Session: 45
Abstract number: 3948
Main author: Cristina Arce
e-mail: ge1arjic@uco.es

Global transcriptional response of porcine intestinal epithelial cell lines to Salmonella enterica serovar Typhimurium and Choleraesuis

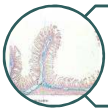
C. Arce, A. Jiménez-Marín, M. Collado-Romero, C. Lucena, J.J. Garrido
Animal Breeding and Genomics Group. Dpt. Genetics.
University of Córdoba. Spain

Background

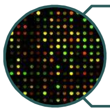
ST and SC two of the most frequent *Salmonella* serotypes isolated in European pigs

ST: Enterocolitis in different species

SC: Sistemic disease in pig



Intestinal region at which *Salmonella* enters topic of controversy



Microarray revolutionize research in the management of diseases, increasing the understanding of host-pathogen interaction

Objectives

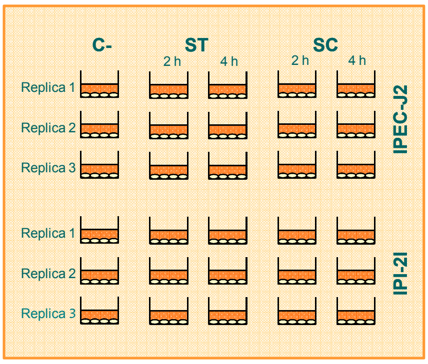
Microarray *in vitro* assay

ILEUM ≠ JEJUNUM

ST ≠ SC

?

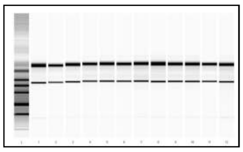
Methods



Experiment Design

RNA Extraction (RNeasy-Qiagen)

RNA Quality (Experion-BioRad)



RNA: RIN 9.8-10

Genoma España

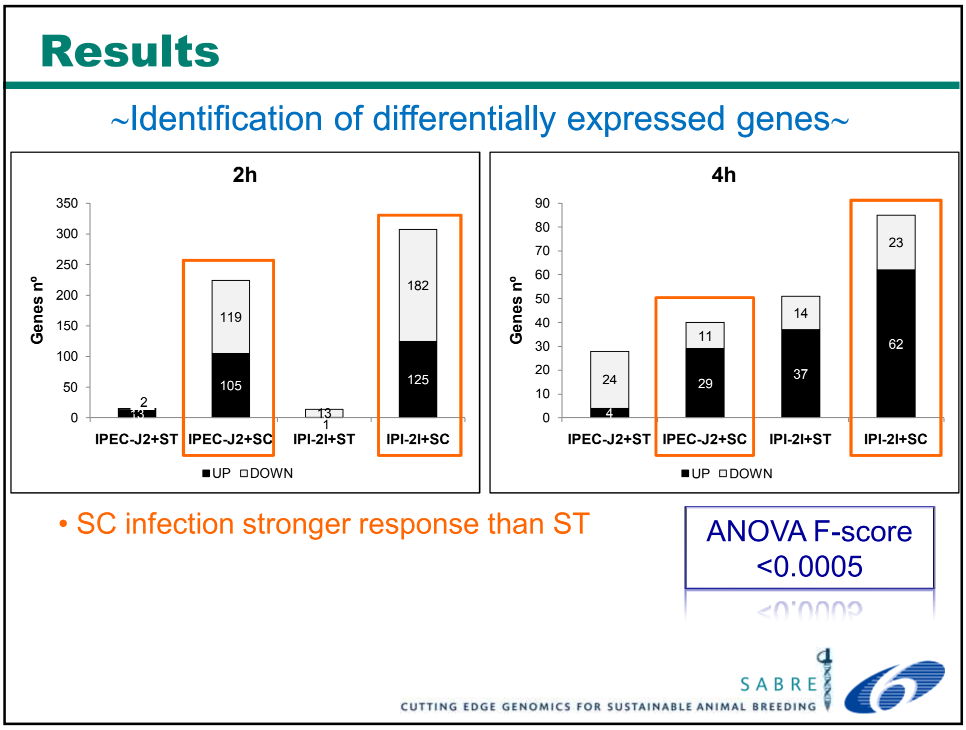
Affymetrix Porcine Genechip Array

scbi uma PLATAFORMA ANDALUZA DE BIOINFORMÁTICA

Results Analysis

INGENUITY PATHWAYS ANALYSIS
For life sciences researchers

Biologic Interpretation

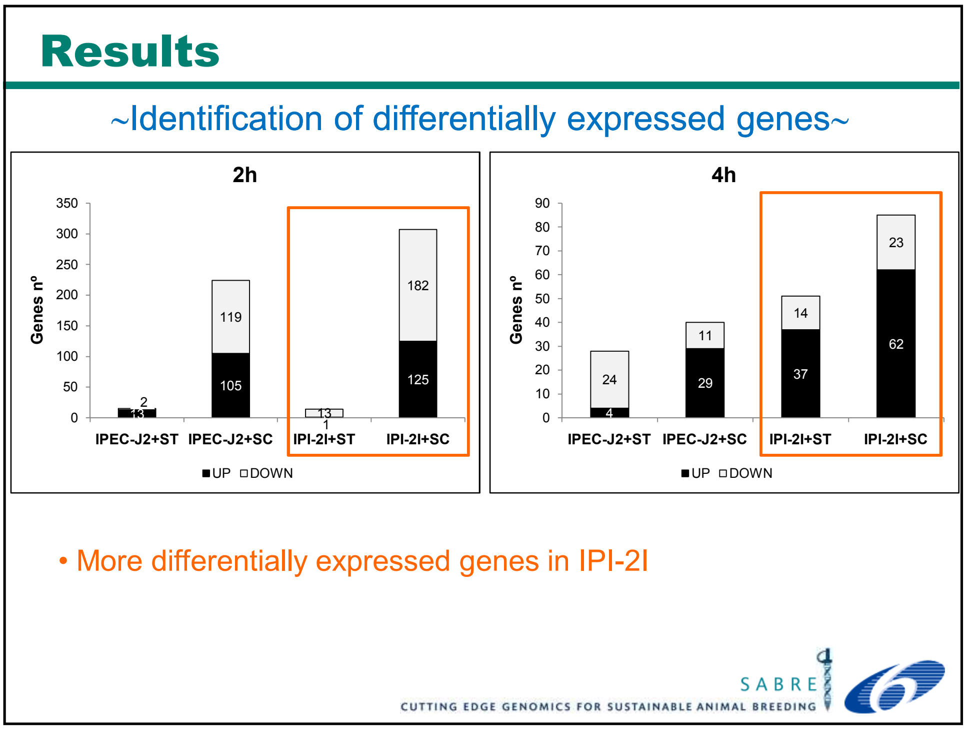


Results

~Identification of differentially expressed genes~

- SC infection stronger response than ST

ANOVA F-score
<0.0005



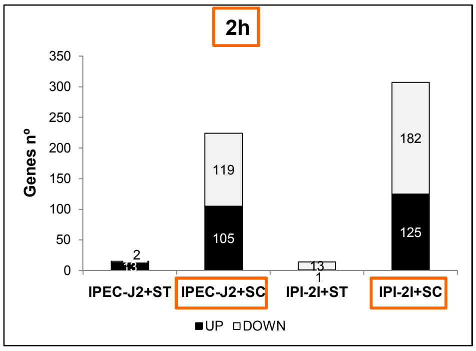
Results

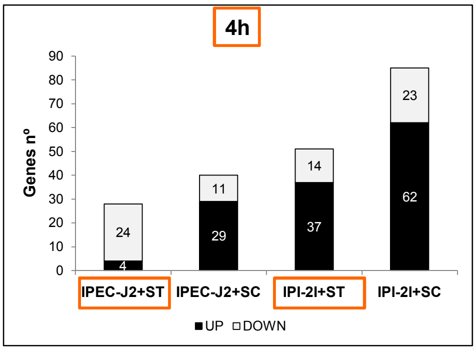
~Identification of differentially expressed genes~

- More differentially expressed genes in IPI-2I

Results

~Identification of differentially expressed genes~



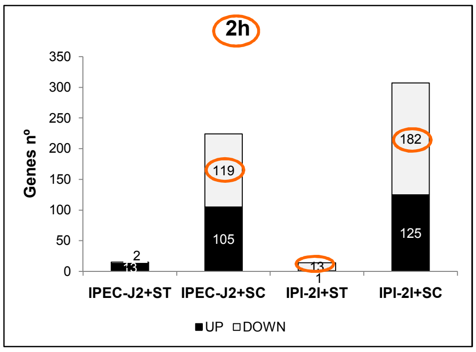


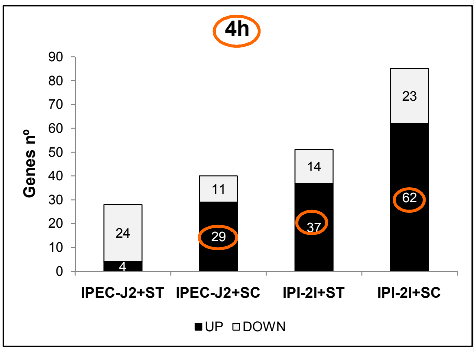
- Response to ST later than to SC

SABRE
CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

Results

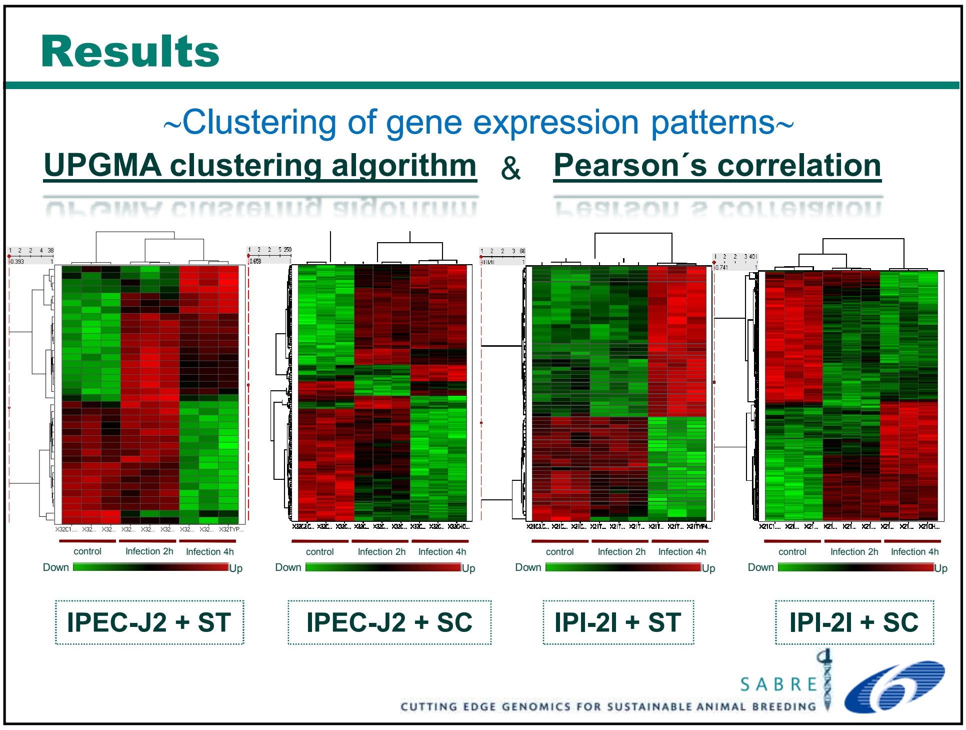
~Identification of differentially expressed genes~





- All except IPEC-J2 + ST, more genes up at 4h and down at 2h

SABRE
CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING



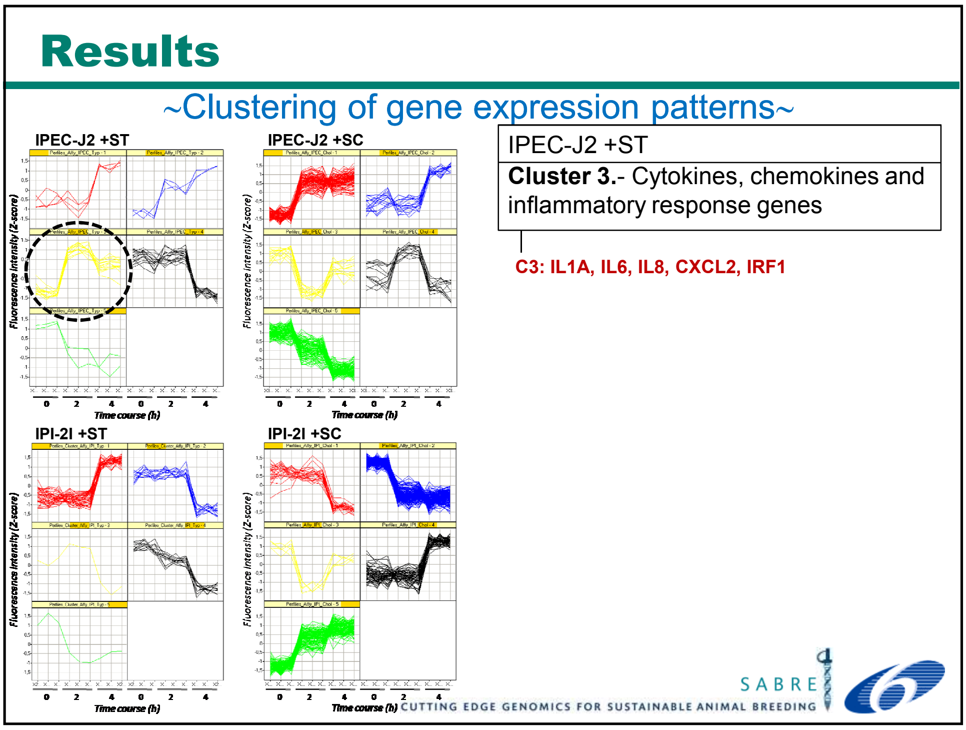
Results

~Clustering of gene expression patterns~

UPGMA clustering algorithm & **Pearson´s correlation**

IPEC-J2 + ST **IPEC-J2 + SC** **IPI-2I + ST** **IPI-2I + SC**

SABRE
CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING



Results

~Clustering of gene expression patterns~

IPEC-J2 +ST

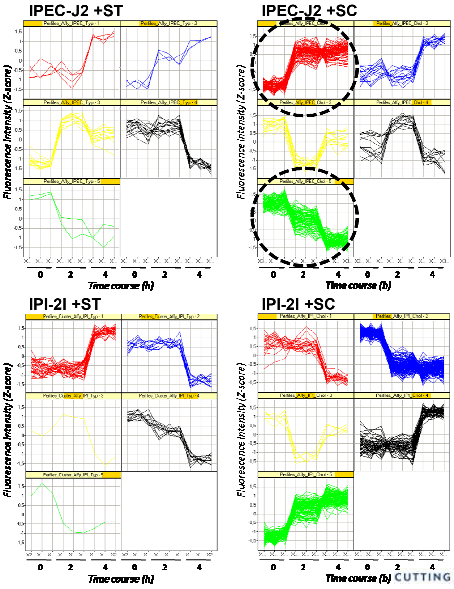
Cluster 3.- Cytokines, chemokines and inflammatory response genes

C3: IL1A, IL6, IL8, CXCL2, IRF1

SABRE
CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

Results

~Clustering of gene expression patterns~



IPEC-J2 +SC

Maximal response at 2h

Cluster 1.- Endocytosis, motility and inflammatory response genes

Cluster 5.- Kinases, endocytosis, apoptosis and inflammatory response genes

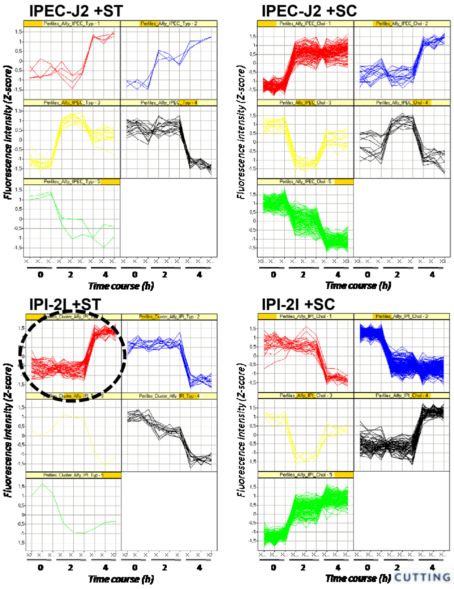
C1: AP2M1, RHOG, IL8, TLR9, IRF1

C5: MAPK9, AAK1, PDIAE, ACVR1

SABRE CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

Results

~Clustering of gene expression patterns~



IPI-2I +ST

Maximal response at 4h

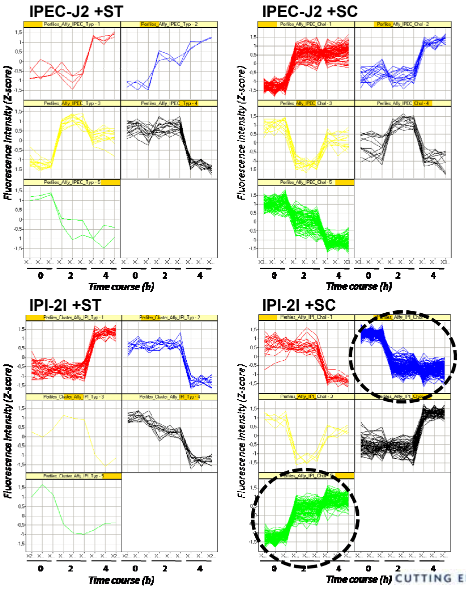
Cluster 1.- Endocytosis, angiogenesis and MΦ differentiation genes

C1: VEGFA, LIPG, CSF1

SABRE CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

Results

~Clustering of gene expression patterns~



C2: MAPK1, MAPK9, ACT3, ARF1

C5: RHOG1, LBP, VEGFB

IPI-2I +SC

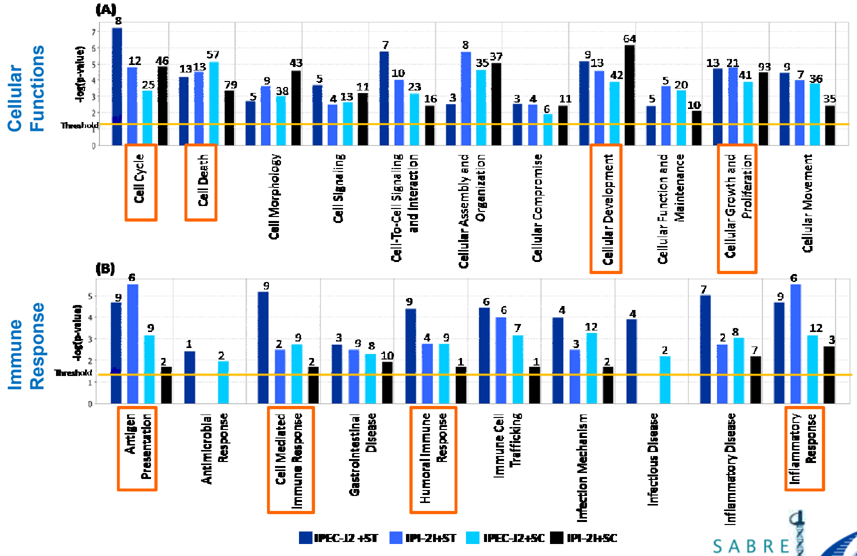
Several genes at 2 and 4h

Cluster 2.- Kinases, cytoeskeleton and vesicle transport genes

Cluster 5.- Motility, cytoeskeleton, and endocytosis genes

Results

~Functional analyses of the cellular gene expression profiles~



Results

~Functional analyses of the cellular gene expression profiles~

	TOP CANONICAL PATHWAYS	p-Value	
IPEC-J2 + ST	NF-κb Signaling	5.19E-06	⇦
	IL-6 Signaling	2.29E-05	
	Role of PKR in Interferon Induction and Antiviral Response	6.12E-05	
IPEC-J2 + SC	Clathrin –mediated Endocytosis	1.73E-05	
	Regulation of Actin-based Motility by Rho	4.63E-05	⇦
	CXCR4 Signaling	6.14E-04	
	NF-κb Signaling	1.66E-03	⇦
IPI-2I + ST	Phospholipid Degradation	2.19E-03	
	Glycerophospholipid Metabolism	8.35E-03	
	Inositol Phosphate Metabolism	1.06E-02	
IPI-2I + SC	Regulation of Actin-based Motility by Rho	3.83E-03	⇦
	IL-8 Signalling	1.6E-02	
	Purine Metabolism	2.15E-02	
	4-1BB Signaling in T Lymphocytes	2.38E-02	
	Integrin Signaling	2.61E-02	

Conclusions

- This *in vitro* microarray assay is the first one comparing the expression pattern in two porcine intestinal cell lines after two *Salmonella* serotypes infection
- Porcine epithelial cell lines from different gut regions useful tool in porcine immune response to *Salmonella* studies
- Differences in response between cell lines were found
- Differences in response to ST and SC were found:
  - ST causes a stronger immune response than SC
  - More differentially expressed genes in SC infected cells
  - SC elicited an earlier response than ST

Conclusions

- Gene clusters help to annotate unknown genes with coexpression data to known genes, and characterize gene network regulatory mechanism involved in infection response
- Functional analysis allowed to determine that:
  - ST and SC infection alter multiple biological processes and cellular functions in intestinal epithelial cell lines
  - Immune response pathways are modulated in IPEC-J2 cell line during ST and SC infection
  - Angiogenesis, antiapoptosis and cell migration are modulated in IPI-2I cells during ST and SC infection
  - SC infection modifies the expression of genes involved in transcription factor activity, protein kinase, apoptosis and actin-based motility by Rho pathways

---

Acknowledgements

- Animal Breeding and Genomics Group (UCO):

  J.J. Garrido, A. Moreno, D. Llanes, L. Morera, M. Barbancho, C. Lucena, A. Jiménez-Marín, M. Collado-Romero, G. Sanz, G. García, R. Martins, N. Serrano, C. Aguilar, R. Álvarez, E. Ruiz

- Plataforma Andaluza de Bioinformática (SCBI-UMA):

  M. G. Claros, R. Bautista

- These results are part of the SABRE research project that has been co-financed by the European Commission, within the 6th Framework Programme, contract No. FOOD-CT-2006-016250.

Animal Breeding & Genomics Group

UNIVERSIDAD DE CORDOBA

PLATAFORMA ANDALUZA DE BIOINFORMÁTICA