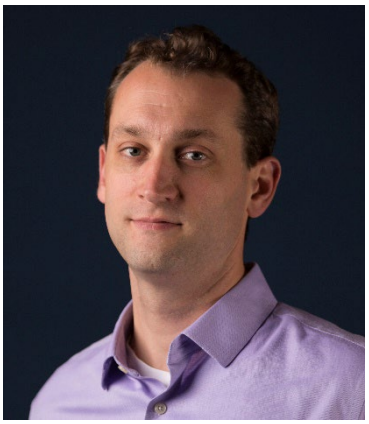
GATERSLEBEN LECTURE

IPK LEIBNIZ-INSTITUT

Speaker: **Prof. Dr. Robert (Bob) Schmitz**
Department of Genetics,
University of Georgia, Athens, GA, USA



Title: ***Deciphering the evolution of cis-regulation in plants at single-cell resolution***

Time: **Tuesday, June 9, 2026, 2 pm**
https://ipk-gatersleben-de.zoom-x.de/j/64783767811?pwd=hndGuIynz0tMsTZ3oKnPjTsgHfQDL8.1
ID: 647 8376 7811
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Place: **IPK Lecture Hall and via Zoom,**
Correnssstr. 3, 06466 Seeland OT Gatersleben

Abstract: Plant epigenomics and single-cell genomics are transformative tools for studying cis-regulatory variation in plant genomes. We are using these technologies to identify cis-regulatory elements, characterize their cell-type-specific activity, and uncover how genetic variants influence their activity. In this talk, I'll explore how cutting-edge tools like epigenomics and single-cell genomics are rapidly advancing our understanding of plant biology by pinpointing the location of "cis-regulatory elements", the non-coding regions of DNA that play a crucial role in gene expression control. Using maize as a model, we're uncovering how these regulatory elements vary between plants and how those differences have influenced key traits during domestication. Dissection of the distal non-coding regulatory region associated with TEOSINTE BRANCHED 1 (TB1) reveals complex interplay between dynamic accessible chromatin regions shaped by transposon insertions. Determining the causal genetic variant for increased expression of TB1 in maize, compared to its progenitor teosinte, remains a conundrum highly the complexity of non-coding regulatory in plant genomes. In parallel we are using population epigenomics to scale up the identification of causal regulatory elements important for expression and trait variation. Although genome-wide association studies (GWAS) have helped connect genetic variation to important traits in crops, they often struggle to identify the precise variants responsible, especially because most trait-linked DNA changes lie outside of genes. By profiling over 700,000 individual cells across 172 genetically diverse maize lines, we've mapped the locations and activity of regulatory elements at unprecedented resolution. Our work reveals how transposons helped rewire gene regulation, how specific transcription factor binding sites influence chromatin accessibility, and how natural variation in these regions contributes to flowering time and other critical traits. Lastly, we are innovating methods for single-cell genetic screens in plants to increase detection of causal genetic variants for expression and trait variation. These discoveries offer new insights into the molecular drivers of crop diversity and hold promise for improving agriculture through targeted genome editing.

Academic positions:

2026-Present	Distinguished Research Professor, UGA Foundation Professorship of Plant Sciences & Georgia Research Alliance Lars G. Ljungdahl Distinguished Investigator, University of Georgia, Athens, GA
2021-2026	Professor, UGA Foundation Professorship of Plant Sciences & Georgia Research Alliance Lars G. Ljungdahl Distinguished Investigator, University of Georgia, Athens, GA
2017-2021	Associate Professor, University of Georgia, Athens, GA
2013-2017	Assistant Professor, University of Georgia, Athens, GA
2008-2013	Postdoctoral Fellow, The Salk Institute for Bio. Studies, La Jolla, CA
2003-2007	Graduate Student, University of Wisconsin, Madison, Wisconsin

Education:

2007	Ph. D., University of Wisconsin, Madison, Wisconsin
2002	B.Sc., University of Arizona, Tucson, Arizona

Prof. Dr. Nils Stein (organizer and host)