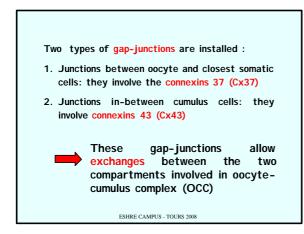
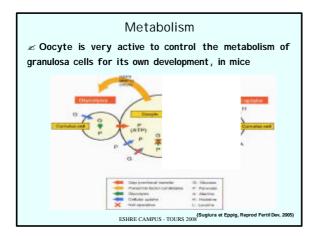


Two major events take place during follicular development :

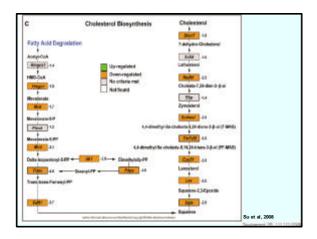
- 1. Oocyte acquisition of meiotic competence as well as une developmental competence ? Oocyte quality
- 2. Granulosa cell proliferation and differentiation with specific differentiation of cumulus cells ? specific gene expression

Oocyte-cumulus dialog







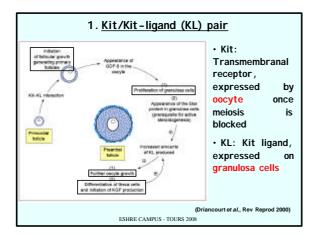




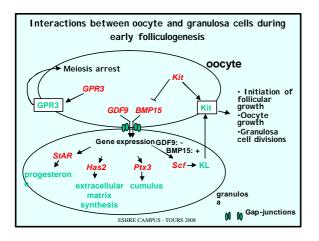


#### ≪Kit-KL pair

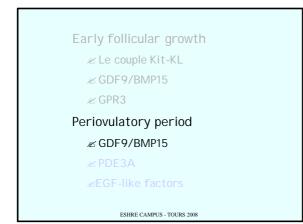
- ≤ GDF9/BMP15
- ⊯ GPR3
- Periovulatory period
  - ≤ GDF9/BMP15
  - ≈PDE3A
  - ⊯EGF-like factors

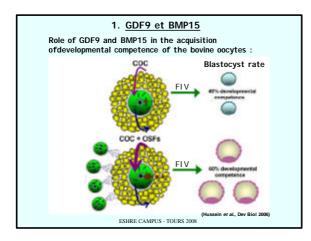




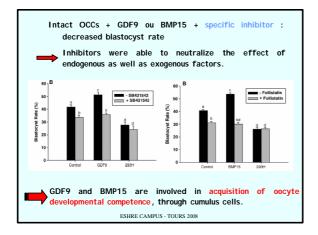




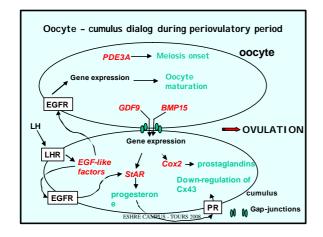














# .

Preliminary statement

Various factors inside OCC are involved in the regulation of follicular growth and differentiation  $% \left( {\left[ {{{\rm{T}}_{\rm{T}}} \right]_{\rm{T}}} \right)$ 

- 2 consequences for human purpose (as well as domestic mammals):
  - 1. IVM of OCCs (adding various factors to culture medium)
  - 2. Indirect assessment of oocyte quality (studying the expression level of cumulus specific genes as a function of oocyte follow up once fertilized)

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#### Why working on human cumulus cells ?

- Major role of the cumulus on oocyte maturation
- Cumulus cells easily accessible during IntraCytoplasmic Sperm Injection (ICSI) procedure

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• Human oocytes uneasy to use for research purpose



# Aim of this study

- To evaluate the expression of specific genes in human cumulus cells according to oocyte maturity
- Objectives :
  - To relate these expression patterns with developmental competence of the oocyte
  - To select embryos with high implantation potential

## Material and Methods

- Human cumulus cells individually retrieved shortly before ICSI
- Cumulus stored at -80°C with lysis buffer of the extraction kit of total RNA (Stratagene or Qiagen)
- Individual follow up of oocyte and embryo quality assessment



#### 2 parts

- Study of expression of target genes by real time Polymerase Chain Reaction (PCR)
- Study of cumulus cells transcriptome according to oocyte maturity

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# 1. Study of specific genes expression by real time PCR

- Total RNA extraction [Absolutely RNA Nanoprep<sup>®</sup> kit (Stratagene)]
- Reverse Transcrition of all RNA [iScript firststrand cDNA Synthesis kit (Bio-Rad Laboratories)]
- Quantitative PCR amplification [iQ<sup>™</sup> SYBR<sup>®</sup> Green Supermix kit (Bio-Rad Laboratories)]
- Results normalized to an endogeneous reference gene

# Target genes

- Steroidogenic Acute Regulatory protein (STAR) :
  - Progesterone synthesis (Cholesterol transport)
- Cyclooxygenase 2 (PTGS2 or COX2) :
  - Prostaglandin (PGE<sub>2</sub>) synthesis
  - Cumulus expansion
  - Ovulation

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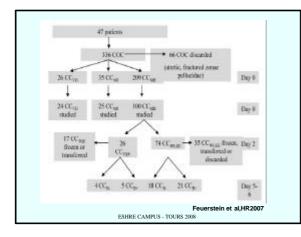
Amphiregulin (AREG) :

 Cumulus expansion
 Oocyte nuclear maturation (GVBD)

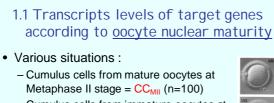
 Stearoyl-CoenzymeA Desaturase 1 and 5 (SCD1 and SCD5) : – Monounsaturated fatty acids synthesis

Endogeneous reference gene :

• Ribosomal Protein L19 (RPL19)





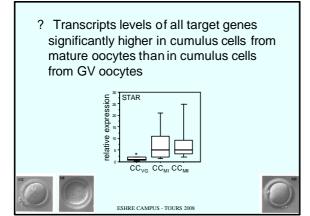


 Cumulus cells from immature oocytes at Germinal Vesicle stage = CC<sub>GV</sub> (n=24)
 Cumulus cells from immature oocytes

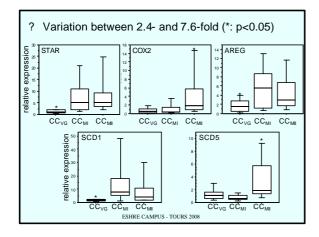


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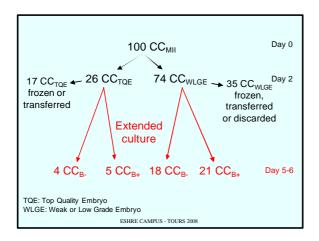
without GV or  $1^{st}$  polar body, arbitrarily called Metaphase I =  $CC_{MI}$  (n=25)









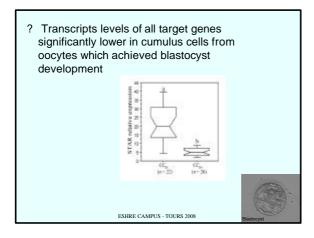




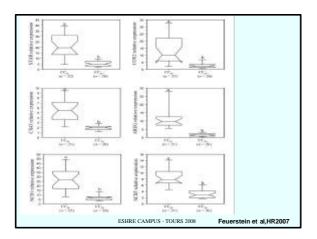
expression, using	CON2, CN43, AREG, SCD1, SCE real-time RT–PCR with RPL19 as idual homan cumulus cells as a fu g fertilization.	an endogeneous
Target gene	CC <sub>WLOE</sub> (n = 71-74)	$CC_{TQE}$ ( $n = 36$ )
STAR	9.2 + 1.3	$8.8 \pm 1.7$
COX2	$4.6 \pm 0.9$	$6.9 \pm 1.9$
CX43	$2.8 \pm 0.2$	$3.2 \pm 0.5$
AREG	$4.8 \pm 0.6$	$7.1 \pm 2.2$
SCD1	$9.5 \pm 1.5$	$10.5 \pm 2.9$
SCD5	$3.6 \pm 0.4$	$4.0 \pm 0.9$
AREG SCD1 SCD5 Values are presen OCwatche, Cumuli	$4.8 \pm 0.6$ $9.5 \pm 1.5$	7.1 ± 22 10.5 ± 29 4.0 ± 0.9
at Day 2.		euerstein et al,HR20



- 1.2 Transcripts levels of target genes according to <u>developmental ability of</u> <u>the fertilized oocytes</u> at day 5-6
- Two situations :
  - Cumulus cells enclosing oocytes which stopped their development at embryo stage =  $CC_{B}$ . (n=22)
  - Cumulus cells enclosing oocytes which achieved blastocyst development = CC<sub>B+</sub> (n=26)









# Conclusion part1

- Increased expression of all target genes in cumulus cells after resumption of meiosis of the oocyte
- Decreased expression in cumulus enclosing fertilized MII oocytes with a high developmental potential (expression and use of these transcripts)

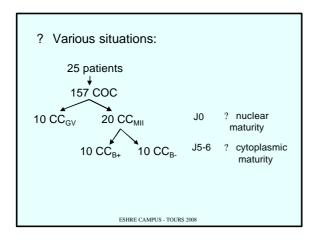
#### Conclusion part 1

? Expression of all investigated genes (STAR, COX2, AREG, SCD1 and SCD5) in cumulus cells in a precise chronological pattern to sustain or reflect further embryo development

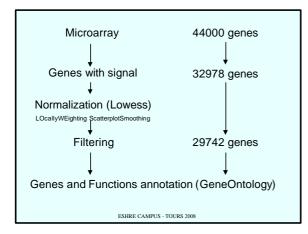
# Part 2. Study of cumulus cells transcriptome

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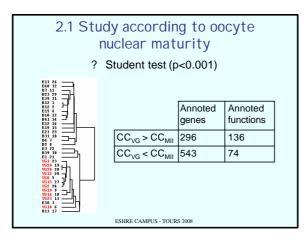
- Total RNA extraction [RNeasy® micro kit (Qiagen)]
- Reverse transcription, Amplification and labelling of all RNA [Low RNA Input Linear Amplification Kit, PLUS,Two-Color (Agilent)]
- Hybridization of cDNA onto microarray [4x44K microarrays (Agilent)]
- -Scanning and Feature extraction



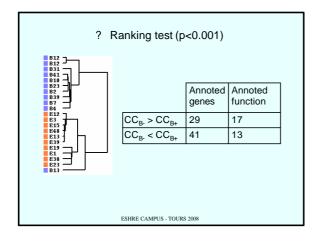














Function	р
antigen_processing	0
antigen_presentation,_exogenous_antigen	0,0003
antigen_processing,_exogenous_antigen_via_MHC_class_II	0,0003
MHC_class_II_receptor_activity	0,0003
response_to_stimulus	0,0007
visual_perception	0,0018
sensory_perception_of_light_stimulus	0,0018
organismal_physiological_process	0,0018
antigen_presentation	0,0024
development	0,0129
skeletal_development	0,016
structural_molecule_activity	0,0175
immune_response	0,0182
sensory_perception	0,0185
defense_response	0,0233
response_to_biotic_stimulus	0,0283
organ_development	0,0462



## 2. Up-regulated functions in $CC_{B+}$

Function	р
basement_membrane	0,0035
nucleic_acid_binding	0,0212
regulation_of_transcription,_DNA-dependent	0,0226
transcription,_DNA-dependent	0,0266
GTPase_activity	0,0292
regulation_of_transcription	0,0305
regulation_of_nucleobase,_nucleoside,_nucleotide_and_nucleic_acid_metabolism	0,0335
transcription	0,0379
regulation_of_cellular_physiological_process	0,0413
regulation_of_cellular_metabolism	0,0458
nucleobase,_nucleoside,_nucleotide_and_nucleic_acid_metabolism	0,0459
regulation_of_physiological_process	0,0494
nucleoside -triphosphatase_activity	0,0499

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# Perspectives

- Validation by quantitative PCR of the expression pattern of identified genes (ongoing)
- Clinical application : use of cumulus biomarkers to better define and discriminate competent oocyte...to influence transfer strategy
- Analysis of mechanisms involved for these target genes to modulate oocyte competence

	edgments CHRU		
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Plateforme Génopole-Ouest, Nantes			
R Houlgatte	Carlos Participantes		
R Teusan	and the first of the second		
	IPUS - TOURS 2008 PHARMACEUTICALS		