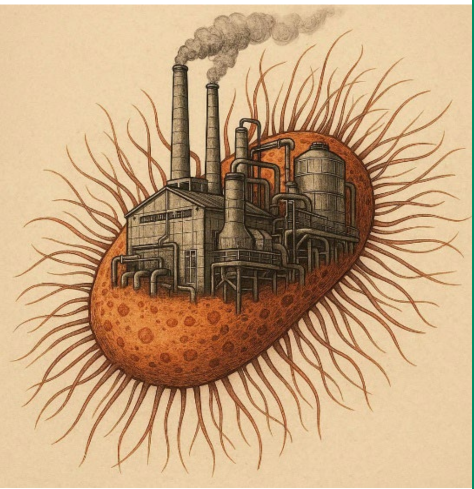
CeBiTec – Quarterly

Summer 2025



- The Nattkemper group is part of a multinational interdisciplinary team analysing the cold-water coral population in the Atlantic using AI
- Tackling epigenetic transgene silencing by systematic Cas9-mediated strain engineering
- Hoffman group publishes study on the link between genetic variations in black grouse and reduced mating success in Nature Ecology & Evolution
- 12th CeBiTec Student Academy during the summer holidays
- Collaborative Project on Human Biology and Human Disease with the Öffentlich-Stiftisches Gymnasium Bethel
- BIIGLE continues to receive support from NFDI4Biodiversity

The Nattkemper group is part of a multinational interdisciplinary team analysing the cold-water coral population in the Atlantic using AI

©Tim Nattkemper

Cold-water corals are an important component of deep-sea ecosystems, biodiversity hotspots that are under increasing pressure from human activities, including fishing, deep-sea mining and climate change. In order to develop measures for future climate change impacts, the distribution of corals and their physical environmental conditions need to be recorded and understood. Relatively large datasets on the distribution of cold-water corals exist for the North Atlantic, but unfortunately, very little for the Central and South Atlantic. As part of the Challenger 150 programme of the UN Ocean Decade, large amounts of image and video data have been collected, most of which have not yet been analysed. This new project, which is led by Prof K Howell (University of Plymouth, UK), aims to unearth this "hidden treasure trove of data" in a multinational interdisciplinary team and to analyse the huge amount of image and video data. The Biodata Mining working group (Prof. T Nattkemper) will contribute its online video/ image annotation system BIIGLE and will be involved in the development and application of AI-based analysis tools for the automatic classification and segmentation of corals in the data, which poses numerous new challenges due to the special characteristics of underwater images.

(T. Nattkemper)

Tackling epigenetic transgene silencing by systematic Cas9-mediated strain engineering

Alexander Einhaus and Arno Krieger, with the Algal Biotechnology and Bioenergy group led by Olaf Kruse, have tackled the longstanding problem of epigenetic transgene silencing in the green microalga *Chlamydomonas reinhardtii*.

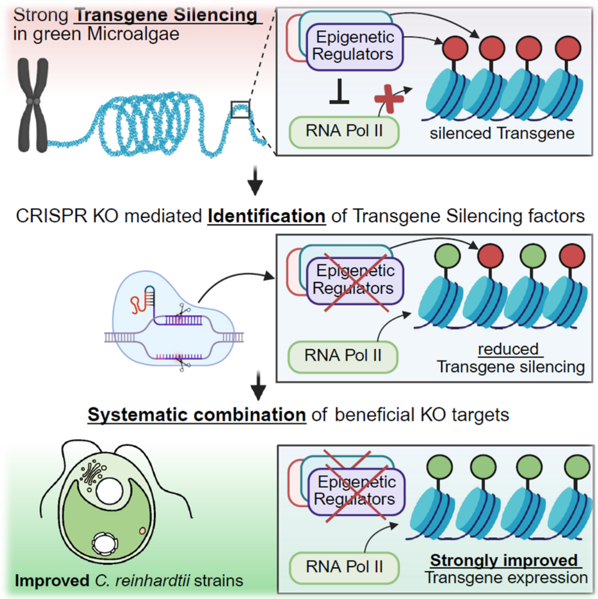


Figure 1 | Graphical abstract of the article “Genome editing of epigenetic transgene silencing in *Chlamydomonas reinhardtii*“ © 2025 The Authors. Published by Elsevier Ltd.

The potential of this microalga as a potent and sustainable chassis for biotechnology has been limited by its distinct ability for gene silencing on the chromatin level and poor stability of engineered transgene expression. Using a systematic reverse genetics approach using CRISPR-Cas9 the authors could identify factors that are involved in mediating this strong response to introduced transgenes. Candidate genes include various histone lysine methyltransferases (HLMs), Sir2-type histone deacetylases (SRTs), a DNMT1-type DNA methylase (DMC5) and an ancillary ribosomal component involved in siRNA-mediated translational repression (VIG1).

A combination of beneficial knock-out (KO) candidates in double and triple KO mutants further distinctly improved strain performance and stability of transgene expression. In particular, the combined KO mutant ΔA51 (ΔSRTA, ΔDMC5 and ΔVIG1) displayed robust transgene expression and stability. It outperformed established strains in engineered production of the commercially relevant terpenoids α-bisabolene, patchoulol, casbene and taxadiene.

A total of 27 novel mutant strains represents a valuable collection of mutant strains to fundamentally study the role of epigenetic factors and their potential interplays. Additionally, a novel split selectable marker system using the *Nostoc punctiforme* DnaE split intein in combination with the Spectinomycin resistance gene was established. Using this split selectable marker system for dual-targeted CRISPR-mediated KO represents the first successful application of inteins in *C. reinhardtii* and adds a valuable contribution to the molecular toolkit.

Einhaus A, Krieger A, Köhne L, Rautengarten B, Jacobebbinghaus N, Saudhof M, Baier T, Kruse O **(2025).** *Trends in Biotechnology*, *43* (8), 1961–1981. DOI: 10.1016/j.tibtech.2025.04.019

(A. Einhaus)

Hoffman group publishes study on the link between predicted deleterious mutations and reduced mating success in black grouse in Nature Ecology & Evolution

©Rebecca Chen

A research project led by PhD student Rebecca Chen from the CeBiTec research group "Evolutionary Population Genetics" has investigated how deleterious mutations predicted from whole genome resequencing data affect the reproductive success of male black grouse. The key finding: it's not visible traits like colourful plumage that determine mating success, but behaviour. Males with a high number of harmful mutations were less frequently present at lekking sites, missing out on vital opportunities to reproduce. The study, titled "Predicted deleterious mutations reveal the genomic mechanisms underlying fitness variation in a lekking bird", has now been published in the journal Nature Ecology & Evolution.

"The study combines modern genomic analyses with a unique long-term dataset on wild black grouse", explains lead author Rebecca Chen. The researchers analysed the whole genomes of 190 males in combination with years of observations on their behaviour, appearance, and mating success.

They found clear evidence that deleterious mutations significantly reduce reproductive success. One of the surprising results: not only mutations inherited from both parents (homozygous) but also those from just one parent (heterozygous) had a negative effect. This contradicts the previous assumption that only harmful mutations expressed in the homozygous state reduce fitness.

Figure 2 | Black grouse
© J. Hoffman

Mutations in DNA segments that control the activity of other genes – so-called regulatory regions, especially promoters – proved to be particularly damaging. These segments help switch genes on or off depending on the environmental context. When they are impaired, animals may struggle to adjust their behaviour appropriately – for example, deciding when to show up at a lek to compete for mates.

"These mutations appear to disrupt the fine-tuning of behavioural responses," says Chen. And it is precisely this behaviour that females observe – not necessarily the male's appearance. The results thus provide new insights into how animals may unconsciously assess the genetic quality of potential mates.

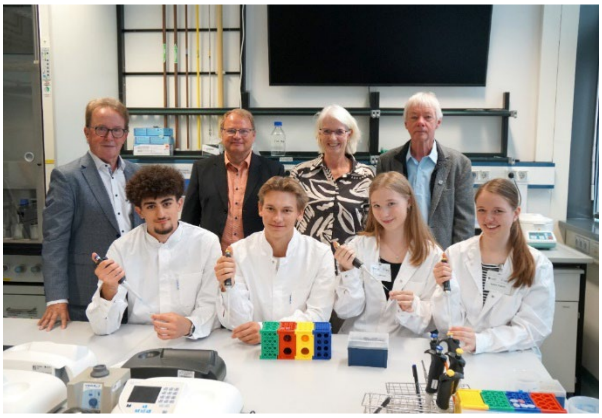
The study was conducted within the framework of the Joint Institute for Individualisation in a Changing Environment (JICE) – a collaborative research initiative by Bielefeld University and the University of Münster. "Our work shows how modern genetic analysis, combined with long-term field data, can generate new insights into evolution" says senior author Professor Dr Joseph Hoffman.

Founded in 2021, JICE brings together researchers from biology, philosophy, the social sciences, and environmental studies. It aims to better understand individual variation in animals and humans as they respond to changing environments. The current study reflects this approach: by linking detailed genomic data with behavioural and environmental factors, it contributes to understanding why some individuals in the wild are more successful than others.

Chen, R.S., Soulsbury, C.D., Hench, K. et al. Predicted deleterious mutations reveal the genetic architecture of male reproductive success in a lekking bird. Nat Ecol Evol (2025). https://doi.org/10.1038/s41559-025-02802-8

(J. Hoffman)

12th CeBiTec Student Academy during the summer holidays


Prof. Dr. Jörn Kalinowski, Rainer Menze from the district government in Detmold, Claudia Holle from the Osthushenrich-Stiftung, Prof. Dr. Norbert Grotjohann, with students Yazan Al Akhal, Jeremy Löwen, Leonie Boo, and Malien Hiddink at the opening of the 12th CeBiTec Student Academy. ©Bielefeld University

In the first week of the summer holidays, the 12th CeBiTec Student Academy brought together 16 senior class students for an intensive programme focusing on biomedical topics. The academy aims to encourage young people with a strong interest in science and to assist them in reflecting on their career aspirations.

The 2025 programme, organised by Prof. Dr. Alf Pühler, Prof. Dr. Jörn Kalinowski and Prof. Dr. Norbert Grotjohann, combined established elements with several new features. As in previous years, students learned microbiological techniques for the detection of bacteria (Dr. Kerstin Röllke) and gained insights into nanopore sequencing, besides its bioinformatic evaluation (Dr. Tobias Busche & Matthias Otto). A notable addition this year was a practical experiment involving the dissection of a heart and the biochemical diagnosis of myocardial infarction through photometric determination of lactate dehydrogenase (LDH) activity (Dr. Maren Panhorst).

The lecture programme was also expanded with two new contributions: Prof. Dr. Tilo Grosser (clinical development of medicinal products) and Dr. Almut Mentz (molecular pathology) enriched the programme with expertise from their respective research and clinical fields. These lectures complemented the programme from previous years, comprising medical genomics (Prof. Dr. Jörn Kalinowski), industrial biotechnology (Prof. Dr. Volker Wendisch), and algae biotechnology (Dr. Jan Mussgnug). Study programmes in biology, biotechnology, and medicine were presented by Dr. Nils Hasenbein, Prof. Dr. Johann Kufs and Dr. Henriette Watermann, respectively.

Two excursions provided further insights into medical and clinical practice. A recently established programme element - the visit to the Medical Faculty - once again offered participants the opportunity to explore the field of human anatomy under the guidance of Prof. Dr. Björn Spittau and to gain practical impressions in the Skills Lab with Mike Reichert. Another new programme item was a visit to the Study House at Campus Klinikum Bielefeld, which included hands-on demonstrations in the local Skills Lab, a tour of the Hospital Museum, and a guided visit to the Institute for Laboratory Medicine, Microbiology and Transfusion Medicine.

The week's programme was complemented by evening events and the traditional overnight stay at the youth hostel in Bielefeld, providing opportunities for informal exchange.

From next year, the organisation of the CeBiTec Student Academy will see changes. After many years of committed and highly valued service, Prof. Dr. Jörn Kalinowski and Prof. Dr. Alf Pühler will step down from their organisational roles. The CeBiTec warmly thanks both for their exceptional contributions to the academy's development and success. Future student academies will be organised by Prof. Dr. Volker Wendisch, Prof. Dr. Tilo Grosser and Prof. Dr. Norbert Grotjohann, thankfully continuing his engagement. Supported by the Osthushenrich Foundation, this team will ensure the continued high quality and relevance of the CeBiTec Student Academy in the years to come.

(K. Röllke)

Collaborative Project on Human Biology and Human Disease with the Öffentlich-Stiftisches Gymnasium Bethel

FBS Gymnasium Bethel

This year, the teutolab-biotechnology once again partnered with the Öffentlich-Stiftisches Gymnasium Bethel for a project entitled "Human Biology and Human Diseases", which forms part of the school's programme "Neue Lernwege gehen" ("Exploring New Learning Pathways") for all 9th-grade classes.

9th-grade students conducting experiments on human biology. ©teutolab-biotechnology

Within this project, students expand and deepen their fundamental knowledge of human biology. Working in groups over the course of half a school year, they study a specific human disease in detail and present their findings to their classmates at the end of the term. In addition, they gain practical experience in medical diagnostics through laboratory sessions supported by the teutolab-biotechnology. From February to July 2025, the teutolab-biotechnology provided experimental modules focusing on cardiovascular diseases and infections caused by bacteria and viruses. In hands-on activities, the students dissected a pig's heart, determined blood groups, performed an ELISA test to identify viral infections, and learned methods for bacterial typing. These experiments took place either at the school or at the teutolab-biotechnology facilities in the CeBiTec.

Beyond acquiring scientific knowledge, the project offered the 58 participating students the opportunity to work with authentic diagnostic methods, apply theoretical concepts in a practical context, and gain valuable insight into real-world biomedical workflows. This experience not only strengthened their understanding of human biology but also fostered their scientific curiosity. Supported by *zdi* ("Future through Innovation") as part of vocational orientation and career guidance, the project aims to inspire participants to consider future studies or careers in the life sciences.

(K. Röllke)

BIIGLE continues to receive support from NFDI4Biodiversity

BIIGLE is a specialised software for image and video analysis, which is developed by the Biodata Mining Group of Tim W. Nattkemper. The software facilitates manual and AI-assisted annotation for the analysis of large datasets and is used by scientists all over the world for environmental monitoring and exploration. As of August 2025, biigle.de has almost 5,000 registered users from 40 different countries and stores more than 37 million annotations on more than 5 million images and videos.

BIIGLE is part of the official service catalog of the NFDI4Biodiversity project, a consortium under the umbrella of the National Research Data Infrastructure (NFDI) dedicated to mobilizing biodiversity and environmental data for collective use. NFDI4Biodiversity has recently been approved for another funding phase lasting three to five years. As a project partner, the Bielefeld Institute for Bioinformatics Infrastructure (BIBI) will continue to support BIIGLE as a consortium service and provide expertise in the setup of core services such as cloud storage and compute or authentication and authorisation infrastructure.

(M. Zurowietz)

Impressum

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