Does oxidative stress metabolism play a role in *Zantedeschia aethiopica* spathe senescence?

Cátia Barbeta, MC Piques, MS Pais, K Palme, RM Tavares and T Lino-Neto

University of Minho
Biology Department
October 2004

### Plant senescence

**Dramatic ultrastructural changes**
- chloroplast disorganization
- leaf-like peroxisomes are converted into glyoxysomes
- alterations of vacuole ultrastructure

**Dramatic metabolic changes**
- decline of photosynthetic and photorespiratory activities
- increase of catabolic pathways
  - induction of glyoxylate cycle
  - induction of other metabolic pathways
  - salvage and redistribution of metabolites
  - secondary metabolic pathways

### Senescence may not proceed through a single common pathway...

Multiple signaling pathways leads to senescence induction

- Developmental signals
- Hormonal changes
- Cell energy status
- Free radical levels
Senescence may not proceed through a single common pathway...

Multiple signaling pathways lead to senescence induction

- Developmental signals
- Hormonal changes
- Cell energy status
- Free radical levels

Senescence and oxidative stress

- Decrease in the protective mechanisms against activated oxygen forms
- Induction of cellular ROS generating mechanisms
- ROS

Senescence triggering factor

Consequence of the senescence process itself

Zantedeschia aethiopica (L.) Spreng.
Development of *Zantedeschia aethiopica* spathe

Senescence  Regreening

Morphological changes of *Z. aethiopica* spathe abaxial surface

Spathe senescence occurs during spathe whitening…
Inhibition of spathe senescence occurs during spathe regreening.

Is oxidative stress causally related to spathe senescence?
Is oxidative stress causally related to spathe senescence?

The results obtained from cytosolic CuZnSOD and cytosolic APX suggests an initial H$_2$O$_2$ burst in the cytosol leading to senescence progression. H$_2$O$_2$ content and lipid peroxidation.

Significant increase in the levels of H$_2$O$_2$ during the initial stages of the whitening process. Differential expression of Apx and cytCuZn-Sod genes in those stages. The increase in H$_2$O$_2$ level continues until the white spathe. The main source is probably the senescence process itself. Lipid peroxidation that measures the level of oxidative damage follows the same pattern as H$_2$O$_2$ levels suggesting a cause/effect relationship. H$_2$O$_2$ seems to have a dual function in Z. aethiopica spathe senescence. As a signalling molecule involved in the activation of cellular mechanisms that ultimately leads to the senescence process during spathe whitening. As a deleterious agent to cellular functions.
Evaluation of oxidative stress enzymes during spathe development

Is oxidative stress causally related to spathe senescence?

Comprehensive transcript profiling during spathe development

Multiparallel expression profiling by macroarray analysis

Large-scale EST sequencing and its annotation

5' End sequencing and sequence analysis

3,840 Spathe cDNA clones

21% Singleton ESTs

250 Gene clusters

1,257 Unique gene products

Differentially expressed in leaves and spathe specific expression

Leaf specific expression 2%

Not differentially expressed 45%

Differentially expressed in leaves and spathe specific expression 35%

Spathe specific expression 18%

Functional classification

Unclassified proteins 12%

Protein synthesis 3%

Cell rescue, defense and virulence 2%

Subcellular localization 4%

Transport facilitation 3%

Protein fate 3%

Control of cellular organization 1%

Metabolism 7%

Other 9%

Global gene expression variance

Combining the analyzed EST dataset and the macroarray data

Senescence associated genes

Oxidative stress related genes
Combining the analyzed EST dataset and the macroarray data

Senescence-associated genes

Oxidative stress-related genes

Combining the analyzed EST dataset and the macroarray data

Senescence-associated genes

Oxidative stress-related genes
Is oxidative stress causally related to spathe senescence?

**ROS** seems to play a dual role in *Z. aethiopica* spathe senescence in signalling and in degradative processes.

Expression profile of oxidative stress related genes is similar to that of senescence associated genes.

**Acknowledgments**

Prof. Dr. Bernd Weisshaar and Dr. Martin Werber
Max-Plank-Institut für Züchtungsforschung, Köln, Germany

Dr. Rui Fernandes
IBMC, Porto, Portugal

Cátia Barbeta is supported by Fundação para a Ciência e Tecnologia, grant ref. SFRH/BD/12081/2003