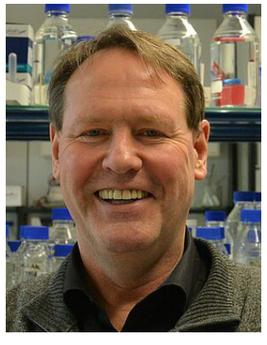
eMicrobevol

EARLY MICROBIAL EVOLUTION

Projektleitung HHU



Prof. Dr. William F. Martin
Institut für Molekulare Evolution (Institutsleitung)
Telefon +49 211 81-1 30 11
bill@hhu.de

What is your project about and what are the research goals?

The work on this project, eMicrobevol (for early microbial evolution), started in 2015 and was completed in 2020. It was my second ERC advanced grant (many thanks to the ERC). My first, Networkorigins, ran from 2009 to 2014 and focused on the use of networks as a tool and vehicle to study genome evolution. eMicrobevol went further by taking the technological challenge of investigating the evolutionary history of all the data in genomes head-on, rather than using a few selected genes as a proxy for the evolution of the genome as a whole. For that, we had to computationally sort all 30 million genes from 6000 sequenced genomes into clusters, natural families of sequence similarity that can be used to explore the deep evolutionary past of our unicellular ancestors. The challenge was the accurate handling of matrices containing 30 trillion elements, each element containing substantial amounts of information. For this, the colleagues at the central computing facilities (ZIM) of the HHU provided us with many terabytes of random access memory on one machine (many thanks to the ZIM), that gave us a big edge on big data.

The goals of the project were to learn about our own past. It is part of human nature to want to know more about our biological past, where we ultimately come from. It is part of the human condition. My main scientific curiosity is to learn more about the phases of evolution about which we know least: early microbial evolution.

The project honed in specifically on three questions that are critical to our understanding of microbial evolution: i) What are the quantitative and lineage specific relative contributions of gene transfer from endosymbionts vs. gene transfers from other prokaryotes during eukaryotic genome evolution? ii) How significant are the differences in verticality in comparisons of genome evolution in prokaryotes vs. eukaryotes and how can we better quantify those differences? iii) What was the biological nature of the earliest prokaryotes? The goal was to obtain answers to these question using data from sequenced genomes. We had good success, publishing 60 papers from the project, many in major journals (Nature, Nature Microbiology, Cell, PNAS, Trends, Nature Ecology and Evolution), a good mark for a small team.

How did the project idea come about?

The project emerged naturally from my own research career, which has always been devoted to some aspect of understanding evolution. But the ERC expects proposals, in particular advanced grants, to go substantially beyond the state of the art and, ideally, to open up new areas of scientific endeavour at the forefront of the field: in a word, to be "groundbreaking", to depart from one's own comfort zone. The idea for eMicrobevol came from my impatience with a field that used at most 1% of each genome for evolutionary investigations. "We can do better than that" I said to my team, "all we have to do is code the data in a new way, from beginning to end, so that the computer can read all the trees and tell us what we want to know". With the ZIM's help to solve the clustering problem, we had a path forward.

Why did you decide to apply for an ERC and why at this time in your career?

ERC projects give one a good bit of freedom, enough funding to allow 2-3 talented postdocs develop the research programme and become successful in their own right. They also afford funding for 5 years, short enough that one always has to hurry up before the time is up, but long enough that one does not have to start writing a report before the team is in place. The key to timing was simple, the funding from my first advanced grant had run out, but I had not yet run out of ideas.

What advice do you have for researchers interested in ERC research funding?

Put your best ideas forward. Don't be stingy with your ideas, get them out there in writing, see if the ideas are as good as you think they are. Panels want to read interesting proposals. Write about interesting and important questions and novel avenues of investigation in an accessible way – make it easy for panels and referees to want to fund your work and to have concrete reasons to do so. And start early. Open the files for your proposal and start writing 13 months before it is due. The ideas need to be new so they need time to mature as text. Submit with one month to spare so that you can look at the final product in a relaxed manner. Once submitted you can always improve and replace.

Laufzeit	Fördersumme HHU	Fördersumme gesamt	Förderprogramm
1. November 2015 - 31. Oktober 2020	EUR 2.393.447,50	EUR 2.393.447,50	Excellent Science - European Research Council - Advanced Grant (ERC-AdG)

This project has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (grant agreement No 666053)