

# “Signalling control of stress tolerance and production of stress protective compounds in plants”

**FA0605**

Start date: 21/03/2007

End date: 16/12/2011

Year: 1-2

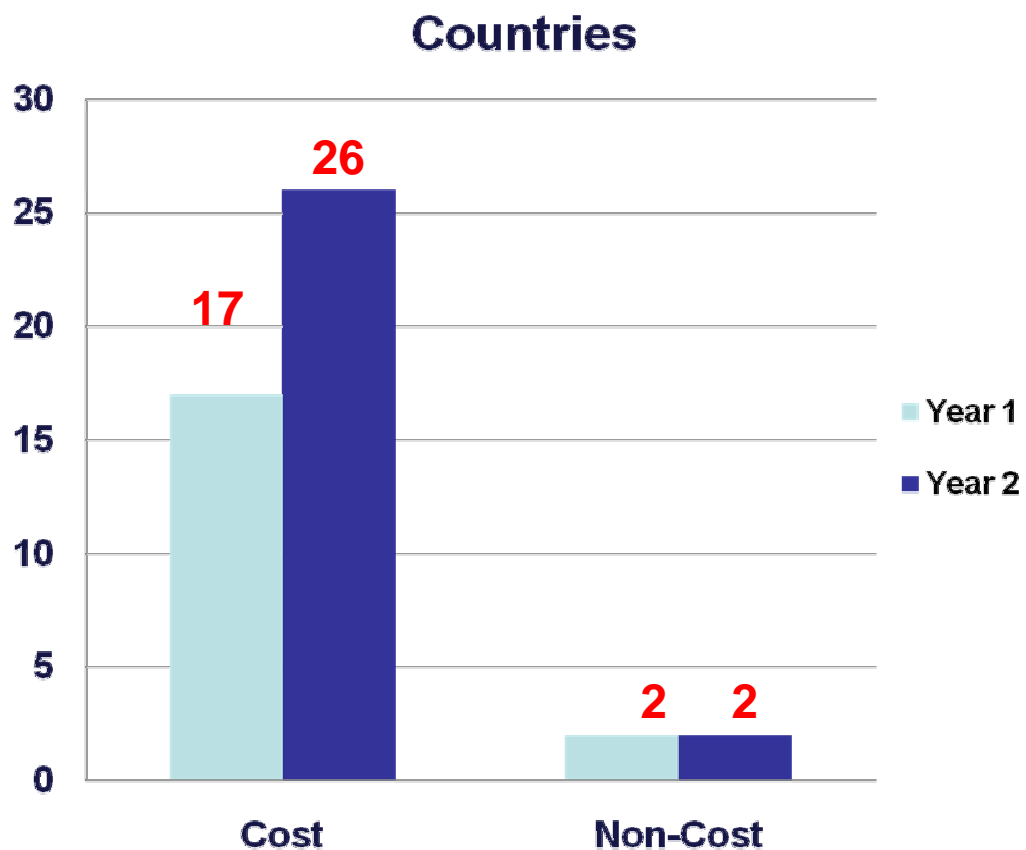
**Antonio Fernández Tiburcio**

Chair

Universitat de Barcelona/ Spain



# Action Parties



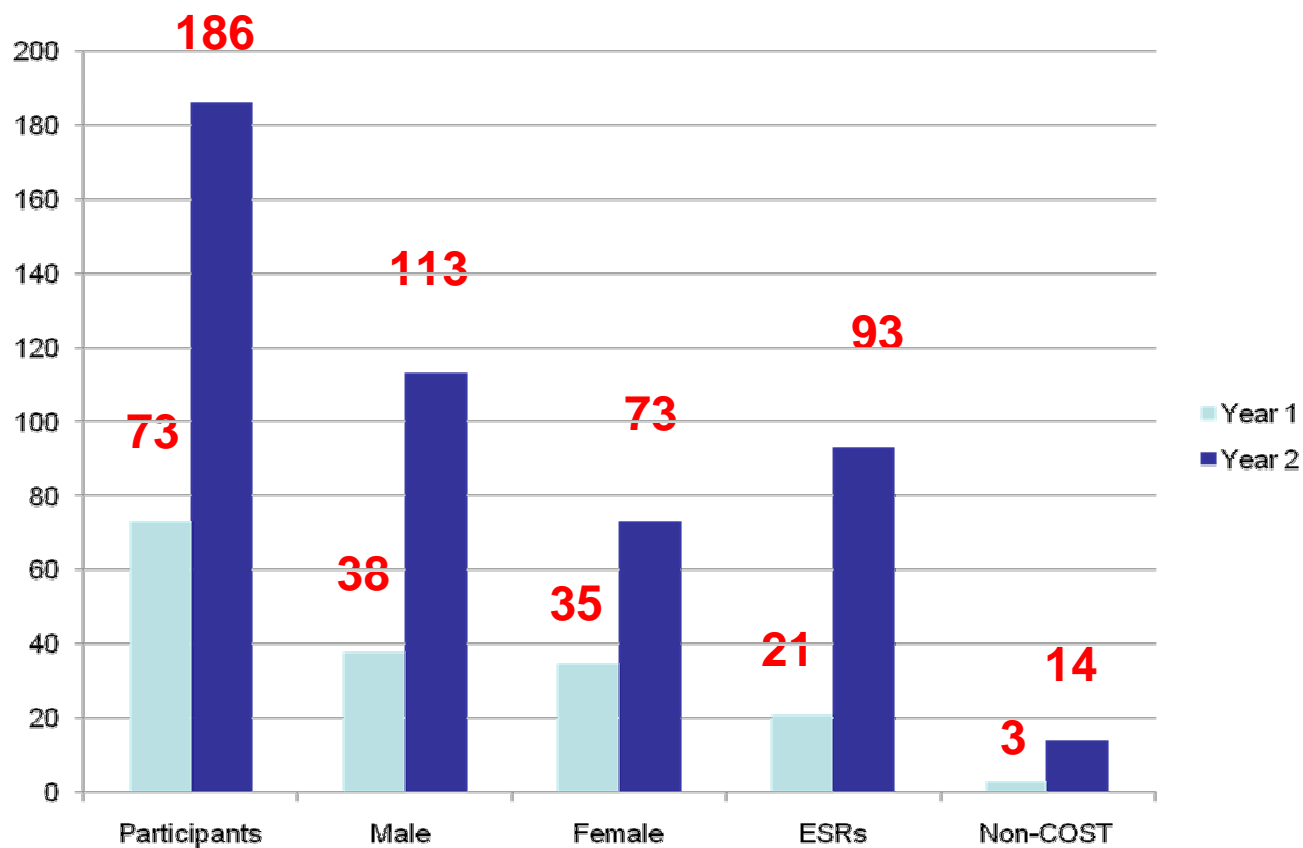
## Grant Holder:

Univ. Barcelona

Antonio F. Tiburcio

Spain

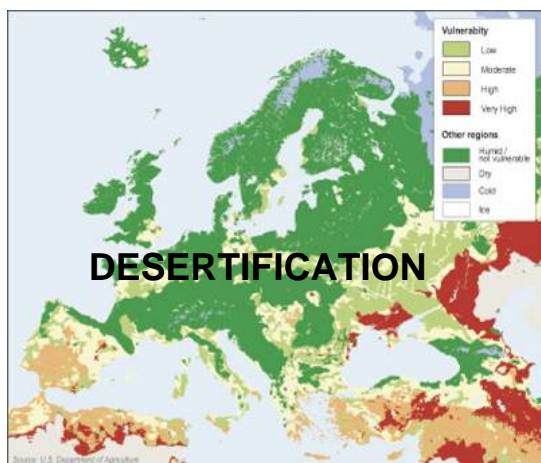
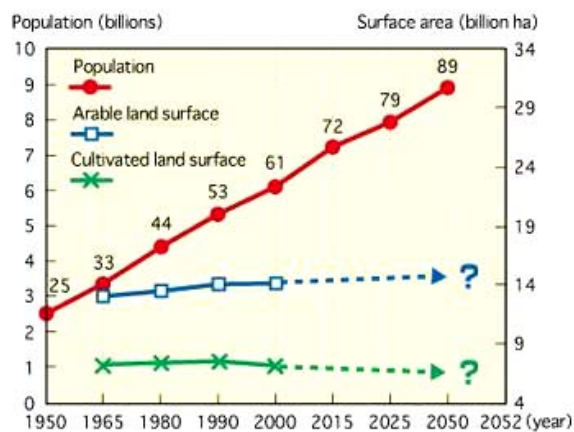
# Action participants



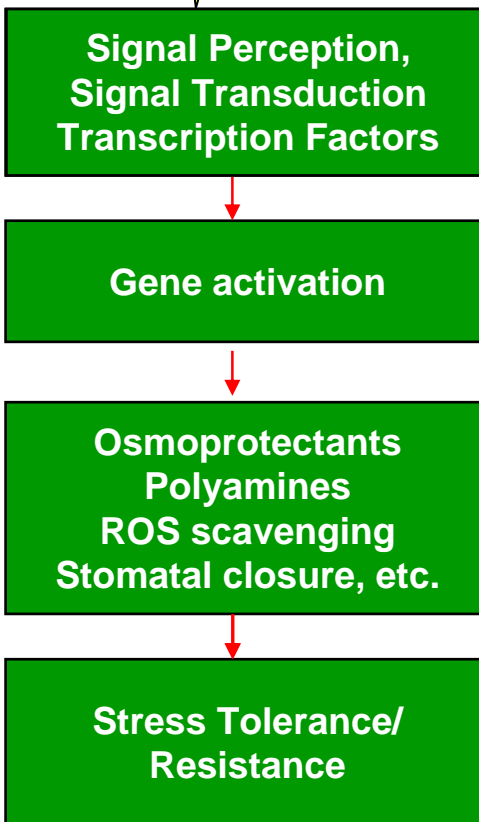
# Use of COST instruments

	YR 1	YR 2
<b>No. of MC / WG meetings</b>	<b>1 MC + 1 SC</b>	<b>1 MC + 2 SC</b>
<b>No. of STSMs</b>	<b>1</b>	<b>6</b>
<b>No. of workshops / conferences</b>	<b>1</b>	<b>1</b>
<b>No. of joint publications</b>	<b>10</b>	<b>16</b>
<b>No. of training schools</b>	<b>0</b>	<b>0</b>
<b>GASG (activities)</b>	<b>Poster, website</b>	<b>Website, FEBS Meeting</b>

# Scientific context and objectives (1/2)



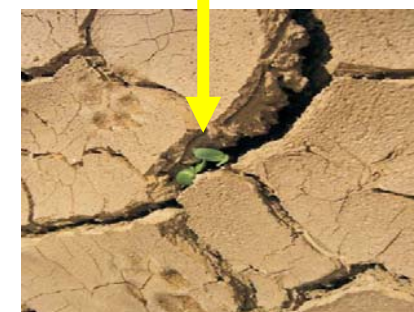
THE INDEPENDENT "The century of drought" (5/10/06)



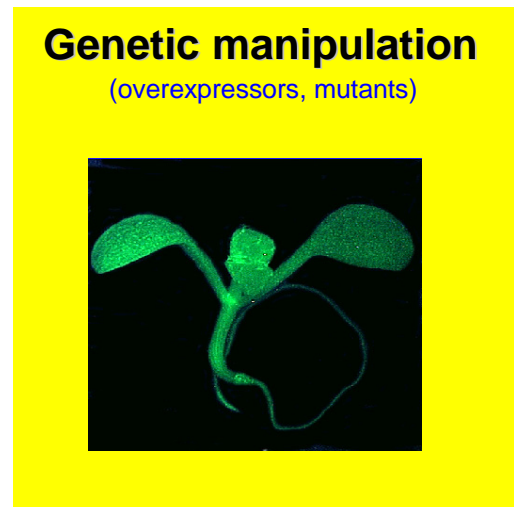
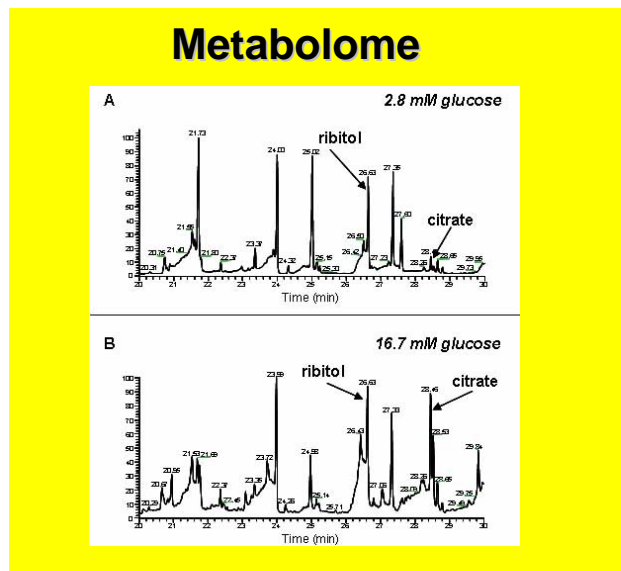
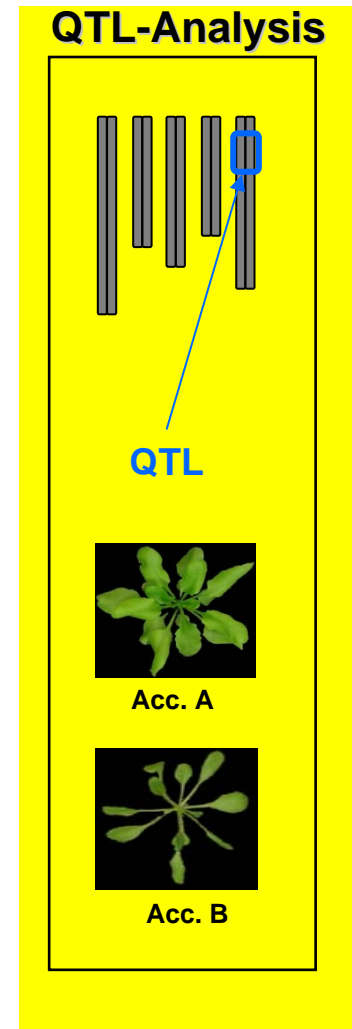
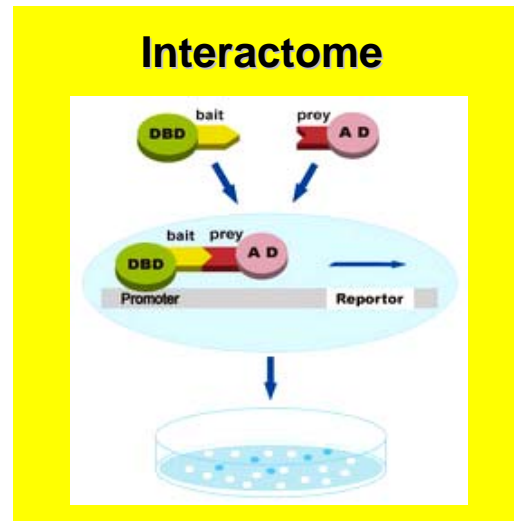
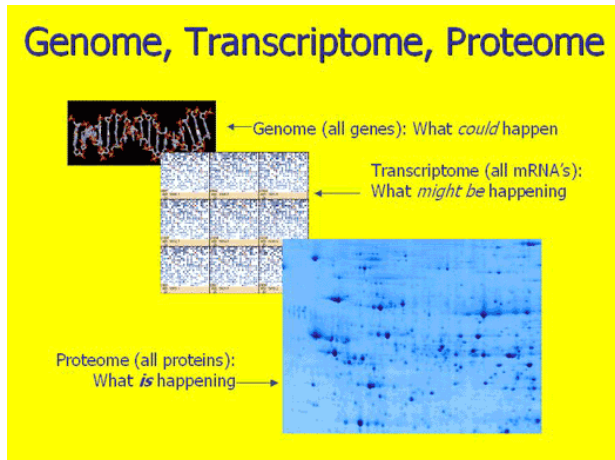
## MAIN OBJECTIVES

Identification of Novel Key Regulatory Stress Factors

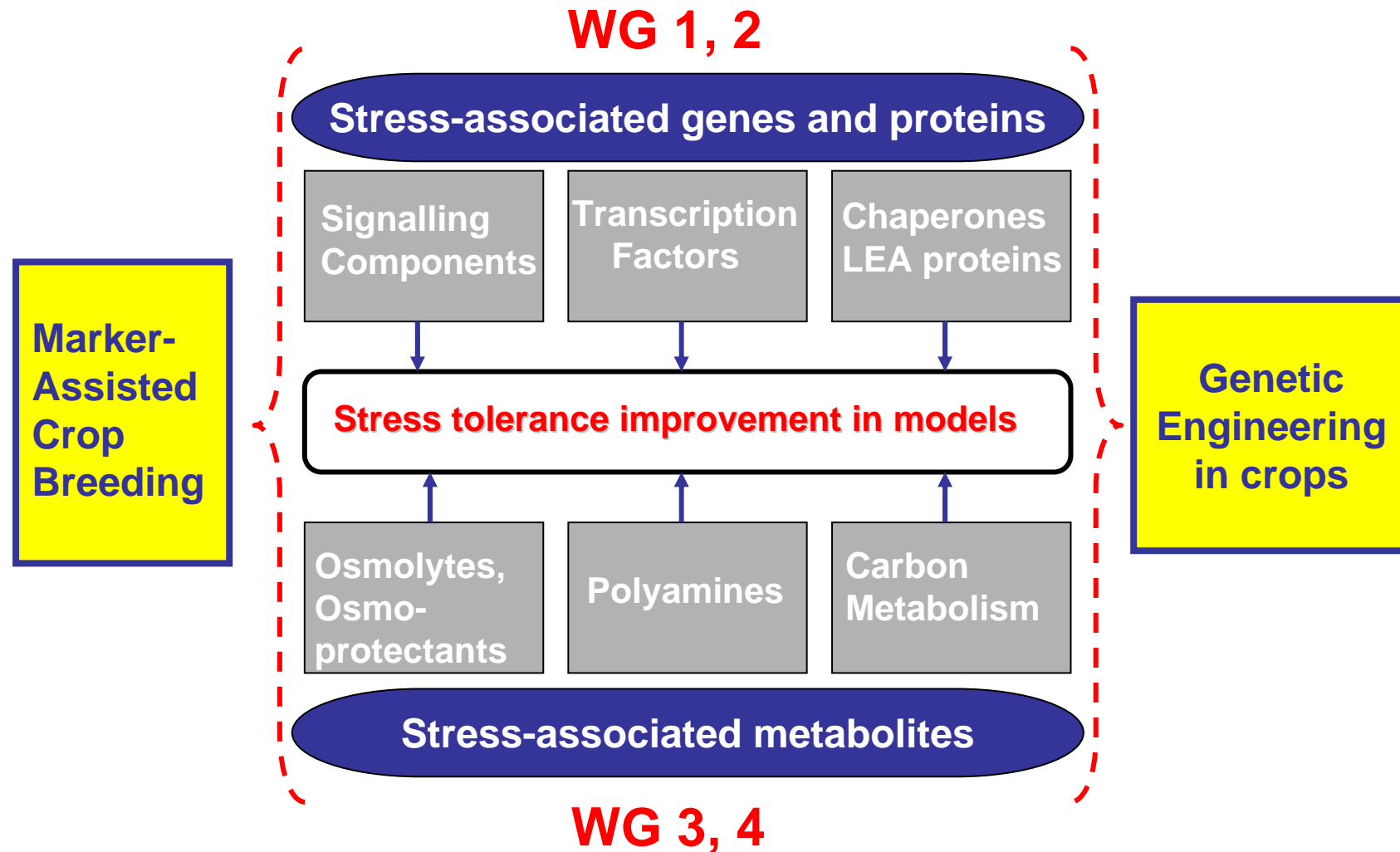
Exploitation of gained Knowledge to Improve Stress Tolerance



# Scientific context and objectives (2/2)



# Working groups

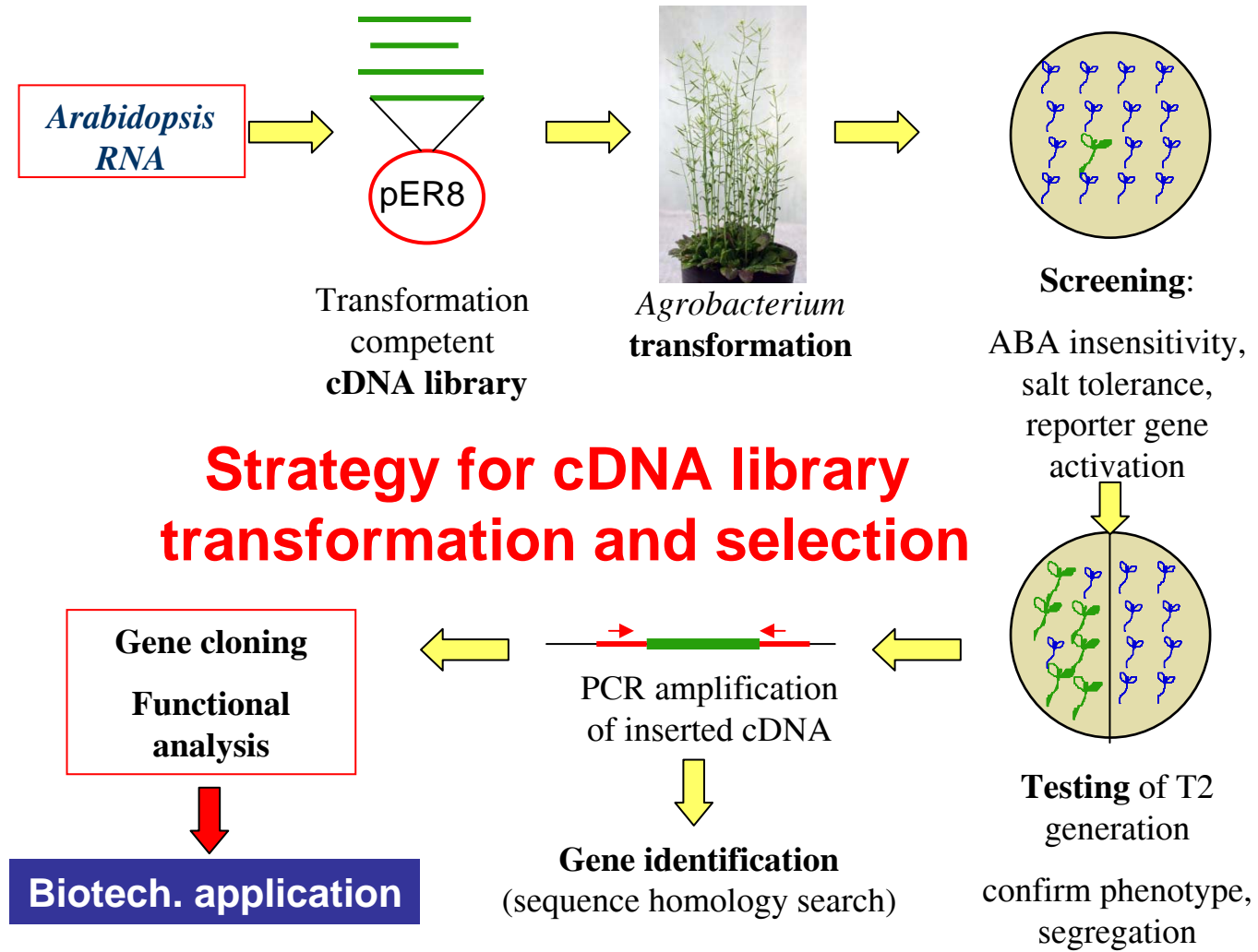


# Results vs. Objectives

	YEAR 1				YEAR 2				YEAR 3				YEAR 4			
<b>WG1: CHARACTERIZATION OF PROTEIN KINASES</b>																
1.1. Regulatory roles of SnRk1/2 kinases	■				■				■							
1.2. Identification of regulatory targets					■				■				■			
1.3. Development of novel genetic technologies									■				■			
1.4. Identification of kinase substrates	■				■				■				■			
1.5. SnRk1/2 regulatory interactions	■				■				■				■			
1.6. Regulation of specific responses	■				■				■				■			
1.7. Development of systems biology					■				■				■			
<b>WG2: IDENTIFICATION OF SIGNALLING FACTORS</b>																
2.1. Development of novel genetic approaches	■				■				■				■			
2.2. Cross-talk between signalling pathways	■				■				■				■			
2.3. Chromatin remodeling complexes	■				■				■				■			
2.4. New signalling factors	■				■				■				■			
2.5. ABA - hypersensitive mutants	■				■				■				■			
2.6. Interspecific genetic and metabolic variability	■				■				■				■			
2.7. New genetic tools for T. halophyla	■				■				■				■			
<b>WG3: PRODUCTION OF OSMOPROTECTANTS</b>																
3.1. Control of proline accumulation	■				■				■				■			
3.2. Cross-talk between responses	■				■				■				■			
3.3. Methionine metabolic network	■				■				■				■			
3.4. Regulation by kinases and transcription factors	■				■				■				■			
3.5. Proteins with chaperone functions	■				■				■				■			
<b>WG4: POLYAMINE METABOLIC PATHWAY</b>																
4.1. Molecular and metabolic markers	■				■				■				■			
4.2. Interspecific genetic and metabolic variability	■				■				■				■			
4.3. Mutans and transgenics	■				■				■				■			
4.4. Cross-talks with signalling pathways	■				■				■				■			
4.5. Polyamine metabolim in relevant crops and trees	■				■				■				■			
	YEAR 1				YEAR 2				YEAR 3				YEAR 4			

- **100 publications**  
(Sci, PNAS, PI Cell, JBC, PI J, PI Phys, TIBS, etc.)
- **2 Books of Abstracts**
- **2 patents**
- **3 EU proposals**
- **SEFV newsletter**
- **COST newsletter**
- **TV, newspapers**

# Significant highlights (1/2)



## Strategy for cDNA library transformation and selection

Szabados et al. (2008)

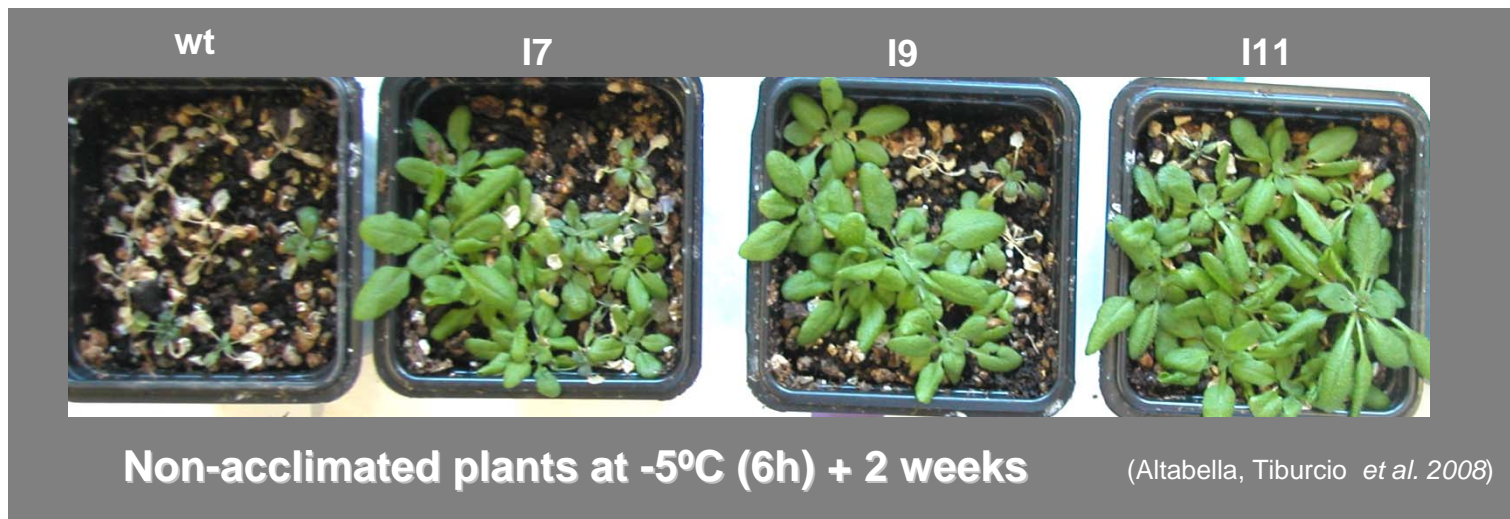
# Significant highlights (2/2)

Gene discovery in cold response in Arabidopsis

**Arginine decarboxylase (ADC) genes**  
(transcriptomics, metabolomics, knock-outs)

(Cuevas *et al.*, 2008;2009)  
4 INPAS groups

ADC-Overexpression in Arabidopsis



ADC-Overexpression in tomato

**Metapontum Agrobios**  
Rina Iannacone

**Freezing tolerance in tomato?**

# Challenges

