

## 2017 Helmholtz – OCPC – Programme for the involvement of postdocs in bilateral collaboration projects

### PART A

**Title of the project:** The pan transcriptome of hexaploid bread wheat

**Helmholtz Centre and institute:** Helmholtz Center Munich, German Research Center for Environmental Health (HMGU), Plant Genome and Systems Biology group (PGSB)

**Project leader:** Prof. Klaus Mayer

**Web-address:** <http://pgsb.helmholtz-muenchen.de/plant/index.jsp>

**Description of the project** (max. 1 page):

Along with maize and rice, wheat is the most important crop plant and calory resource for human consumption worldwide. Due to the enormous size of the bread wheat genome (allohexaploid, 17 Gigabases) until very recently access to the full genomic information was impossible. However, truly revolutionary sequencing and genome assembly technologies now enable economic and rapid access to the full and ordered genomic information. This is seen as a quantum leap in genome biology but, even more importantly, also for agricultural sciences and the future of wheat breeding with potential massive impact beyond basic research. The Plant Genome and Systems Biology group at HMGU is a world leading genome biology and bioinformatics research group that has a long history in plant genomics and contributed to a range of crop genomics and – in particular – cereal and bread wheat genomics projects. Along with the currently ongoing finalization of the reference genome (cultivar “Chinese Spring”) we embarked towards the sequencing and characterisation (both structural & functional) of additional cultivars with a main focus towards cultivars of agricultural importance. Besides full genome information exhaustive transcriptomic information will be generated with a particular emphasis on the grain development and grain transcriptome dynamics. Previous analysis has shown that there is a tightly regulated separation of labour as well as a tight regulatory interplay among subgenomes. More importantly in very recent work we find pronounced differences for grain quality genes and the balancing of subgenome contributions and subgenome transcriptional networks.

Aim of the collaboration and of the scientific work to be executed will be the comparative bioinformatic and systemic analysis with a strong emphasis towards the grain transcriptome and in

particular the cultivar specific differences for grain quality genes and the embedding of these into transcriptional networks. We expect new and systems level insights into the variability of genes and networks underlying important characteristics of grain and baking quality. We see this as an important contribution for next generation wheat breeding, food supply and food quality and finally as a logical next step to transcend basic research into applied research (“from bench to field”).

**Description of existing or sought Chinese collaboration partner institute (max. half page):**

Postdocs from Chinese academic institutions with strong expertise in the field of plant and crop genomics are welcome to apply. We seek partnering contacts with institutes that have a focus at the intersection of basic and genomic research and applying modern genome technologies for addressing fundamental questions in biology as well as the use and exploitation of genomic data and analytical opportunities for application and e.g. future breeding activities in crop plants in particular -but not restricted to - cereal grasses.

Know-how in the following listed items are advantageous:

**Required qualification of the post-doc:**

- PhD in bioinformatics, computational biology, biology or comparable
- Experience with (genome) sequence analysis, NGS data analysis and bioinformatic workflows and toolkits
- Extensive knowledge in (plant-) genomics and biology
- Additional skills in at least one scientific programming language (Python, Perl, Java, C) and statistics (such as R)
- Familiar with LINUX/UNIX and high-performance compute environments
- Experience with database systems (MySQL, PostGres, Oracle) desirable
- Strong communication skills to be able to work in an international team and to interact with cooperation partners and consortia
- Strong presentation skills to communicate results both to the group and cooperation partners and summarize findings in scientific manuscripts

The ideal candidate would have demonstrated experience in one of the fields of comparative genomics, systems biology, network analysis and/or plant genomics.