

**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



**Are gene networks always meaningful?**  
 A. Gamot, N. Villa, L. Liaubet, F. Rossi,  
 G. Tosser-Klopp, P. Cherel, M. SanCristobal


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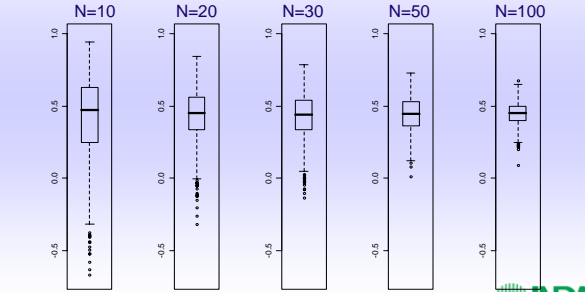
Gene networks are meaningful with a **minimum of 20-30 individuals** and a good method for deciphering large **network structure**

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At least 20-30 observations are required to estimate "accurately" a (partial) correlation




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- This explains why no coherent result was obtained by Jaffrézic & Tosser-Klopp (2009) during the last Eadgene "post-analysis" workshop.
- Same thing with a Sabre data set (transcriptome of folliculogenesis in pig and cattle), with N=7

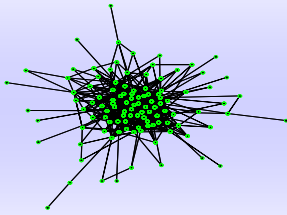
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Construction of a network for a data set with 56 individuals

graph: liste 128, corrélations partielles



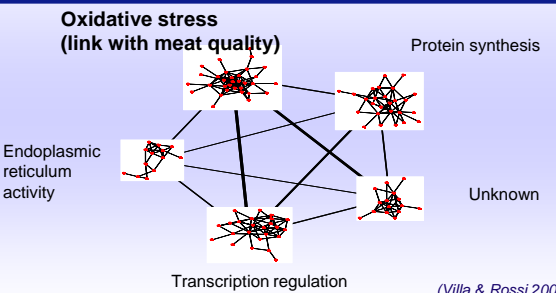
Top 128 genes with an eQTL (Liaubet *et al.*, unpublished data), network built on partial correlation, cut-off s.t. density 5%-10%  
 (Schaefer & Strimmer 2005)

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A clustering of the large network lead to 5 sub-networks related to biological functions




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## Are gene networks always meaningful?

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INRA



If you want a good gene network ....

- ... have **enough individuals** (min. 20-30),
- construct your network with an appropriate method (e.g. partial correlation ),
- decipher the **structure** of your large network with a good clustering method



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