# TABLE OF CONTENTS

Opening Statement	
Summary	
Acknowledgements	IX
Preface	XI
Table of Contents	1
List of Figures	2
List of Tables	3
Abbreviations	4
Introduction	7
Objectives	23
Chapter 1	27
Origin of Gibberellin-Dependent Transcriptional Regulation by Molecular Exploitation of a Transactivation Domain in DELLA Proteins	
Chapter 2	59
DELLA Proteins Recruit the Mediator Complex Subunit MED15 to Co-activate Gene Expression in Land Plants	
Coordination Between Growth and Stress Responses by DELLA in the Liverwort <i>Marchantia polymorpha</i>	93
General Discussion	125
Conclusions	139

## LIST OF FIGURES

Introduction	
Figure 1. Gibberellin induced DELLA degradation	10
Figure 2. Structure of DELLA proteins	11
Figure 3. Main mechanisms of DELLA transcriptional regulation	13
Figure 4. DELLA coordination of multiple pathways	15
Figure 5. Evolution of GA-related biosynthesis and signalling genes	16
Chapter 1	
Figure 1. Gibberellin-signalling elements are present in vascular plants	
Figure 2. DELLA proteins are land plant specific	
Figure 3. DELLA proteins are present in all extant land plant lineages	
Figure 4. GID1 binding residues in DELLA proteins are highly conserved	37
Figure 5. Some non-vascular DELLA proteins can interact with GID1 receptors ()	
Figure 6. DELLA domain conserved region act as a transcriptional activator domain	41
Sup. Figure 1. GID1 bona fide orthologs may be unique to vascular plants	50
Sup. Figure 2. Presence of SLY1/GID2 orthologs in land plants	52
Sup. Figure 3. Non-vascular land plants have conserved DELLA proteins	54
Sup. Figure 4. DELLA domain is structurally conserved	55
Sup. Figure 5. Some non-vascular DELLA proteins can interact with Arabidopsis ()	
Sup. Figure 6. The conserved DELLA domain acts as a transcriptional activator domain	57
Sup. Figure 7. DELLA domain $lpha$ helix D harbours a transactivation domain needed for ()	58
Chapter 2	
Figure 1. RGA and MED15 interaction enhances gene activation	
Figure 2. MED15 is involved in DELLA transcriptional activation	
Figure 3. MED15 is needed for DELLA-dependent co-activation responses	
Figure 4. MpDELLA acts as a co-activator by recruiting MpMED15	
Figure S1. Mammalian p53 structure involved in ARC105 recruitment	
Figure S2. RGA-MED15a yeast-two hybrid deletion analysis	
Figure S3. Yeast-two hybrid of DELLA-MED15 paralogs in Arabidopsis	85
Figure S4. RNA-seq coverage of <i>MED15</i> gene cluster in Arabidopsis in the 5x <i>della</i> mutant	
Figure S5. RNA-seq TPM comparison scatter plots	
Figure S6. Biological processes G0 term enrichment in DELLA-MED15 targets	87
Figure S7. Venn's diagram of ARR10 targets compared to PAC induced genes	
Figure S8. MED15 involvement in DELLA co-activation responses	88
Figure S9. Gene expression analysis of DELLA-PIF targets in <i>med15a<sup>Ri</sup></i>	89
Figure S10. RNAP II ChIP-seq coverage of selected genes with or without GAs	89
Figure S11. MED15 KIX-domains alignment and phylogeny tree	90
Figure S12. <i>MED15</i> genes fragments found in <i>M. polymorpha</i>	
Figure S13. MpMED15-MpDELLA interaction analysis	91
Figure S14. MpDELLA-related dual luciferase assays	92
Figure S15. MpDELLA-MpMYB14 interaction analysis	92
Chapter 3	
Figure 1. Mp <i>DELLA</i> overexpression inhibits plant growth via cell division	
Figure 2. Functional interaction between MpDELLA and MpPIF	99
Figure 3. Genome-wide co-regulation of gene expression by MpPIF and MpDELLA	101
Figure 4. Involvement of Mp <i>DELLA</i> in the response to oxidative stress	103
Figure S1. Related to Figure 1	118

Figure S2. Related to Figure 2	120
Figure S3. Related to Figure 3	122
Figure S4. Related to Figure 4	123
General Discussion	
Figure 1. Evolution of GA-related biosynthesis and signalling genes	128
Figure 2. Comparison of DELLA regulation & regulatory networks in <i>A. t.</i> and <i>M. p.</i> ()	131

## LIST OF TABLES

#### Mendeley Data Resource

Chapter 1. Supplementary Tables 1-9 Chapter 2. Supplementary Tables 1-9 Chapter 3. Table S1. Non-targeted metabolomic analysis Table S2. Oligonucleotide primers Data S1

 $3 \propto$ 

#### ABBREVIATIONS

3-AT 3-aminotrizole **ARF. AUXIN RESPONSE FACTOR ARR.** ARABIDOPSIS RESPONSE REGULATOR bHLH, basic helix-loop-helix BIFC, Bimolecular Fluorescence Complementation BLAST, Basic Local Alignment Search tool **BZR.** BRASSINAZOLE RESISTANT C4H, CINNAMATE 4-HYDROXYLASE CBP, CREB-Binding Protein ChIP, Chromatin Immunoprecipitation CHS. CHALCONE SYNTHASE Cit, Citrine CKI, Cyclin-dependent Kinase Inhibitors CPS, COPALYL DIPHOSPHATE SYNTHASE cW, Continuous white light CXE, Carboxyl esterase CycB /CYCB, Cyclin B DBD / BD, DNA Binding Domain DEX. Dexamethasone DIR, DELLA-Interacting Residue DPBA, Diphenylborinic acid 2-aminoethyl ester EdU, 5-ethynyl-2'-deoxyuridine EF1, ELONGATION FACTOR1 ELF7 / PAF1, EARLY FLOWERING 7 ERF, ETHYLENE RESPONSE FACTOR F3H, FLAVANONE 3-HYDROXYLASE FL. Full lenath FLC, FLOWERING LOCUS C FLS. FLAVONOL SYNTHASE FR, Far red (R, Red) GA(s), gibberellin(s) GA20ox, GIBBERELLIN 20-OXIDASE GA20X, GIBBERELLIN 2-OXIDASE GA3ox, GIBBERELLIN 3-OXIDASE GAF1 / IDD2, GAI ASSOCIATED FACTOR1 GAI, GIBBERELLIN A INSENSITIVE GBR. GA-Binding Residue GIDn, GIBBERELLIN INSENSITIVE DWARFn GL1, GLABRA1 GLP. GID-Like Protein GR, Glucocorticoid receptor GRAS, GAI/RGA/SCARECROW **GUS**, β-GLUCURONIDASE HAM, HAIRY MERISTEM HD-ZIP, Homeodomain-Leucin Zipper HMM. Hidden Markov Model IDD, INDETERMINATE DOMAIN JA. JASMONIC ACID JAZ, JASMONATE ZIM-DOMAIN Ke, rate of nonsynonymous substitution KAO, KAURENOIC ACID OXIDASE

KIX, Kinase-inducible domain (KID) Interacting Domain KO, KAURENE OXIDASE (alternatively: Knock Out) **KRP.** KIP-RELATED PROTEIN KS, KAURENE SYNTHASE Ks, rate of synonymous substitution LAS, LATERAL SUPRESSOR LUC, Firefly (Photinus pyralis) LUCIFERASE MAPK, mitogen-activated protein kinase MID, MED25-interacting domain MiP, Microprotein ML, Maximum Likelihood MV, Methyl Viologen (Paraquat) NAC. NAM. ATAF & CUC PAC, Paclobutrazole PAF1 / ELF7, POLYMERASE-ASSOCIATED FACTOR 1 PAL, PHENYLALANINE AMMONIA LYASE PAT1, PHYTOCHROME A SIGNAL TRANSDUCTION1 PDB, Protein Database PFD. PREFOLDIN PIC, RNA polymerase II Pre-Initiation Complex **PIF**, PHYTOCHROME-INTERACTING FACTORs PIL1, PIF3-LIKE1 PKL, PICKLE Pol II / RNAP II, DNA-dependent RNA polymerase II PRE5, PACLOBUTRAZOL RESISTANCE 5 RAM, Root Apical Meristem REN, Sea pansy (Renilla reniformis) LUCIFERASE RGA, repressor of ga1-3 RGLn. RGA-LIKEn Ri, RNA interference RNAP II / Pol II, DNA-dependent RNA polymerase II SAM, S-Adenosyl methionine SCF, Skp/Cullin/F-box containing complex SCLn, SCARECROW-LIKEn SCR, SCARECROW SHR, SHORTROOT SLY. SLEEPY SMR, SIAMESE RELATED SPL, SQUAMOSA PROMOTER-LIKE SWI/SNF, SWITCH/SUCROSE NON-FERMENTABLE SWI3, SWITCH3 TAD, Transcriptional Activation Domain TES, Transcriptional End Site TF(s), transcription factor(s) TOC159, TRANSLOCASE OF CHLOROPLAST159 TR(s), transcriptional regulator(s) TSS, Transcriptional Start Site UAS, Upstream Activating Sequence XTR7, XYLOGLUCAN ENDOTRANSGLYCOSYLASE-RELATED Y2H, Yeast-two Hybrid YFP, Yellow Fluorescent Protein

 $\sim$  4