



BonnMu – a resource for functional genomics in maize



**Dr. Caroline Marcon: University of Bonn,
Germany - Institute of Crop Science and Resource
Conservation (INRES)**



04 December 2025

14:00 to 14:45 CET

Bergamo

Hosted by

Dr. Vincenzo Rossi - CREA-CI



Link for attending online: [BonnMu – a resource for functional genomics in maize](#) | [Partecipazione alla riunione](#) | [Microsoft Teams](#)

Curriculum vitae

PD Dr. Caroline Marcon

University of Bonn, Germany

Institute of Crop Science and Resource Conservation (INRES)

Project group: *BonnMu* Resources

At the Chair for Crop Functional Genomics (CFG)

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Academic Career

Since 2023	Habilitation and <i>venia legendi</i> in Genetics at the Faculty of Agriculture, University of Bonn Thesis title: „Functional genomics of maize (<i>Zea mays</i> L.) seedling roots“
Since 2019	Leader of the project group: <i>BonnMu</i> Resources, University of Bonn
2012 – 2019	Postdoctoral research associate in the research group of Prof. Dr. Frank Hochholdinger, University of Bonn Topics: genetic, transcriptomic, and proteomic analysis of the maize root system
2007 – 2012	Ph.D. thesis at the Center for Plant Molecular Biology (ZMBP), Department of General Genetics, University of Tübingen, in the research group of Dr. Frank Hochholdinger
04/2006 – 04/2007	Diploma in Biology, University of Tübingen

Recent award

2025	Maize Genetics Cooperator Award: presented by the Maize Genetics Cooperation, this award honors maize cooperators who have dedicated their careers to service by supporting community resources, organizing collaborative efforts, or enabling maize research.
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Research activities

In the past 13 years as a research associate and project leader in the research group of Frank Hochholdinger (University of Bonn, Germany), I worked on the genetic, transcriptomic, and proteomic analysis of the maize root system. This included the molecular cloning of the *root hair defective* (*rth*) genes *rth5* (Nestler et al. 2014) and *rth6* (Li et al. 2016), and the functional characterization of the *rootless with undetectable meristems1* (*rum1*) gene (Zhang et al. 2014; Zhang et al. 2016). In comparison to wild-type plants, *rth* mutants exhibit impaired root hair development, while *rum1* mutants lack both lateral and seminal roots (reviewed in Hochholdinger et al. 2018a). I also participated in numerous transcriptome studies, including those focused on heterosis (Paschold et al. 2012; Paschold et al. 2014; Baldauf et al. 2016; Marcon et al. 2017; Baldauf et al. 2018), the functional diversity of distinct root types (Tai et al. 2016), and responses to drought stress (Opitz et al. 2014; Opitz et al. 2016; Marcon et al. 2017). Additionally, I generated a high-resolution proteome and phosphoproteome atlas of maize primary root tissues, which uncovered functional specialization along the root axes (Marcon et al. 2015; reviewed in Hochholdinger et al. 2018b). Since 2019, I lead the project group BonnMu Resources. The BonnMu resource represents a large publicly available collection of maize Mutator (Mu) transposon induced mutants (Marcon et al. 2020; Win et al. 2024; Marcon et al. 2025b; Win et al. 2025; reviewed in Marcon et al. 2025a).

For references, please see: <https://www.inres.uni-bonn.de/cfg/en/c-f-g/marcon>

For information on the BonnMu resource, please visit: www.bonnmu.uni-bonn.de

Talk in Bergamo, entitled: BonnMu – a resource for functional genomics in maize

Summary: The BonnMu resource is a publicly available collection of maize mutants created using Mutator (Mu) transposons, which are mobile DNA elements that can “jump” into genes and disrupt their function. Currently, our resource includes 425,924 heritable Mu insertions affecting 36,612 (83%) of the 44,303 annotated maize genes in the B73v5 genome. Most of these insertions (94%) occur within genes, such as in 5' UTRs, exons, or introns, while only about 6% insert into non-coding regions. Mu insertions and photos of seedling phenotypes from segregating BonnMu F₂ stocks can be accessed through the Maize Genetics and Genomics Database (MaizeGDB). In this talk, I will discuss the creation and application of the BonnMu resource for identifying and characterizing mutations induced by Mu transposons, which represents a useful tool for functional genomics studies in maize.