CURRICULUM VITAE

GENERAL INFORMATION

Surname: Smaczniak
First names: Cezary Dominik
Academic Degree: Dr.
ORCID ID: orcid.org/0000-0002-4663-8275
Date of birth: 26 December 1983
Gender: male
Institution: Humboldt-Universität zu Berlin, Institute of Biology, Plant Cell and Molecular Biology
Philippstr. 13, 10115 Berlin, Germany
Telephone: +49 30 209 349 743
E-Mail address: cezary.smaczniak@hu-berlin.de
Current position: Research fellow (de: ‘wissenschaftlicher Mitarbeiter’, 100% TV-L HU)

SCIENTIFIC DEGREES

Degree: Doctor
Subject: Molecular Biology
University: Wageningen University, Wageningen, the Netherlands
Year of graduation: 2013
Doctoral thesis: *MADS interactomics. Towards understanding the molecular mechanisms of plant MADS-domain transcription factor function.*
Supervisor: Prof. Gerco Angenent

ACADEMIC EDUCATION

Degree: Magister
Subject of studies: Biotechnology
University: Jagiellonian University, Kraków, Poland
Year of graduation: 2007
Supervisor: Prof. Maria Kapiszewska

ACADEMIC APPOINTMENTS

Since 2018	Research Fellow/Project Leader, Institute of Biology, Humboldt-Universität zu Berlin, Berlin, Germany
2015 – 2017	Postdoc, Potsdam University, Institute for Biochemistry and Biology, Potsdam-Golm, Germany
2013 – 2015	Postdoc, Wageningen University, Laboratory of Molecular Biology Wageningen, the Netherlands

MISCELLANEOUS ACADEMIC AND REVIEWING ACTIVITIES

Since 2015	Reviewer for scientific journals: e.g. Plant Cell, Nucleic Acids Research, Genes, Plant Reproduction, and Plant Physiology. See: https://publons.com/researcher/1574772

SELECTED PUBLICATIONS

1. **Smaczniak, C.***, Muino, J.M.*, Chen, D., Angenent, G.C., and Kaufmann, K. (2017). *Differences in DNA Binding Specificity of Floral Homeotic Protein Complexes Predict Organ-Specific Target Genes.* **Plant Cell** 29, 1822-1835.
2. **Smaczniak, C.**, Angenent, G.C., and Kaufmann, K. (2017). *SELEX-Seq: A Method to Determine DNA Binding Specificities of Plant Transcription Factors.* **Methods Mol Biol** 1629, 67-82.
3. **Smaczniak, C.**, Immink, R.G., Muino, J.M., Blanvillain, R., Busscher, M., Busscher-Lange, J., Dinh, Q.D., Liu, S., Westphal, A.H., Boeren, S., Parcy, F., Xu, L., Carles, C.C., Angenent, G.C., and Kaufmann, K. (2012). *Characterization of MADS-domain transcription factor complexes in Arabidopsis flower development.* **Proc Natl Acad Sci USA** 109, 1560-1565.
4. **Smaczniak, C.***, Li, N.*, Boeren, S., America, T., van Dongen, W., Goerdayal, S.S., de Vries, S., Angenent, G.C., and Kaufmann, K. (2012). *Proteomics-based identification of low-abundance signaling and regulatory protein complexes in native plant tissues.* **Nat Protoc** 7, 2144-2158.
5. **Smaczniak, C.**, Immink, R.G., Angenent, G.C., and Kaufmann, K. (2012). *Developmental and evolutionary diversity of plant MADS-domain factors: insights from recent studies.* **Development** 139, 3081-3098.

OTHER PUBLICATIONS

1. Mikulski, P., Hohenstatt, M.L., Farrona, S., **Smaczniak, C.**, Stahl, Y., Kalyanikrishna, K., Kaufmann, K., Angenent, G.C., and Schubert, D. (2019). *The chromatin-associated protein PWO1 interacts with plant nuclear lamin-like components to regulate nuclear size.* **Plant Cell** 31, 1141-1154.
2. Lai, X., Stigliani, A., Vachon, G., Carles, C., **Smaczniak, C.**, Zubieta, C., Kaufmann, K., and Parcy, F. (2019). *Building Transcription Factor Binding Site Models to Understand Gene Regulation in Plants.* **Mol Plant** 12, 743-763.
3. Yan, W., Chen, D., **Smaczniak, C.**, Engelhorn, J., Liu, H., Yang, W., Graf, A., Carles, C.C., Zhou, D.X., and Kaufmann, K. (2018). *Dynamic and spatial restriction of Polycomb activity by plant histone demethylases.* **Nat Plants** 4, 681-689.
4. Bai, X., Huang, Y., Hu, Y., Liu, H., Zhang, B., **Smaczniak, C.**, Hu, G., Han, Z., and Xing, Y. (2017). *Duplication of an upstream silencer of FZP increases grain yield in rice.* **Nat Plants** 3, 885-893.
5. Muino, J.M., **Smaczniak, C.**, Angenent, G.C., Kaufmann, K., and van Dijk, A.D. (2014). *Structural determinants of DNA recognition by plant MADS-domain transcription factors.* **Nucleic Acids Res** 42, 2138-2146.
6. Debernardi, J.M., Mecchia, M.A., Vercruyssen, L., **Smaczniak, C.**, Kaufmann, K., Inze, D., Rodriguez, R.E., and Palatnik, J.F. (2014). *Post-transcriptional control of GRF transcription factors by microRNA miR396 and GIF co-activator affects leaf size and longevity.* **Plant J** 79, 413-426.
7. Kloosterman, B., Abelenda, J.A., Gomez Mdel, M., Oortwijn, M., de Boer, J.M., Kowitwanich, K., Horvath, B.M., van Eck, H.J., **Smaczniak, C.**, Prat, S., Visser, R.G., and Bachem, C.W. (2013). *Naturally occurring allele diversity allows potato cultivation in northern latitudes.* **Nature** 495, 246-250.
8. Liu, W., Kohlen, W., Lillo, A., Op den Camp, R., Ivanov, S., Hartog, M., Limpens, E., Jamil, M., **Smaczniak, C.**, Kaufmann, K., Yang, W.C., Hooiveld, G.J., Charnikhova, T., Bouwmeester, H.J.,

Bisseling, T., and Geurts, R. (2011). *Strigolactone biosynthesis in Medicago truncatula and rice requires the symbiotic GRAS-type transcription factors NSP1 and NSP2.* **Plant Cell** 23, 3853-3865.

9. Kaufmann, K., **Smaczniak, C.**, de Vries, S., Angenent, G.C., and Karlova, R. (2011). *Proteomics insights into plant signaling and development.* **Proteomics** 11, 744-755.
10. Assuncao, A.G., Herrero, E., Lin, Y.F., Huettel, B., Talukdar, S., **Smaczniak, C.**, Immink, R.G., van Eldik, M., Fiers, M., Schat, H., and Aarts, M.G. (2010). *Arabidopsis thaliana transcription factors bZIP19 and bZIP23 regulate the adaptation to zinc deficiency.* **Proc Natl Acad Sci USA** 107, 10296-10301.
11. Kaufmann, K., Muino, J.M., Jauregui, R., Airoldi, C.A., **Smaczniak, C.**, Krajewski, P., and Angenent, G.C. (2009). *Target genes of the MADS transcription factor SEPALLATA3: integration of developmental and hormonal pathways in the Arabidopsis flower.* **PLoS Biol** 7, e1000090.

FUNDING AND FELLOWSHIPS

2019 – 2022	DFG research project: “Organ-specific binding site selection and transcriptional regulation by floral homeotic transcription factors.”
2015 – 2017	Alexander von Humboldt Research Fellowship for postdoctoral researchers: ”Post-translational control of transcription factor activity in flower development.”
2008	Leonardo da Vinci fellowship (EU), Jagiellonian University, Kraków, Poland. Visiting: Plant Research International, Wageningen, the Netherlands
2007	Erasmus scholarship (EU), Jagiellonian University, Kraków, Poland. Visiting: Centre for Molecular Biophysics, CNRS, Orléans, France.

(CO-)SUPERVISION OF STUDENTS

Since 2017	4 PhD, 1 Master, 1 Bachelor

MEMBERSHIPS OF SCIENTIFIC SOCIETIES

2008 – 2013	Member of the Experimental Plant Sciences graduate school (Wageningen University, Wageningen, the Netherlands)

SCIENTIFIC EXPOSURE

International symposia and congresses:

2019	Workshop on Molecular Mechanisms Controlling Flower Development (Hyères, France) – presentation
2016	4th International Symposium on Genomics and Crop Improvement (Wuhan, China) – presentation
2015	Workshop on Molecular Mechanisms Controlling Flower Development (Aiguablava, Spain) – poster presentation
2014	Transcription and Chromatin, 11th EMBL Conference (Heidelberg, Germany)
2013	Workshop on Molecular Mechanisms Controlling Flower Development (Hyères, France) – presentation
2012	Plant development and environmental interactions, EMBO Conference (Matera, Italy) – poster

2011	Workshop on Molecular Mechanisms Controlling Flower Development (Maratea, Italy) – poster
2010	COST action: Plant proteomics in Europe - Systems biology and -Omic approaches (Namur, Belgium) – poster
2009	Workshop on Molecular Mechanisms Controlling Flower Development (Aiguablava, Spain) – poster

In-depth courses:

2017	9th MaxQuant Summer School, Berlin, Germany
2011	Transcription Factors and Transcription Regulation, Leiden, The Netherlands
2010	Systems Biology: Statistical Analysis of -Omics Data, Wageningen, The Netherlands
2009	3rd European Summer School in Proteomic Basics: Quantification and Post-translational Modifications of Proteins, Bressanone, Italy

LABORATORY EXPERTISE

Protein interactions: Chromatin immunoprecipitation (**ChIP**), systematic evolution of ligands by exponential enrichment (**SELEX**), electrophoretic mobility shift assay (**EMSA**), yeast n-hybrid screening (**YnH**).

Protein characterization: Protein immunoprecipitation (**IP**), tandem mass spectrometry (**LC-MS/MS**), protein expression systems and purification, **SDS-PAGE** electrophoresis, **western-blot**.

Other: Confocal microscopy, gene expression, protoplast transfection and reporter assays, working with radioactivity, comet assay.

Bioinformatics: **LC-MS/MS data analysis packages** (**Xcalibur, Bioworks, MaxQuant, Perseus, Progenesis LC-MS, Sequest, Mascot**); DNA sequence alignment, protein structure alignment and prediction;

PERSONAL SKILLS AND COMPETENCES

Languages: Polish (native speaker), English (proficient user, C1-C2), German (basic user, A2-B1), Portuguese (basic user, A2).

Other: Problem solving, project planning, supervising.