

Plant Biology Europe 2018 Conference

Abstract Book

How to cite this e-Book:

Christiansen, S.K. & Bendevis, M. (2018). A new tool for In:
Abstract Book for the Plant Biology Europe Conference in Copenhagen, p xx-xx.
ISBN 978-87-996274-1-7

All Rights Reserved

©2018 University of Copenhagen, Denmark

This material must not be reproduced, displayed, modified or distributed without the written permission of the copyright holder.



ISBN: 978-87-996274-1-7

Published by Department of Plant and Environmental Sciences, University of
Copenhagen,
Bülowsvej 17, DK-1870 Frederiksberg (<http://plen.ku.dk/english/>).

LOCAL ORGANIZING COMMITTEE (LOC)

Svend Christensen – LOC Chair, EPSO
*University of Copenhagen
Dept. of Plant and Environmental Sciences*

Birte Svensson
*Technical University of Denmark
Dept. of Biotechnology and Biomedicine*

Stefan Jansson – FESPB, SPPS
*Umeå University
Umeå Plant Science Centre*

Kåre Lehmann Nielsen
*Aalborg University
Dept. of Chemistry and Biosciences*

Stephan Wenkel - SPPS
*University of Copenhagen
Dept. of Plant and Environmental Sciences*

Henrik Brinch Pedersen
*Aarhus University
Dept. of Molecular Biology and Genetics*

Solveig Krogh Christiansen
*University of Copenhagen
Dept. of Plant and Environmental Sciences*

Søren Kjærsgaard Rasmussen
*University of Copenhagen
Dept. of Plant and Environmental Sciences*

Mira Arpe Bendevis
*University of Copenhagen
Dept. of Plant and Environmental Sciences*

SCIENTIFIC ORGANIZING COMMITTEE (SOC)

Cathie Martin - SOC Chair
John Innes Centre

Urte Schlüter - SOC Co-chair
University of Düsseldorf

Jeremy Harbinson
University of Wageningen

Ilse Kranner
University of Innsbruck

Fabio Fornara
University of Milan

Robbie Waugh
The James Hutton Institute

Alan Schulman
Natural Resources Institute Finland (LUKE)

Karin Metzclaff
EPSO

Torgny Näsholm
Umeå University

Jens Stougaard
Aarhus University

Michael Palmgren
The University of Copenhagen

Christian W.B. Bachem
Wageningen University

<http://www.europlantbiology2018.org/>



SPONSORS



Improving food & health

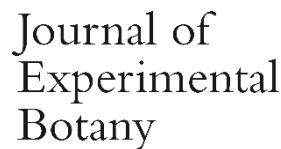
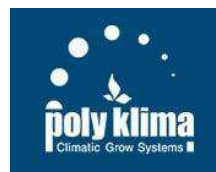
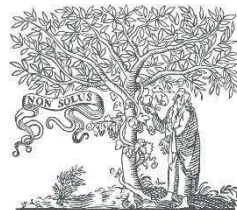


UNIVERSITY OF COPENHAGEN
FACULTY OF SCIENCE



YOUR OWN CLIMATE





Inducibility, tissue-specificity and product variation of three phytochelatin synthase homeologs from the cadmium-tolerant reed *A. donax* L.

Claudio Varotto¹, Luca Stragliati¹, Mingai Li¹, Ada Ricci², Luigi Sanità di Toppi³

¹Edmund Mach Foundation, SAN MICHELE ALL'ADIGE (TN), Italy

²Università degli studi di Parma, PARMA, Italy

³Università di Pisa, PISA, Italy

Phytochelatin (PC) are a family of Cys-rich oligopeptides constituting the main defence of plants against toxicity of heavy metals and metalloids like cadmium and arsenic. PCs are non-ribosomally synthesized from glutathione by the enzyme phytochelatin synthase (PCS). Dicotyledonous PCS have been characterized in detail, while much less information is available on monocotyledonous ones. In this study, we characterized three different *PCS* genes from giant reed (*Arundo donax* L.), a biomass/bionergy crop with remarkable tolerance to cadmium, to study the evolution of this trait in monocots. Phylogenetic reconstruction with *PCS* genes from fully sequenced monocotyledonous genomes indicated that the three *A. donax* *PCS*, *AdPCS1-3*, are most likely homeologs - resulting from lineage-specific whole-genome polyploidization. *AdPCS1-3* genes are tissue-specifically expressed, and *AdPCS1* is expressed about 5 times more than *AdPCS2* and *AdPCS3*. All three genes displayed cadmium-responsive expression in roots, and coded for functional PCSs, as once overexpressed in yeast they confer enhanced tolerance to cadmium stress. Overexpression of *AdPCS1-3* in *Arabidopsis thaliana* further confirmed the typical phenotype associated to overexpression of functional *PCS* genes. Mass-spectral analyses detected statistically significant differences in the amount and spectral feature of the PCs synthesized, with *AdPCS2* and *AdPCS1* producing, respectively, the highest and lowest amount of total PCs in yeast cells. *AdPCS1* synthesized the same amount of PC2, PC3 and PC4, while both *AdPCS2* and *AdPCS3* enzymes produced significantly higher amounts of PC2 and PC3 compared to PC4.

Taken together, these results indicate that the genetic bases of *A. donax* high capability to tolerate the presence of heavy metals is, at least in part, related to the high functional specialization of its *PCS* genes from a transcriptional as well as enzymatic point of view. Thus, transcriptional neofunctionalization and specialization seems to have played a major role in the evolution of Cd tolerance in *A. donax*.