

# Inhaled carbon nanotube-induced gene expression profile in rat lung

**Carole Seidel**

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# Carbon nanotubes

## Unique physical properties

- Mechanical
- Electrical

## Large variety of CNTs

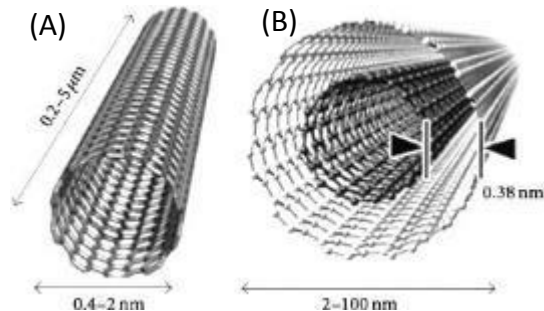
- Number of “walls”
- Length, diameter
- Functionalization

## Industrial and medical applications

- Nanoelectronics
- Composite materials
- Sport goods
- Hydrogen storage
- Drug carriers

## Toxicological properties

- Pulmonary inflammation
- Granuloma, pulmonary fibrosis
- Mesothelioma
- Lung cancer



# Objectives

- **Study of carbon nanotube toxicity**
  - **Sub-acute nose-only inhalation study in rats**
  - **Conventional approach**
  - **Molecular approach (High content screening method: transcriptomics)**
  - **NM-401**
  - **NM-403**

# Experimental protocol



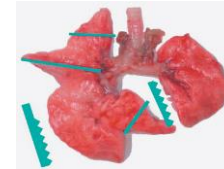
Female Sprague  
Dawley Rats

**Nose-only inhalation  
exposure**



**(2x3h) / day,  
5 days / week,  
4 weeks**

Control  
+ 2 concentrations (0.5 and 1.5 mg/m<sup>3</sup>)



**Tissue sampling**



**3**



**30**

**Short term**



**90**

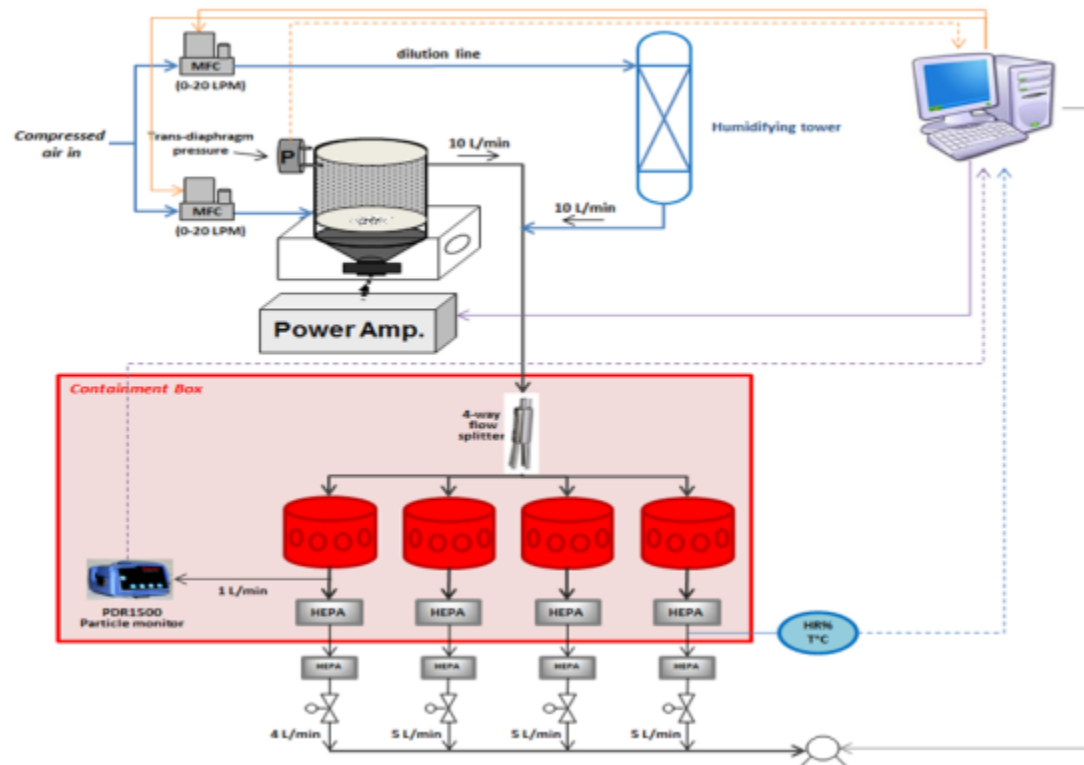


**180**

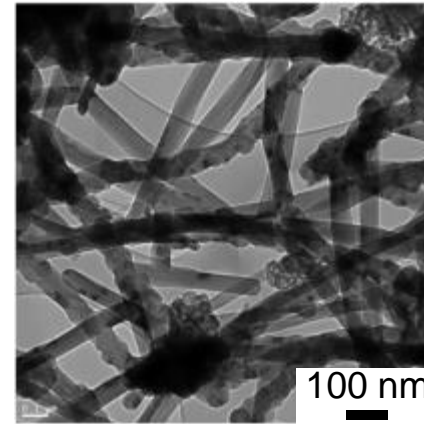
**Long term**

**Post exposure time (days)**

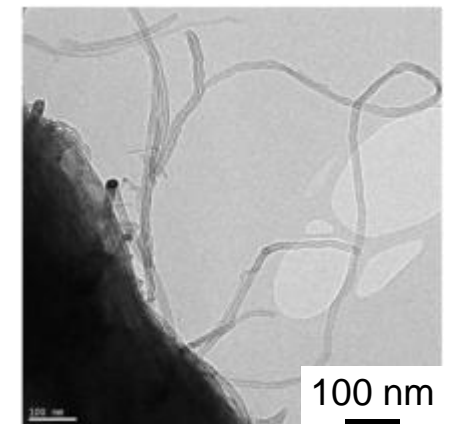
# Aerosol generation



NM-401



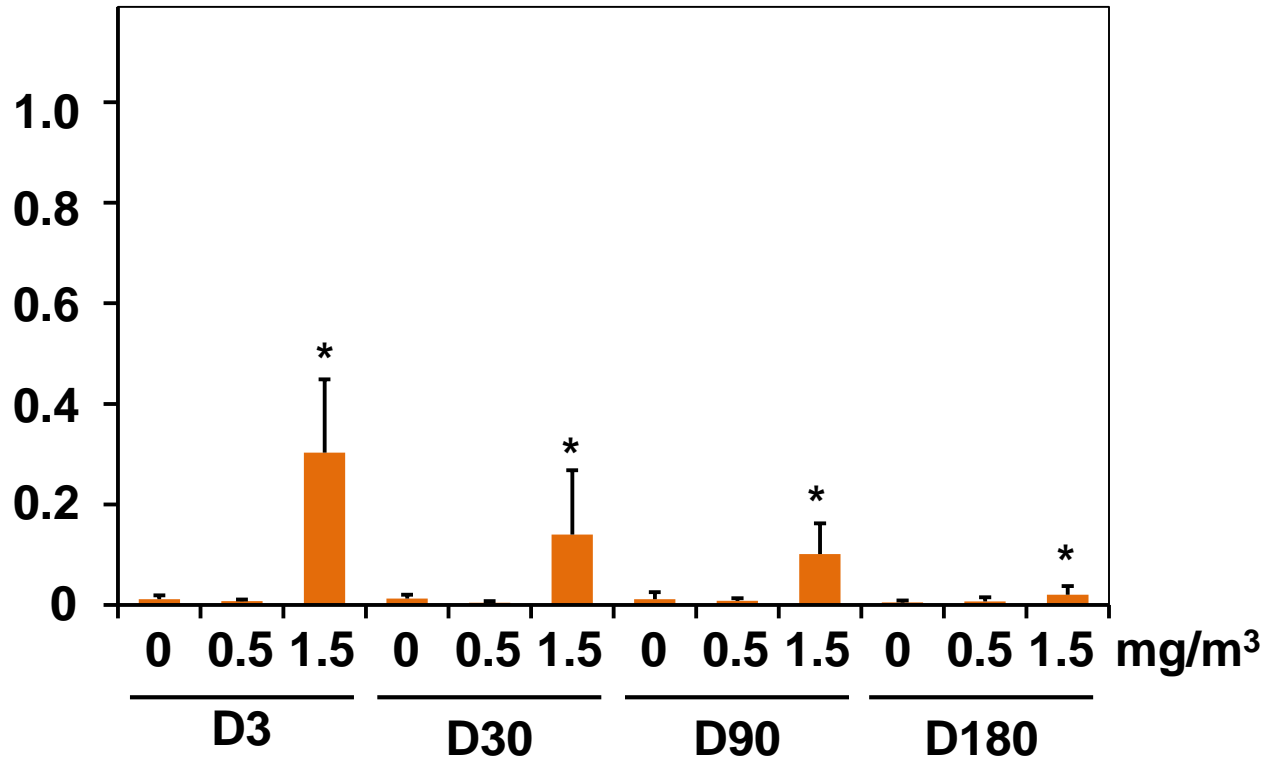
NM-403



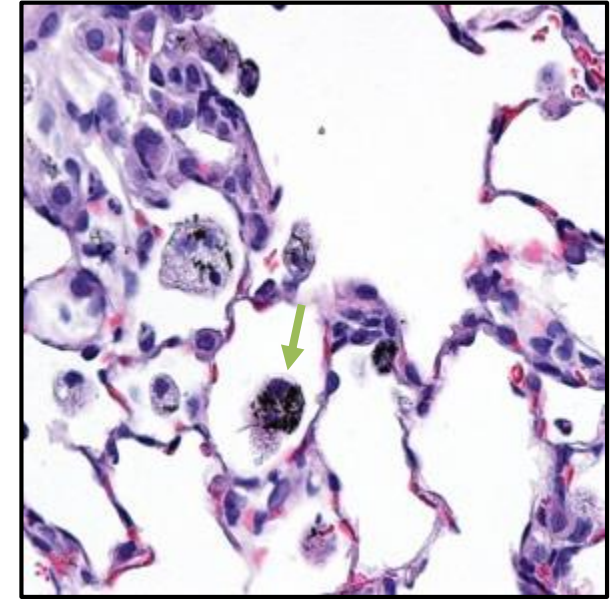
	Target concentration (mg/m <sup>3</sup> )	Concentration (mg/m <sup>3</sup> )	Concentration (particles/cm <sup>3</sup> )	MMAD (nm)	NMAD (nm)
NM-401	0.5	0.54 ± 0.11	~815	790	280
	1.5	1.59 ± 0.24	~2200		
NM-403	0.5	0.50 ± 0.14	~130	1940	1440
	1.5	1.48 ± 0.63	~540		

# Broncho-alveolar lavage fluids cytology – NM-401

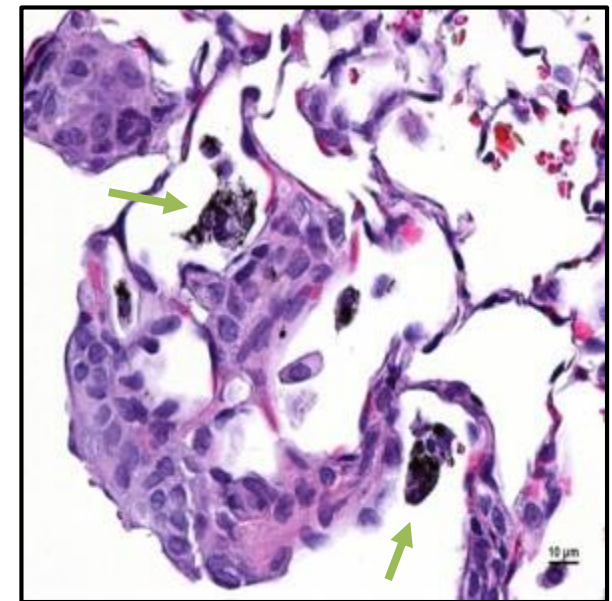
Neutrophilic granulocytes  
(x10<sup>6</sup> / left lobe)



1.5 mg/m<sup>3</sup>



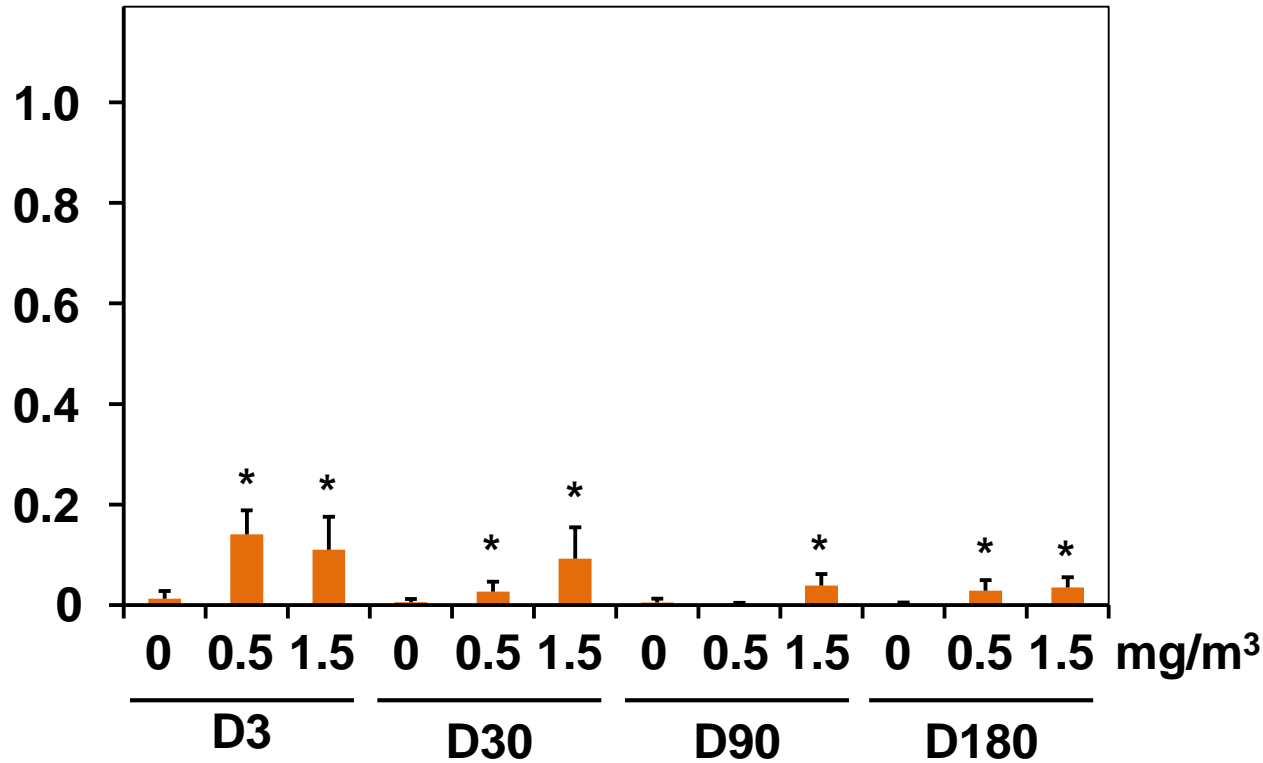
Day 3



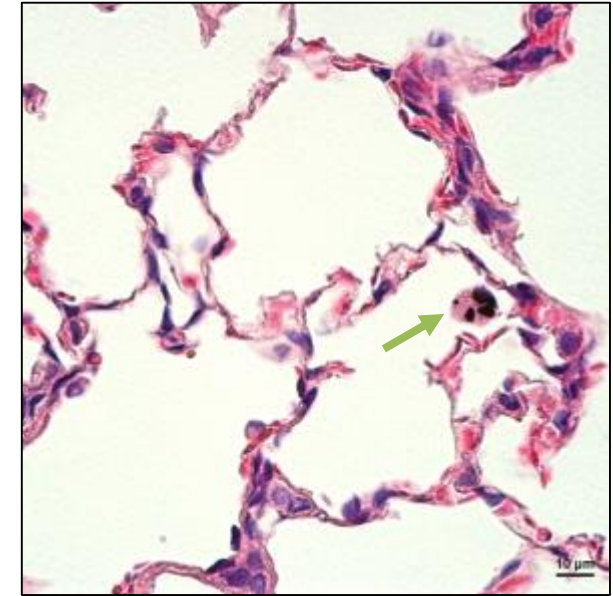
Day 180

# Broncho-alveolar lavage fluids cytology – NM-403

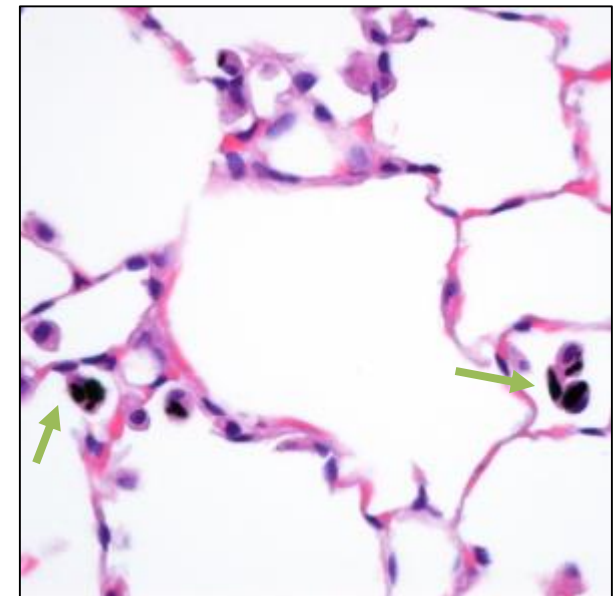
Neutrophilic granulocytes  
( $\times 10^6$  / left lobe)



1.5 mg/m<sup>3</sup>



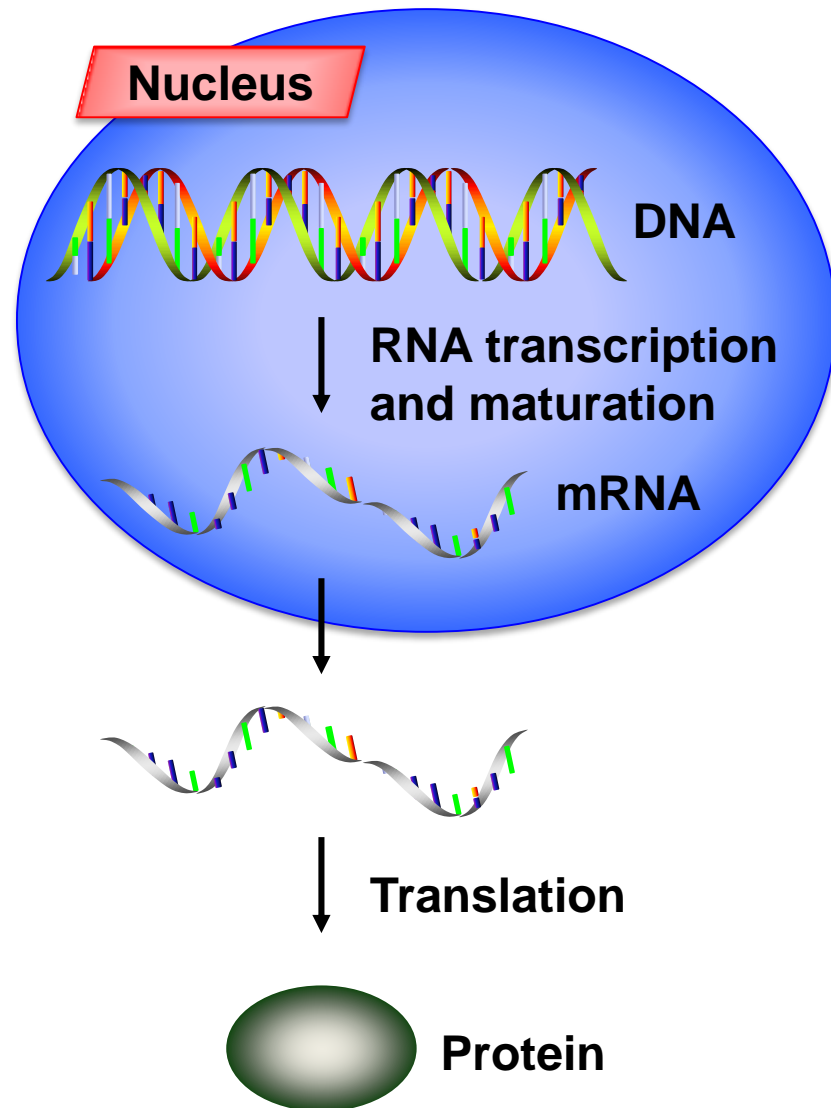
Day 3



Day 180

Conventional approach

# Transcriptomic analysis (Agilent microarray)



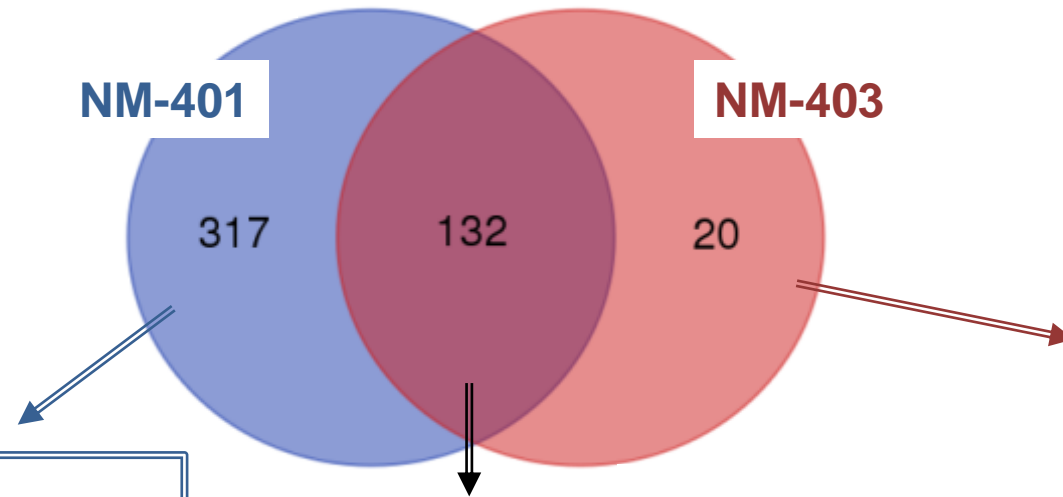
Molecular approach

**Transcriptomics =**  
study of the complete set of RNA transcripts  
produced by the genome  
⇒ identification of gene differentially  
expressed in response to treatment

**Microarray: Agilent technology**  
**Data analysis: GeneSpring software**  
**Gene clustering: DAVID database**



# Gene expression profile : NM-401 versus NM-403 (day 3)



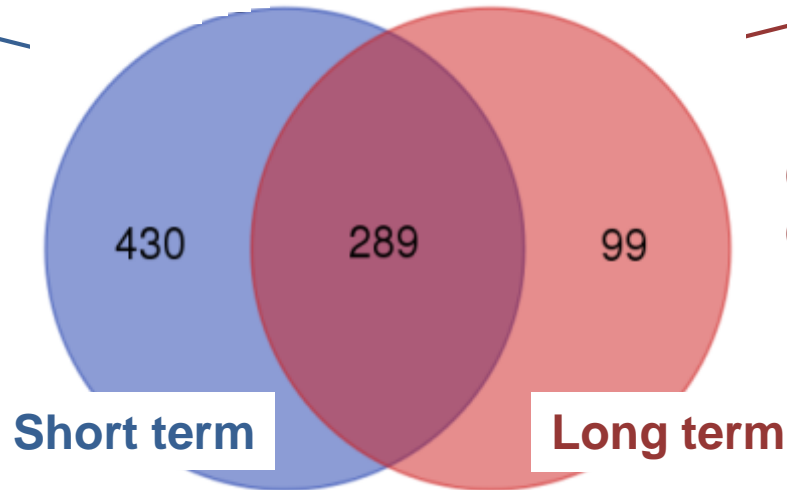
Not enough genes for clustering

Protein folding  
Response to ER stress  
Positive regulation of cytokinesis  
Cell division  
Protein phosphorylation  
Negative regulation of glucocorticoid receptor signalling pathway  
Innate immune response  
Positive regulation of GTPase activity

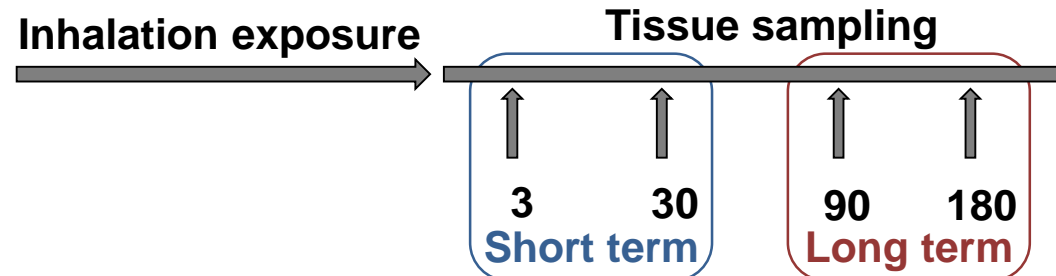
Neutrophil chemotaxis  
Inflammatory response  
Chemokine-mediated signaling pathway  
Monocyte – lymphocyte chemotaxis  
Cellular response to interleukin-1  
Cellular response to interferon- $\gamma$   
Cellular response to TNF  
...

# Short term *versus* long term effects – NM-401

Vasodilation  
Protein folding  
Negative regulation of blood coagulation  
Negative regulation of proteolysis  
Negative regulation of endopeptidase activity  
Regulation of ion transmembrane transport  
Potassium ion transport



Regulation of cell shape  
Chromosome segregation  
Cytoskeleton organization  
Mitotic cytokinesis



Molecular approach

GO BP: Gene Ontology Biological Processes

1.5 mg/m<sup>3</sup>



# Conclusions and perspectives

## NM-401 versus NM-403 day 3

- Both CNTs modulated expression of genes involved in the inflammatory response
- NM-401 : protein folding, cell division, protein phosphorylation...
- NM-403 : some genes not clustered

## NM-401 short versus long term effect

- NM-401 modulated expression of genes involved in the inflammatory response from 3 to 180 days after the end of the exposure period even at the lower dose
- Short term effects : vasodilation, protein folding and ion transport
- Long term effects : cell cycle progression and cytoskeleton organization

## Perspectives

- Comparison of gene expression profile in short and long term effects in NM-403 exposed lung rats
- Further analysis of genes specifically modulated in the long term period

# Acknowledgement



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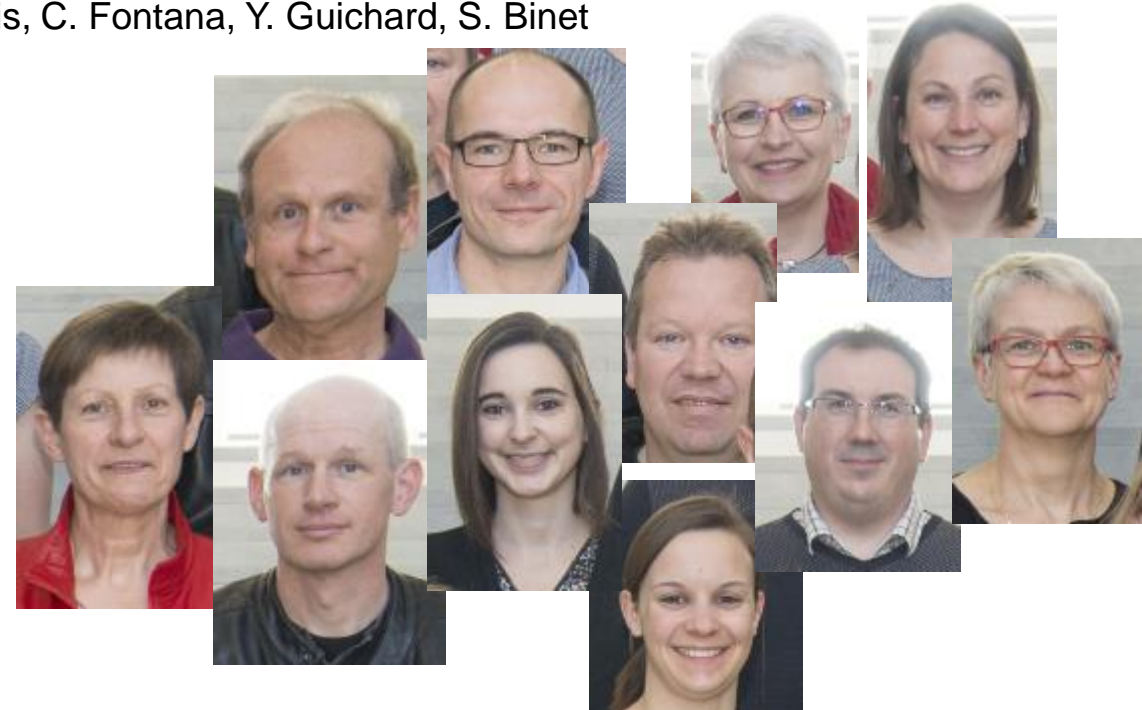
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