

# EUROCORES Programme

Ecological and Evolutionary Functional Genomics (EuroEEFG)

#### Consensus statement EuroEEFG Review Panel

(Final evaluation)

### List of contributors

Hardtke	Christian	University of Lausanne	Lausanne	СН
Littlewood	D. Tim J.	The Natural History Museum	London	UK
Mori	Hirotada	Nara Institute of Science and Technology	Nara	JP
Raes	Martine	Universitaire Notre Dame de la Paix	Namur	BE
Sruoga	Aniolas	Vilnius University	Vilnius	LT
Nogueira	Maria Manuela	European Science Foundation	Strasbourg	FR

In total, 5 out of 12 Review Panel members evaluated the EurooEEFG Programme. This consensus statement was sent to all Review Panel members for approval.

## **Progress in the Collaborative Research Projects (CRPs)**

#### Progress towards CRP goals

The strongest CRPs are exceptional and highlight the best of what the EUROCORES Programme can yield, providing in their words 'creating networks' of 'complementary expertise' and a 'critical mass of researchers' not possible to achieve 'in any single country'. It is obvious from the majority of CRPs that considerable momentum has been achieved with the promise of completion of the majority of planned objectives and goals in the near future, and in some cases far exceeding the original goals (e.g. A\_alpina). Two of the 8 CRPS have progressed extremely well. MECOMECON has been very active; their achievements are well explained and their future priorities clearly outlined in their high-quality report. STRESSFLEA is also a good example of an impressive collaborative project. It is unfortunate that the lack of individual funding of some projects compromised the original goals of a few CRPs (e.g. FREDI) but in these cases the teams each worked to their capacity in fulfilling their individual objectives and collective goals wherever possible. Most CRPs explain shortfalls (due to funding or time limitations) and provide evidence of remedial action having been taken. NEMADAPT explains that some objectives were too ambitious, for instance RNAi knockdowns were not achieved ("a bridge too far").

Progress to date has been excellent and many more high profile, solid academic deliverables (articles, trained staff, networks and new collaborations) can be expected in the future.

## • integration and collaboration within the multinational CRP teams

Each CRP has demonstrated considerable integration within the teams, with the majority making concerted and sustained efforts to build momentum. Strong networks have arisen and many partners recognise the uniqueness of these partnerships emerging thanks to EuroEEFG.

The majority of CRPs have clearly taken their programmes very seriously, coordinating, training and sharing resources and ideas, developing substantial trans-national collaboration and exchange of expertise and, where possible, linking with other CRPs through scheduled meetings or via commonly attended conferences. The project MOCA had already started international collaborations before this programme was launched but EuroEEFG certainly accelerated its individual projects.

## Scientific highlights of the CRPs, including main achievements, contribution to knowledge, joint outputs

Regarding scientific output, the CRPs' performance is rather diverse. Most projects have shown very good performance and efficiency, especially projects analysing diversities through geographical differences such as A. alpina, MECOMECON, NEMADAPT and DEEP\_C. While some have produced excellent work that already manifested in prestigious joint publications, others have performed at a lower level which is probably due to the initial funding constraints applied by the funding organisations at the end of the selection process.

Nonetheless, the overall goal of boosting genomics in the context of ecology and evolution research has been largely achieved. The quality of output is generally high including articles in *Nat Genetics, Science, TREE, Nat Comm, MBE*. The final scientific output of the CRPs in terms of number of publications and coauthorship between different principal investigators varies considerably from CRP to CRP. Joint output is generally disappointing except for FREDI, MECOMECON and MOCA but several reports mention that collaborations continue (e.g. EpiCOL) with several joint manuscripts in preparation. Therefore, the full success of individual CRPs has yet to be achieved, probably within the next couple of years.

This collaborative programme has enforced research groups from various European countries to be connected. Some CRPs such as A. alpina, MECOMECON or DEEP\_C have successfully established many resources both in informatics and experiments for the future which will be highly beneficial when shared within communities. For instance, MECOMECON developed a tool (automated classifier) that could be used by all microbial CRPs (MECOMECON, FREDI, MOCA, DEEP\_C). STRESSFLEA also strengthened the European position in the field and led to many joint publications, communications and posters. Their genomic platform will be applied to study adaptive responses of natural populations to climate change. The data collected from biological archives will be used in predictive modelling to forecast future adaptive responses to environmental stress. The outcome of this research will have immediate application in the design of environmental policies and conservation plans to preserve biodiversity which is of high priority in the EU agenda. The DEEP\_C team has also been working very efficiently in tight collaboration. Huge amounts of material and genomic information have been shared between all partners, including Associated Partners (APs). The DEEP\_C team has already published 5 joint articles and more publications will come.

The list of main highlights, achievements and contribution to knowledge is impressive:

- Isolation and characterisation of natural isolates of model organisms and their associated microorganisms (*C. elegans* for NEMADAPT)
- Generation of novel RIL populations for fine-scale QTL mapping of naturally variable traits
- Development of new tool kits or environmental genomic research (for instance for freshwater bacteria in FREDI)
- Development of new genomics and transcriptomics tools for ecological model systems (STRESSFLEA)
- Development of a bioinformatics analysis pipeline suited for metagenomics datasets from remote environments with few matches to known genomes (MOCA)
- Share of huge amounts of biological material and genomics information (e.g. DEEP C)
- Collection of diverse arrays of material (for instance with a latitudinal gradient for A. alpina) for sequencing and phenotypic analysis
- Making methylome data available (STRESSFLEA)
- Development of protocols and bioinformatics for next-generation methods of epigenotyping

#### **Programme integration**

#### Contribution of the CRPs to the programme and integration of the CRPs within the programme

The weakness of interactions between the different CRPs is probably related to the highly diverse topics of the 8 CRPs, reducing the scientific relevance, interest and motivation for cross-CRP interaction. However, the CRPs did make an effort to integrate which was obvious at the final conference in May 2013. Interactions at previous international meetings between some CRPs were also encouraging.

The 4 microbial CRPs (MECOMECON, MOCA, FREDI and DEEP\_C) were extremely well integrated thanks to the common scientific topic and the intellectual overlap although DEEP\_C complained that there was little possible integration. Interactions between these 4 CRPs have been strong with common trainings and participation to symposia, sessions in congresses or workshops. Interactions were clearly less obvious for other CRPs that have worked in a more isolated fashion, e.g. FREDI representing the freshwater microbial module, who considered the interactions with other CRPs low.

Nonetheless, a few bilateral approaches were tentatively established between CRPs: NEMADAPT and STRESSFLEA with a focus on adaptation in 2 invertebrate models (worm and flea); A. alpina and EpiCol as the 2 "plant CRPs"; STRESSFLEA and EpiCol interacted in 2011 at the 13<sup>th</sup> Congress of the ESEB in Tübingen (DE) and in 2013 at the 7<sup>th</sup> International Symposium on Eco-Evolutionary Dynamics in Leuven (BE). Interestingly, several CRPs mention recent interactions (FREDI, MOCA and STRESSFLEA) showing the potential for further exchanges.

An earlier joint meeting rather that the final cross-CRP conference that took place only in May 2013 could have enabled a better integration between all CRPs (MMN: note that previous attempts of such programme-wide events had failed).

# Added value of the programme for the CRPs (have the CRPs benefited from being part of the programme?)

The combination of CRPs is amongst the top set of networks integrating ecological and evolutionary functional genomics across a wide diversity of habitats and taxonomic and geographical scales. All groups have transitioned to the routine use of next-generation sequencing data in their research, which was facilitated by the shared technical expertise of collaborating groups within the programme. Some more "isolated" CRPs (e.g. FREDI) explain their uniqueness in the programme but acknowledge the overall fit and complementarity to EUROCORES through international meetings and networks.

The major added value of EuroEEFG resided in the following aspects:

- reinforcement of European researchers' consortia by:
  - o achieving a critical mass,
  - o giving the opportunity to combine complementary expertise within a CRP (ecology, molecular biology, bioinformatics etc.) (A. alpina)
  - o increasing their visibility and competitor power versus US-based consortia (NEMADAPT, STRESSFLEA)
  - o having access to a common pool of samples and new methods (collection, analysis and treatment of large datasets, analytical methods, high-throughput sequencing, data mining...)
- for STRESSFLEA, the CRP facilitated its connection to the broader Daphnia consortium offering new possibilities for collaborations in particular in the field of bioinformatics
- for EpiCol, the CRP allowed the first cross-European collaborative project on ecological and evolutionary plant epigenetics
- the programme offered unexpected opportunities for considering applications in the area of ecological genetics and genomics (A. alpina)
- knowledge transfer, in particular within the field of bioinformatics, between the principal investigators (MOCA)
- possibilities for studies across latitudinal gradients and transplant experiments (A. alpina)
- CRPs can be the basis of larger EU-wide research networks for EU funding (NEMADAPT application, however unsuccessful up to now), new bi- or tri-lateral programmes (FREDI), Marie-Curie post-doctoral proposals (FREDI)

#### Networking, training and dissemination

#### Intensity of networking, training and dissemination activities and the level of participation of the various CRPs

All CRPs took the need for networking, training and dissemination very seriously as they are key to the success of the programme. Therefore, this aspect was globally good although unequal between CRPs and even low in some cases. Networking was privileged within the CRPs during the first part of the programme, and across CRPs only at the end which is quite classical in EUROCORES programmes.

The most important networking activities within the EuroEEFG programme were:

- the EuroEEFG round table during the ISME14 Symposium in Copenhagen in August 2012
- the final EuroEEFG programme-wide conference "Frontiers in Ecological and Evolutionary Genomics" in Noordwijkerhout, the Netherlands, on 26-30 May 2013. This conference was very successful, and both the scientific content and the networking opportunities will have impacts on future research.

The following networking and dissemination aspects should be highlighted:

- intensive exchange of methods, protocols and biological material
- organisation of specialised courses: geostatistics (MECOMECON), summer course on environmental genomics (STRESSFLEA), microbial genome annotation (organised by MECOMECON with participation of members from 5 CRPs: MECOMECON, FREDI, DEEP\_C, MOCA and STRESSFLEA)

- workshops, e.g. "Traits-based approaches in microbial ecology" (organised by MECOMECON with participation of members from the same 5 CRPs as above)
- presentations and participation in international meetings
- beneficial effects on Master's students (MOCA)
- visibility and dissemination favoured by the ESF website and brochures (MECOMECON)
- public outreach original initiatives, such as nematode attraction in the MicroZoo in Artis (Amsterdam) (NEMADAPT), radio appearance for several CRPs.
  - Usefulness and impact of the networking, training and dissemination activities on the field of research and the programme goals

Networking activities are important to share skills, information, opinions and concepts. Inter-disciplinary communication between members working in different fields as it is the case in EuroEEFG is essential to perform and expand research. EuroEEFG has yielded well-established networks with evidence for additional funding arising directly from the programme. The students and post-docs that had been part of the training during the final conference in May 2013 have clearly benefited from collaborations and exposure to the new techniques. Several trainees who had taken part in exchanges and training courses within individual CRPs or the whole programme gave positive feedback about these aspects.

#### General comments and other feedback

#### How well has the programme achieved its potential?

Overall, the programme has led to the establishment of highly productive networks of international research teams, leading in their respective fields and producing work that could not have been achieved on a country-by-country basis. EuroEEFG can certainly be considered as positive within the CRPs, even though some CRPs achieved their potential better than others. In the future, more intra-CRP joint publications should be encouraged but networking takes time especially in "omics" programmes. Several CRPs (e.g. EpiCol, MOCA) continue their collaborative work which is positive but also means that a final assessment of the CRP achievements is not yet possible. Inter-CRP interactions are clearly weaker but interactions cannot be "forced" if not scientifically meaningful.

#### Any other comments in relation to the facilitation and promotion of collaborative research?

EUROCORES programmes reinforce fundamental hypothesis-driven research, free from societal and economic aspects, which clearly has to be maintained in future programmes. The low level of bureaucracy mentioned by MECOMECON also clearly needs to be maintained. The scheme provides a unique platform for European integration, knowledge transfer and skill enhancement, while tackling common goals. Whilst 'buy-in' to this scheme is limited by the choices of national funding agencies and budgets, the scheme does work well with considerable success. The critical and important opportunity for 'novel collaborations' being possible through EUROCORES is frequently cited. The full impact of EuroEEFG will only be realised within the next 3-5 years since many projects have yet to be completed and results published.

On the other hand, the following difficulties impaired the achievement of objectives in some CRPs:

- change of Project Leader (EpiCOL)
- lack of funding for Associated Partners to participate in networking activities although this is in compliance with EUROCORES guidelines
- dependence on national agencies' decisions and their suboptimal funding
- start at different time schedules due to difficulties in recruiting staff or delayed funding decisions

## Potential follow-up activities and future perspectives

EuroEEFG was the first large international project dedicated to the subject of ecological and evolutionary epigenetics. Through dissemination of research outputs at international conferences, workshops and publications, results, ideas and questions have been successfully spread and thereby contributed to the development of ecological and evolutionary epigenetics in Europe. A (still developing) side-product of EuroEEFG is the development of protocols and bioinformatics for next-generation methods of epigenotyping which will be very useful in the future.