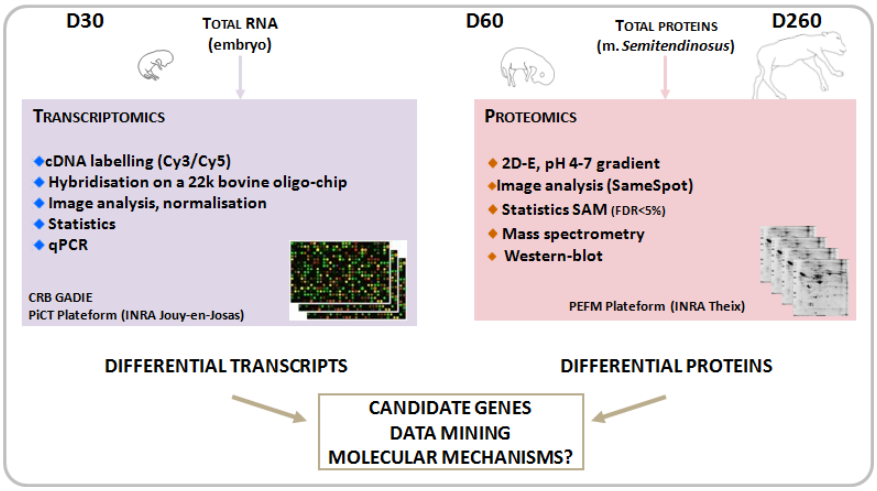
Bovine clones have a delay in their muscle differentiation during their first year postnatal (Jurie *et al* 2009 Animal 2, 244-250). Recently, we have shown that disturbances in both primary and secondary myogenesis occur in bovine foetal clones (Cassar-Malek *et al* 2010 Cellular Reprogramming 12,191-201). This may impact on the meat quality derived from clones and their offspring. To further identify molecular pathways that may underlie early disturbances in myogenesis, we have compared the genomic profiles of foetal clones (C) and their control counterparts obtained after artificial insemination (AI).

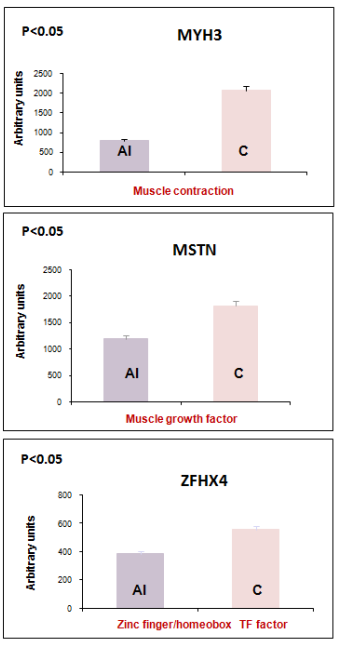
ANIMALS AND METHODS

- at day (D) 30 of gestation: C *vs* AI (n = 4 Holstein embryos per group)
- at D 60 of gestation: C *vs* AI in two breeds (Holstein and Charolais ; n = 4 per group in each breed)
- at D 260 of gestation: C *vs* AI (n = 4 Holstein foetuses per group)



RESULTS

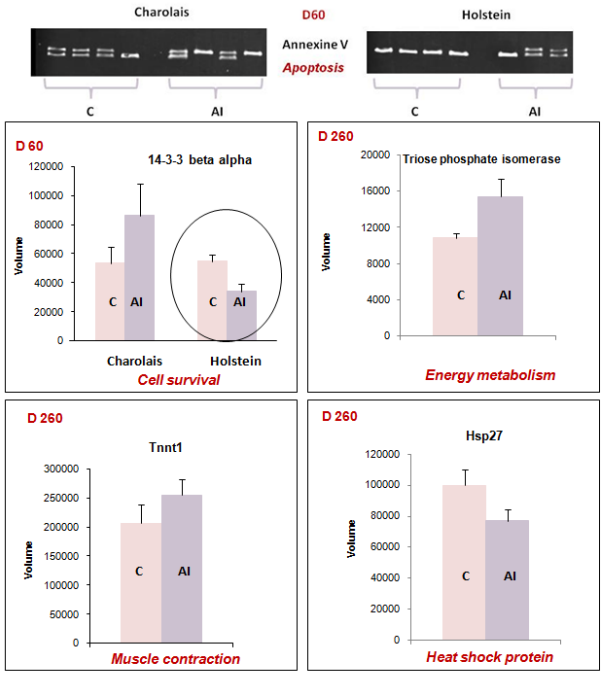
- **D 30:** 340 oligonucleotides ⇨**215 differential genes** (P<0.015) between C and AI
- **D 60:** 10 up- and 8 down-regulated proteins (FDR<5%) in C *vs* AI
- **D 260:** 2 up- and 10 down-regulated proteins (FDR<5%) in C *vs* AI



Examples of differential transcript abundance (qPCR data)

Data mining showed that few functions were affected

- **lipid metabolism and angiogenesis at D 30**
- **4 interconnected networks related to lipids (Ingenuity Pathway) at D 30**
- **regulation of cell cycle/apoptosis at D 60**
- **energy metabolism and chaperone activity at D 260**



Examples of differential protein abundance (western blot data)

CONCLUSION

In clones, muscle gene expression and protein abundance differed from those of their AI counterparts. Molecular profiling combined with data mining illustrated a delay in early and late myogenesis of clones and revealed pathways putatively altered in clones.

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