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RESEARCH CONFERENCES

ESF-EMBO Symposium

System Biology of Drosophila Developments

Dom Polonii, Pultusk (PL) 22-25 May 2012

Chair: **Johannes Jaeger,** Centre for Genomic Regulation (CRG), Barcelona Co-Chair: **Eileen Furlong,** Genome Biology Unit, EMBL, Heidelberg

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Highlights & Scientific Report

Conference Highlights

Please provide a brief summary of the conference and its highlights in non-specialist terms (especially for highly technical subjects) for communication and publicity purposes. (ca. 400-500 words)

Eileen Furlong (EMBL Heidelberg) and Yogi Jaeger (CRG Barcelona) organized the ESF/EMBO Conference on 'The Systems Biology of *Drosophila* Development', which took place from May 22nd to 24th at the scenic location of Polonia Castle in Pułtusk, Poland.

The meeting brought together an eclectic mix of developmental geneticists, mathematical modelers, and 'omicists' working on *Drosophila* development, which is a paradigm model for the emerging science of systems biology. The well-studied processes of axis and pattern formation, morpho- and organogenesis in this species provide a test bed for new approaches, and allow us to gain insights into the structure, function, and evolution of developmental processes which are of fundamental importance to modern biology in general.

The small format allowed early-stage researchers to present their work, and to interact with the invited speakers in an informal manner. Contributions by pioneers in the field such as John Reinitz (Chicago), and Bas van Steensel (NKI Amsterdam) and a range of exciting newcomers were complemented by a thought-provoking historical lecture by Alfonso Martinez-Arias (Cambridge). Polish hospitality was excellent and contributed a great deal to the success of the conference. The conference dinner and bonfire at the river will surely be remembered by all of us for a long time to come!

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Scientific Report

Executive Summary

(2 pages max)

The ESF/EMBO Conference on 'The Systems Biology of *Drosophila* Development' was organised by Eileen Furlong (EMBL Heidelberg) and Yogi Jaeger (CRG Barcelona). It took place from May 22nd to 24th at Polonia Castle in Pułtusk, Poland. The meeting brought together developmental geneticists, mathematical modellers, and 'omicists' working on the development of the fruit fly *Drosophila melanogaster*. The small format allowed early-stage researchers to present their work, and to interact with the invited speakers in an informal manner.

The topics of conference talks ranged from genomic approaches to the study of chromatin and transcription factor binding, to modelling of transcriptional regulation, gene networks, and morphogenesis during *Drosophila* embryogenesis. Contributions by pioneers in the field such as John Reinitz (Chicago), Denis Thieffry (ENS, Paris), Steve Russell (Univ of Cambridge), Bas van Steensel (NKI Amsterdam) and a range of exciting newcomers were complemented by a thought-provoking historical evening lecture by Prof. Alfonso Martinez-Arias (Cambridge).

Prof. Martinez-Arias emphasised the role of tissue-level processes, which complement pattern formation based on gene regulatory networks. His talk focused on the role of stochasticity and cell sorting in development, and provided a complementary perspective to the genetic and genomic approaches presented by most other speakers.

Genomic contributions to the conference focused on the identification of transcription factor and chromatin binding events. Highlights include the systematic discovery and characterization of different types of chromatin in the *Drosophila* genome (Bas van Steensel), genome-wide mapping of dynamic transcription factor binding and cis-regulatory elements (Alex Stark, Uwe Ohler, Stein Aerts), insights into the context-dependence of regulatory element architecture (Eileen Furlong), and mapping of genomic variation in a population-genetic context (Bart Deplancke).

The cutting edge of image bioinformatics was represented by Pavel Tomancak (presenting his 4Dquantification of gene expression patterns in live embryos) and Alistair Boettiger (who demonstrated imaging and quantification of single mRNA-transcripts in the embryo).

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ESF-UB-08269 Pharmacogenetics and Pharmacogenomics Scientific Report First steps towards quantitative models of eukaryotic transcriptional regulation have been taken over the past few years. Many of the contributors to this new field of research were present at the conference. John Reinitz and David Arnosti presented detailed models of regulatory elements in the context of early *Drosophila* development. Saurabh Since is using such models for genomewide detection of regulatory sequences with pattern-forming potential.

The quantitative study of pattern formation has always been an important focus of the *Drosophila* systems biology community. This field is rapidly diversifying. Models of axis formation and patterning in the early embryo (Angelike Stathoupoulos, John Reinitz, Johannes Jaeger), are now complemented by quantitative studies of later developmental processes such as heart development (Denis Thieffry, Eileen Furlong), or wing (Sven Bergmann) and eye development (Fernando Casares).

Notably, we had several Polish scientists presenting at the conference (Krzysztof Jagla, Bartosz Wilczynski, among others) and many participants from Eastern European countries, which is an encouraging sign for the development of *Drosophila* research in that region.

Scientific Content of the Conference

Summary of the conference sessions focusing on the scientific highlights
Assessment of the results and their potential impact on future research or applications

Due to the reduced size of this conference, we chose an integrated workshop format, rather than separate sessions. Summaries of conference topics can be found in the previous section. A detailed program of the conference with titles of individual speakers can be found at: <u>http://www.esf.org/activities/esf-conferences/details/2012/confdetail394/394-preliminary-programme.html</u>.

The conference resulted in many new contacts between conference participants both at the PI and junior researcher level. These will no doubt lead to exciting new collaborations in the future. See the next session for more details.

As is usual for such conferences, the impact on future impact is hard to assess. If the course of basic science can be predited, it is usually an indication of a stagnant field. Since our field is very dynamic, and this conference was exactly intended to foster unexpected new synergies, it is not a useful exercise to predict future impact.

(1 page min.)

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Forward Look

Assessment of the results

- Contribution to the future direction of the field - identification of issues in the 5-10 years & timeframe

Identification of emerging topics

The conference was generally perceived as a great success, both by the organizers and the participants. The small format allowed both senior and junior researchers to interact intensively in a relaxed and informal way. Many new collaborations were initiated, and old ones reinforced. Throughout the conference, during the poster session and after contributed sessions, junior researchers (many from Eastern European countries) were given the opportunity to discuss their work with leading figures in the field.

In the field of systems biology, it is especially important to co-ordinate the interests and requirements of experimental biologists generating high-throughput quantitative data, and the theoreticians who use them to build their models. Often, the datasets created by the former and not tailored to the need of the latter, and the models of the latter are not suited for analyzing the data of the former, nor to propose new experiments and questions for experimental biologists to investigate. Conferences such as this one greatly help go overcome such issues.

Key topics to be addressed over the next 5–10 years include:

- High-throughput data are becoming available on genome-wide transcription factor binding, chromatin states, DNA modification, and (spatial) gene expression dynamics. How can such large datasets be analyzed to gain specific biological insights? In other words, how can such datasets be reconciled with functional investigations at the single-gene, or small gene network model?
- On the other hand, how can small-scale models of transcriptional regulation and gene regulation be integrated across developmental processes and stages?
- A central question for systems biology modeling of complex organisms is the right choice of level for the model. This depends on the biological question to be asked. Do we need to consider molecular details of *cis*-regulation? Do we need to consider tissue-level processes? Etc. We need a more rigorous understanding on how to chose and move between these levels of description.

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Pharmacogenetics and Pharmacogenomics

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• Similarly, a more rigorous understanding of which modeling formalism is most useful in a given biological context is urgently required.

These conceptual questions cannot simply be addressed by gathering more data. Conceptual discussions among members of the community such as those held at this conference are essential for further progress in the field.

Is there a need for a foresight-type initiative?

Two of the conference participants (Fernando Casares, Pavel Tomancak) have volunteered to look into possibilities for organizing a follow-up conference in two to thee years time.

Business Meeting Outcomes

Election of the Organising Committee of the next conference

Identified Topics

Next Steps

See above.

Atmosphere and Infrastructure

• The reaction of the participants to the location and the organization, including networking, and any other relevant comments

Feedback from participants on the location was overwhelmingly positive. Polonia castle is an ideal place to hold such conferences. The location is gorgeous, the infrastructure is excellent, and the service was absolutely flawless.

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This report will be submitted to the relevant ESF Standing Committees for review.

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Date & Author:

Oct 23, 2012, Johannes Jaeger, Barcelona