

Marc W. Schmid, PhD

PRACTICAL EXPERIENCE

- 2017-TODAY | **Senior Bioinformatician**
MWSCHMID GMBH
Bioinformatics and Scientific Services.
- 2015-2017 | **Bioinformatician / Shared Scientist**
UNIVERSITY OF ZURICH, CENTRAL IT, S3IT
Statistical analysis and visualization of diverse data sets from life sciences. Writing scientific articles. Consulting and training of PhD students and PostDocs at the University of Zurich (experimental design, data analysis and interpretation).
- 2010-2015 | **PhD Graduate Student**
UNIVERSITY OF ZURICH, INSTITUTE OF PLANT BIOLOGY
In addition to my own research, I also contributed with programming, data analysis, and interpretation to various collaborative projects addressing many aspects of plant biology from the evolution of sex-specific genes to the architecture of the nucleus. Consequently, my work comprised many research topics, experimental procedures, and data analysis approaches. The unifying theme was the attempt to understand life with the help of quantitative data.

EDUCATION

- 2010-2015 | **Doctorate at the Faculty of Science**
UNIVERSITY OF ZURICH, INSTITUTE OF PLANT BIOLOGY
Title: Genome-Scale Quantitative Biology of *Arabidopsis thaliana*.
- 2008-2010 | **Master of Science UZH (Biology)**
UNIVERSITY OF ZURICH, INSTITUTE OF PLANT BIOLOGY
Title: A microgenomics approach to analyse the polarity of the four-nucleate embryo sac of *Arabidopsis thaliana*.
Overall final grade: 5.9 out of 6.
- 2005-2008 | **Bachelor of Science ETH (Environmental Sciences)**
SWISS FEDERAL INSTITUTE OF TECHNOLOGY (ETH) ZURICH, D-UWIS
Interdisciplinary studies covering the basics of mathematics, physics, chemistry, biology, economy, law and psychology. Emphasis on the integration of different fields to understand and transform complex environmental systems. Bachelor theses in molecular plant biology and consumer behaviour.
Overall final grade: 5.6 out of 6.

PUBLICATIONS

- [48] Snoeck, S., Kyung Lee, H., **Schmid, M.W.**, Bender, K.W., Neeracher, M.J., Fernandez-Fernandez, A.D., Santiago, J., Zipfel, C. (2024): Leveraging co-evolutionary insights and AI-based structural modeling to unravel receptor-peptide ligand-binding mechanisms. *bioRxiv*
- [47] Ngou, B.P.M., Wyler, M. **Schmid, M.W.**, Kadota, Y. Shirasu, K. (2023): Evolutionary Trajectory of Pattern Recognition Receptors in Plants. *Nature Communications*, in press
- [46] Hartman, K., **Schmid, M.W.**, Bodenhausen, N., Bender, S.F., Held, A.Y., Schlaeppli, K., van der Heijden, M.G.A. (2023): A symbiotic footprint in the plant root microbiome. *Environmental Microbiome*, 18: 65
- [45] Köninger, J., Ballabio, C., Panagos, P., Jones, A., **Schmid, M.W.**, Orgiazzi, A., Briones, M.J.I. (2023): Ecosystem type drives soil eukaryotic diversity and composition in Europe. *Global Change Biology*, 29: 5706-5719
- [44] Labouyrie, M., Ballabio, C., Romero, F., Panagos, P., Jones, A., **Schmid, M.W.**, Mikryukov, V., Dulya, O., Tedersoo, L., Bahram, M., Lugato, E., van der Heijden, M.G.A., Orgiazzi, A. (2023): Patterns in soil microbial diversity across Europe at the interplay of vegetation, climate and soil properties. *Nature Communications*, 14: 3311
- [43] Klotz, C., **Schmid, M.W.**, Winter, K., Ignatius, R., Weisz, F., Saghaug, C.S., Langeland, N., Dawson, S., Lalle, M., Hanevik, K., Cacció, S.M., Aebischer, T. (2023): Highly contiguous genomes of human clinical isolates of *Giardia duodenalis* reveal assemblage and sub-assemblage specific presence-absence variation in protein-coding genes. *Microbial Genomics*, 9: 3
- [42] Boquete, M.T., **Schmid, M.W.**, Wagemaker, N.C.A.M., Carey, S., McDaniel, S.F., Richards, R.L., Alonso, C., Herrera, C.M. (2022): Heavy metal tolerance in *Scopelophila cataractae*: Transcriptomic and epigenetic datasets. *Data in brief*, 45: 108710
- [41] Ramakrishnan, C., Ebnetter, J.A., Winiger, R., **Schmid, M.W.**, Russo, G., Leitao, A., Hemphill, A., Soldati-Favre, D., Hehl, A.B. (2022): Dissection of *Besnoitia besnoiti* intermediate host life cycle stages: from morphology to gene expression. *Plos Pathogens*, 18: e1010955
- [40] Walder, F., **Schmid, M.W.**, Riedo, J., Held, A.Y., Banerjee, S., Büchi, L., Bucheli, T.D., van der Heijden, M.G.A. (2022): Soil microbiome signatures are associated with pesticide residues in arable landscapes. *Soil Biology and Biochemistry*, 174: 108830
- [39] Jaric, I., Voelkl, B., Clerc, M., **Schmid, M.W.**, Novak, J., Rosso, M., Rufener, R., von Kortzfleisch, V. Richter, S.H., Buettner, M., Bleich, A., Amrein, I., Wolfer, D.P., Touma, C., Sunagawa, S., Würbel, H. (2022): The rearing environment persistently modulates mouse phenotypes from the molecular to the behavioural level. *Plos Biology*, 20: e3001837
- [38] Boquete, M.T., **Schmid, M.W.**, Wagemaker, N.C.A.M., Carey, S., McDaniel, S.F., Richards, R.L., Alonso (2022): Non-genetically-based intraspecific differentiation for heavy metal tolerance in the copper moss *Scopelophila cataractae*. *Environmental and Experimental Botany*, 201: 104970
- [37] Mounger, J.M., van Riemsdijk, I., Boquete, M.T., Wagemaker, N.C.A.M., Fatma, S., Robertson, M.H., Voors, S.A., Oberstaller, J., Gawehns, F., Hanley, T.C., Grosse, I., Verhoeven, K.J.F., Sotka, E.E., Gehring, C.A., Hughes, A.R., Lewis, D.B., **Schmid, M.W.**, Richards, C.L. (2022): Genetic and epigenetic differentiation across intertidal gradients in the foundation plant *Spartina alterniflora*. *Frontiers in Ecology and Evolution*, 10: 868826
- [36] Ngou, B.P.M., Heal, R., Wyler, M., **Schmid, M.W.**, Jones, J.D.G. (2022): Concerted expansion and contraction of immune receptor gene repertoires in plant genomes. *Nature Plants*, 8: 11461152
- [35] Rhodes, J., Roman, A.-O., Bjornson, M., Brandt, B., Derbyshire, P., Wyler, M., **Schmid, M.W.**, Menke, F.L.H., Santiago, J., Zipfel, C. (2022): Perception of a conserved family of plant signalling peptides by the receptor kinase HSL3. *eLife*, 11: e74687
- [34] Voegel, C.D., Kroll, S.L., **Schmid, M.W.**, Kexel, A.-K., Baumgartner, M.R., Kraemer, T., Binz, T.M., Quednow, B.B. (2021): Alterations of Stress-Related Glucocorticoids and Endocannabinoids in Hair of Chronic Cocaine Users. *International Journal of Neuropsychopharmacology*, 25: 226-237
- [33] Mounger, J.#, Boquete, M.T.#, **Schmid, M.W.#**, Renan, G., Robertson, M.H., Voors, S.A., Langanke, K.L., Alvarez, M.F., Wagemaker, N.C.A.M, Schrey, A.W., Fox, G.A., Lewis, D.B., Fonseca Lira, C., Lee Richards, C. (2021): Inheritance of DNA methylation differences in the mangrove *Rhizophora mangle*. *Evolution and Development*, 23: 351374. # equal contribution
- [32] **Schmid, M.W.#**, van Moorsel, S.J.#, Hahl, T., Enrica De Luca, Wagg, C., Niklaus, P.A., Schmid, B. (2021): Plant diversity and community age shape soil microbial communities. *Journal of Ecology*, 109: 30073023. # equal contribution

- [31] van Moorsel, S.J.#, **Schmid, M.W.#**, Wagemaker, N.C.A.M., van Gurp, T., Schmid, B., Vergeer, P. (2019): Evidence for rapid evolution in a grassland biodiversity experiment. *Molecular Ecology*, 28: 4097-4117 # equal contribution
- [30] Dalcher, D., Tan, J.Y., Bersaglieri, C., Peña-Hernández, R., Vollenweider, E., Zeyen, S., **Schmid, M.W.**, Bianchi, V., Butz, S., Kuzyakiv, R., Baubec, T., Marques, A.C., Santoro, R. (2020): BAZ2A safeguards genome architecture of ground-state pluripotent stem cells. *The EMBO Journal*, 39: e105606
- [29] Kobiita, A., Godbersen, S., Araldi, E., Ghoshdastider, U., **Schmid, M.W.**, Spinass, G., Moch, H., Stoffel, M. (2020): The Diabetes Gene *JAZF1* Is Essential for the Homeostatic Control of Ribosome Biogenesis and Function in Metabolic Stress. *Cell Reports*, 32: 107846
- [28] Kartal, Ö., **Schmid, M.W.**, Grossniklaus, U. (2020): Cell Type-specific Genome Scans of DNA Methylation Diversity Indicate an Important Role for Transposable Elements. *Genome Biology*, 21: 1-29.
- [27] Hahl, T.#, van Moorsel, S.J.#, **Schmid, M.W.**, Zuppinger-Dingley, D., Schmid, B., Wagg, C. (2019): Plant responses to diversity-driven selection and associated rhizosphere microbial communities. *Functional Ecology*, 34: 707-722 # equal contribution
- [26] Nikolaou, K.C., Vatandaslar, H., Meyer, C., **Schmid, M.W.**, Tuschl, T., Stoffel, M. (2019): The RNA-Binding Protein A1CF Regulates Hepatic Fructose and Glycerol Metabolism via Alternative RNA Splicing. *Cell Reports*, 29: 283-300
- [25] Caldelari, R., Dogga, **Schmid, M.W.**, Franke-Fayard, B., Janse, C.J., Soldati-Favre, D., Heussler, V. (2019): Transcriptome analysis of *Plasmodium berghei* during exo-erythrocytic development. *Malaria Journal*, 18: 330
- [24] Krattinger, S.G., Kang, J., Bräunlich, S., Boni, R. Chauhan, H., Selter, L.L., Robinson, M.D., **Schmid, M.W.**, Wiederhold, E., Hensel, G., Kumlehn, J., Sucher, J., Martinoia, E., Keller, B. (2019): Abscisic acid is a substrate of the ABC transporter encoded by the durable wheat disease resistance gene *Lr34*. *New Phytologist*, 223: 853-866
- [23] **Schmid, M.W.#**, Hahl, T.#, van Moorsel, S.J.#, Wagg, C., de Deyn, G.B., Schmid, B. (2019): Feedbacks of plant identity and diversity on the diversity and community composition of rhizosphere microbiomes from a longterm biodiversity experiment. *Molecular Ecology*, 28: 863-878 # equal contribution
- [22] **Schmid, M.W.#**, Heichinger, C.#, Coman, D., Gagliardini, V., Guthörl, D., Bruggmann, R., Aluri, S. Künzli, M., Schmid, B., Turnbull, L.A., Grossniklaus, U. (2018): Contribution of epigenetic variation to adaptation in *Arabidopsis*. *Nature Communication* 9: 4446 # equal contribution
- [21] van Moorsel, S.J., **Schmid, M.W.**, Hahl, T., Zuppinger-Dingley, D., Schmid, B. (2018): Selection in response to community diversity alters plant performance and functional traits. *Perspectives in Plant Ecology, Evolution and Systematics*, 33: 51-61
- [20] **Schmid, M.W.#**, Giraldo Fonseca, A.#, Smetanin, D., Grossniklaus, U. (2018): Extensive epigenetic reprogramming during the life cycle of *Marchantia polymorpha*. *Genome Biology*, 19:9 # equal contribution
- [19] Lippuner, C., Ramakrishnan, C., Basso, W., **Schmid, M.W.**, Okoniewski, M., Smith, N., Hässig, M., Deplazes, P., Hehl, A.B. (2018): RNA-Seq analysis during the life cycle of *Cryptosporidium parvum* reveals significant differential gene expression between proliferating stages in the intestine and infectious sporozoites. *International Journal for Parasitology*, 48(6):413-422
- [18] **Schmid, M.W.** (2017): RNA-Seq data analysis protocol: Combining in-house and publicly available data. *Methods in Molecular Biology*, 1669
- [17] Bowman, J.L., Kohchi, T., Yamato, K.T., Jenkins, J., Shu, S., *et al.* (2017): Insights into land plant evolution garnered from the *Marchantia polymorpha* genome. *Cell*, 171: 287-304.
- [16] Graf, U., Casanova, E.A., Wyck, S., Dalcher, D., Gatti, M., Vollenweider, E., Okoniewski, M.J., Weber, F.B., Patel, S.S., **Schmid, M.W.**, Li, J., Sharif, J., Wanner, G.A., Koseki, H., Wong, J., Pelczar, P., Penengo, L., Santoro, R., Cinelli, P. (2017): Pramel7 mediates ground state pluripotency through proteasomal-epigenetic combined pathways. *Nature Cell Biology*, 19: 763773.
- [15] Hedhly, A., Vogler, H., **Schmid, M.W.**, Pazmino, D., Gagliardini, V., Santelia, D., Grossniklaus, U. (2016): Starch turnover and metabolism during flower and early embryo development in *Arabidopsis thaliana*. *Plant Physiology*, 172(4): 2388-2402.
- [14] Gossmann, T.I., Saleh, D., **Schmid, M.W.**, Spence, M.A., Schmid, K.J. (2016): Plant reproductive development is characterised by a transcriptomic evolutionary bulge. *Molecular Biology and Evolution*, advanced online access

- [13] **Schmid, M.W.**[#], Schmidt, A.[#], Grossniklaus, U. (2015): The female gametophyte: An emerging model for cell type-specific systems biology in plant development. *Frontiers in Plant Science*, 6:907. [#] equal contribution
- [12] **Schmid, M.W.**, Grob, S., Grossniklaus, U. (2015): HiCdat: a fast and easy-to-use Hi-C data analysis tool. *BMC Bioinformatics*, 16: 277.
- [11] **Schmid, M.W.**, Grossniklaus, U. (2015): Rcount: simple and flexible RNA-Seq read counting. *Bioinformatics*, 31(3): 436-437.
- [10] Schmidt, A., **Schmid, M.W.**, Grossniklaus, U. (2015): Plant germline formation: molecular insights define common concepts and illustrate developmental flexibility in apomictic and sexual reproduction. *Development*, 142: 229-241.
- [9] Grob, S., **Schmid, M.W.**, Grossniklaus, U. (2014): HiC Analysis in *Arabidopsis* Identifies the *KNOT*, a Structure with Similarities to the *flamenco* Locus of *Drosophila*. *Molecular Cell*, 55(5): 678-693.
- [8] Schmidt, A., **Schmid, M.W.**, Klostermeier, U.C., Qi, W., Guthörl, D., Sailer, C., Waller, M., Rosenstiel, P., and Grossniklaus, U. (2014): Apomictic and sexual germline development differ with respect to cell cycle, transcriptional, hormonal and epigenetic regulation. *PLoS Genetics*, 10(7): e1004476.
- [7] Gossmann, T.I., **Schmid, M.W.**, Grossniklaus, U., and Schmid, K.J. (2014): Selection-driven evolution of sex-biased genes is consistent with sexual selection in *Arabidopsis thaliana*. *Molecular Biology and Evolution*, 31(3): 574-583.
- [6] Grob, S., **Schmid, M.W.**, Luedtke, N.W., Wicker, T., and Grossniklaus, U. (2013): Characterization of chromosomal architecture in Arabidopsis by chromosome conformation capture. *Genome Biology*, 14:R129.
- [5] Wuest, S.E., **Schmid, M.W.**, and Grossniklaus, U. (2013): Cell-specific expression profiling of rare cell types as exemplified by its impact on our understanding of female gametophyte development. *Current Opinion in Plant Biology*, 16: 1-9.
- [4] You, W., Tyczewska, A., Spencer, M., Daxinger, L., **Schmid, M.W.**, Grossniklaus, U., Simon, S., Meyers, B.C., Matzke, A.J.M., and Matzke, M. (2012): Atypical DNA methylation of genes encoding cysteine-rich peptides in *Arabidopsis thaliana*. *BMC Plant Biology*, 12: 51.
- [3] Schmidt, A., **Schmid, M.W.**, and Grossniklaus, U. (2012): Analysis of plant germline development by high-throughput RNA profiling: technical advances and new insights. *The Plant Journal*, 70(1): 18-29.
- [2] **Schmid, M.W.**, Schmidt, A., Klostermeier, U.C., Barann, M., Rosenstiel, P., and Grossniklaus, U. (2012): A powerful method for transcriptional profiling of specific cell types in eukaryotes: laser-assisted microdissection and RNA sequencing. *PLOS ONE*, 7(1): e29685.
- [1] McKeown, P.C., Laouielle-Duprat, S., Prins, P., Wolff, P., **Schmid, M.W.**, Donoghue, M.T.A., Fort, A., Duszynska, D., Comte, A., Lao, N.T., Wennblom, T.J., Smant, G., Köhler, C., Grossniklaus, U., and Spillane, C. (2011): Identification of imprinted genes subject to parent-of-origin specific expression in *Arabidopsis thaliana* seeds. *BMC Plant Biology*, 11: 113.