Project Acronym: MuG

Project title: Multi-Scale Complex Genomics (MuG)

Call: H2020-EINFRA-2015-1

Topic: EINFRA-9-2015

Project Number: 676556

Project Coordinator: Institute for Research in Biomedicine (IRB Barcelona)

Project start date: 1/11/2015

Duration: 36 months

Deliverable 2.4: Monitoring of the Plan for the Dissemination and Use of Knowledge

Lead beneficiary: Institute for Research in Biomedicine (IRB Barcelona)

Dissemination level: PUBLIC

Due date: 30/04/2017

Actual submission date: 29/04/2017

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 676556.

Document history

Version	Author(s)	Partner	Date	Comments
0.1	Anna Montras	IRB Barcelona	24/04/2017	Draft for internal revision
0.2	Mike Goodstadt, Marc Martí-Renom	CNAG-CRG	27/04/2017	Minor additions/corrections to training and dissemination events list
0.3	Josep Ll. Gelpí	BSC	28/04/2017	Corrections and additions in dissemination events list
1.0	Anna Montras		28/04/2017	Approved by Supervisory Board.

Table of contents

Glossary

CoE: Center of Excellence

DMP: Data Management Plan

KPI: Key Performance Indicators

SAB: Scientific Advisory Board

VRE: Virtual Research Environment

Executive summary

This deliverable is a follow-up to D2.3 and contains a review of the status of the dissemination and training activities roadmap. The activities completed during the first 18 months of the project and the results achieved in terms of impact and community engagement are analyzed. A general overview on the activities initiated related to use of knowledge (IPR strategy, ownership, exploitation) is presented in this document, although sustainability of the MuG services under development and the potential routes to exploitation are discussed thoroughly in D2.6.

Training and dissemination activities completed between M1 and M18 are presented and discussed extensively, defining the purpose, contents and impact for MuG. Dissemination activities undertaken so far have addressed most target audiences identified in D2.3 (computer scientists, bioinformaticians, experimental biologists). Training activities and, most importantly, practical training courses on MuG tools are key towards user engagement. Hands-on training courses on MuG tools have proved very successful and will be key to progressively increase the VRE user base.

The combination of well-received training courses with a high-presence of MuG at some key community events are the key tools to enhance user uptake. Past and future essential events are identified. A proper engagement strategy, combined with the effort in fostering collaboration are key to guarantee the long-term sustainability of the MuG VRE and its strength as a community.

Based on the results of activities undertaken until April 2017, a detailed revision of KPIs is undertaken. Where necessary, new and more quantifiable KPIs and metrics have been defined. The conclusion from this document is a set of improvement measures based on M1-M18 results to enhance project performance.

1 INTRODUCTION

The present report provides an update on the implementation of the dissemination and training action plan outlined in D2.3. A critical review of the activities undertaken during the first 18 months is undertaken, analyzing the impact of different activities on community engagement. The results will be used to extract potential means of improvement.

Activities performed by MuG partners between M1-M18 have addressed all target audiences (as identified in D2.3):

(i) The research community – through numerous invited conferences of MuG PIs and team members in high-profile scientific events worldwide

(ii) End users of the VRE (mostly academia users have been targeted at this early stage), most efficiently through training courses Interaction with industry will be pursued more intensively once a stable version of the VRE is available and data become available for exploitation. To foster links with industry and pave the way towards collaboration, some tools more in the radar of industry are in place (e.g. LinkedIn group, Twitter, youtube channel, etc.)

(iii) The general public – thanks to selected press releases related to, e.g. publications from our pilot projects, interviews to project PIs, etc. and through social media.

(iv) Research infrastructures or e-infrastructure projects – through joint initiatives or collaboration in advertising.

The impact made by the implemented activities is evaluated through the analysis of the Key Performance Indicators. Based on the analysis of KPIs, the key areas in which the messages need to be enhanced have been identified.

2 ENGAGEMENT STRATEGY

Providing a set of services that responds to the actual needs of the target community is a key objective of the MuG Virtual Research Environment. The service portfolio developed by the project has to be strictly driven by users, hence the importance of characterising the composition and size of our user base from the early stages of the project.

In order to guarantee the uptake of the developed services by the community, it is essential that a thorough assessment of the community composition is carried out throughout the project, progressively involving users and other stakeholders from different ends and allowing them to interact with the developed services and user interfaces.

The key pillars of the engagement strategy are dissemination and training activities:

Training:

- workshops organized by MuG: for developers / for end users
- workshops/courses organized by partners on the use of individual tools integrated in the VRE
- Joint training activities –
    - with other projects (e.g. BioExcel CoE)
    - PATC courses organized by BSC

Dissemination (details in section 4)

- Participation in high-profile events attended by the 3D/4D genomics community
- Peer-reviewed scientific publications
- Press releases on results of interest to a wider audience
- Social media and e-mailing campaigns (e.g. Newsletters)
- Industry oriented events (trade fairs, sectorial SME meetings, innovation forums, etc.)

3 TRAINING

3.1 Objectives and targets

Training is a key tool to tackle one of the main objectives of the project: the nucleation of the 3D/4D genomics community with the objective of bridging the gap with the HPC and big data world. Training activities also contribute to disseminate MuG and will enrich MuG services through attendees' feedback.

Training courses on the MuG tools become an essential engagement tool, as they allow a close interaction between developers and external users, progressively increasing the interest community. In order to define a hybrid 3D/4D genomics-HPC community, working closely with the key initiatives in both fields is essential, as well as a proper dissemination and training strategy.

The common driving point of all MuG training activities is that they address **computational aspects of 3D/4D genomics**. These include (i) activities performed by MuG beneficiaries (BSC, CNAG-CRG, IRB Barcelona, EMBL-EBI) and (ii) specific activities designed to train the users on the use of the integrated features of the VRE.

Different levels of training are foreseen. During the first year training focused in individual tools, making our potential user community aware of the benefits that will be offered by the MuG VRE in terms of ease of use thanks to the integrated tools and customized workflows. In M18, a first Beta version of the VRE integrating key tools to showcase the multi-scale concept of the VRE, has been successfully tested with participants with a real biological case-study.

Joint activities with other EU e-infras in terms of training are also being secured. MuG will participate in the BioExcel CoE webinar series with a training session on Nucleic Acids Flexibility, one of the services integrated in the VRE. Integration of MuG with ELIXIR-ES training activities will also be explored at a later stage.

3.2 List of training events

The most relevant practical training activities undertaken during the first 18 months of the project are summarized in Table 1.

In total, an **audience of 35** people have attended events directly funded/organized by MuG, and **over 150** have participated in training events organized by MuG partners involving MuG tools, methodology and technology.

Table 1: List of completed training events

DATE	Title	LOCATION	Participant	Organizer	Audience size / Feedback/Notes
04/02/2016	PATC Course: Programming Distributed Computing Platforms with COMPSs	Barcelona, Spain	BSC	PRACE, BSC	25 9/10 satisfactory answers in survey
10-14/10/2016	3DAROC16: 3C-based data analysis and 3D reconstruction of chromatin folding	Oeiras, Portugal	IRB, CNAG-CRG	GTPB, CNAG-CRG, **MuG**	14 70% satisfactory answers (MuG questions)
14/03/2016	PATC Course. Simulation Environments for Life Sciences	Barcelona, Spain	IRB, BSC	PRACE, BSC	26
27/09/2016	Workshop: Design your e-infrastructure	Krakow, Poland	IRB, BSC	EGI.GEANT,EUDAT, OpenAIRE	(MuG discussed as a case study)
02/02/2017	PATC: Programming Distributed Computing Platforms with COMPSs	Barcelona, Spain	BSC	PRACE, BSC	28
14/03/2017	PATC Course. Simulation Environments for Life Sciences	Barcelona, Spain	IRB, BSC	PRACE, BSC	30
3-7/04/2017	Chromosomal conformation	Barcelona, Spain	CNAG-CRG	CNAG-CRG	16
10-11/04/2017	Multi-scale study of 3D Chromatin structure	Hinxton, UK	All	**MuG**, EMBL-EBI	18

The two events that were partially funded by MuG and that included full-sessions describing the VRE features are described in detail in section 3.3 and 3.4. In addition to hands-on training described in the previous table, most seminars given by partners in different workshops are also considered to have a training component, especially talks given to audiences composed by undergraduates or PhD students as part of their training.

Table 2 includes some of the training events foreseen for the rest of 2017.

Table 2: List of future training events already confirmed or under preparation

DATE	TITLE	LOCATION	Participant/Instructor	ORGANIZER	AUDIENCE SIZE
14-17/05/2017	Tutorial at CCGRID2017: Programming distributed platforms with PyCOMPSs	Madrid, Spain	BSC (Rosa Badia)	ARCOS/UC3M, IEEE	tbc
28/08-1/09/2017	Tutorial at EURO-PAR 2017 – 23rd Internaltional European Conference on Parallel and distributed computing	Santiago de Compostela, Spain	BSC (Rosa Badia)	Univ. Santiago de Compostela, CiTIUS	tbc
9/07/2017	Tutorial at ACACES 2017 – 13th International Summer School on Advanced Computer Architecture and Compilation for High-	Fiuggi, Italy	BSC (Rosa Badia)	HiPEAC Network of Excellence	tbc

	Performance and Embedded systems				
15/11/2017 (tbc)	Multi-scale study of 3D Chromatin structure (co-localized with Barcelona BioMed conference)	Barcelona, Spain	All	MuG	tbc
tbc	BioExcel Webinar Series – Nucleic Acids Flexibility analysis and Tools.	n.a.	UNOT (Marco Pasi – tbc)	BioExcel CoE	tbc
tbc	3DAROC17: 3C-based data analysis and 3D reconstruction of chromatin folding	Oeiras, Portugal	CNAG-CRG	GTPB, CNAG-CRG	tbc

3.3 3DAROC16: 3C-based data analysis and 3D reconstruction of chromatin folding

3DAROC (http://gtpb.igc.gulbenkian.pt/bicourses/3DAROC16) is an annual course organized by the developers of TADbit analysis software and TADkit 3D genome visualizer (Marc Martí-Renom's team at CNAG-CRG) in collaboration with Instituto Gulbenkian de Ciência (Portugal) as part of the **Gulbenkian Training Programme in Bioinformatics (GTPB)**. It verses around the analysis of experimental data generated by 3C-based methods used to study genome organization in the nucleus. Participants are instructed on the use of TADbit for 3C analysis. Alternative software is also discussed.

The 2016 edition of 3DAROC took place between **10th and 14th October 2016** and incorporated a presentation by MuG co-PI Marc Marti-Renom on MuG's multi-scale multi-resolution concept and objectives, in addition to the usual hands-on sessions on MuG tools TADbit/TADkit (CNAG-CRG) and additional sessions on MD simulation tools (IRB Barcelona), all of which are at present (M18) already integrated in the first Beta version of the VRE.

Fact sheet:

- Type of training event: Hands-on practical
- Course Duration: 5 days
- Number of participants: 14
- Number of instructors: 5

3.3.1 MuG contribution and benefits

The MuG VRE concept was introduced to participants, explaining the benefits of the forthcoming integration of the TADbit/TADkit tool suite in the VRE. In addition, the multi-scale concept of MuG was introduced with an additional 1-day session versing around the need to bridge the gap between multi-resolution data at different scales. To showcase the need to jump across scales and the innovations

MuG is developing to help experimental scientists, a final 1-day session was added. In addition to introducing participants to the MuG concept, the multi-resolution issue was addressed through training sessions on (i) coarse-grained DNA and chromatin dynamics and (ii) Nucleosome position and dynamics. The last session was led by members of Modesto Orozco's Molecular Modelling and Bioinformatics group at IRB Barcelona (MuG coordinator). The course was a unique opportunity for MuG to introduce researchers working on the study of the chromatin folding to the MuG VRE concept and its benefits, from the single point of access to tools and information of relevance to the 3D/4D genomics community to community-tailored, ready-to-use workflows for simulation and structural analysis across different levels of resolution.

For MuG, the event served the double function of dissemination (introducing the MuG concept to future users) and training (instructing future users of the VRE on the use of analysis tools later integrated in the VRE).

3.3.2 Course description

3C-based methods, such as Hi-C, produce a huge amount of raw data as pairs of DNA reads that are in close spatial proximity in the cell nucleus. Overall, those interaction matrices have been used to study how the genome folds within the nucleus, which is one of the most fascinating problems in modern biology. The rigorous analysis of those paired-reads using computational tools has been essential to fully exploit the experimental technique, and to study how the genome is folded in the space. Currently, there is a clear expansion on the wealth of data on genome structure with the availability of many datasets of Hi-C experiments down to 1Kb resolution (see for example: http://hic.umassmed.edu/welcome/welcome.php; http://promoter.bx.psu.edu/hi-c/view.php or http://www.aidenlab.org/data.html). In this course, participants will learn to use TADbit, a software designed and developed to manage all dimensionalities of the Hi-C data:

1D - Map paired-end sequences to generate Hi-C interaction matrices
2D - Normalize matrices and identify constitutive domains (TADs, compartments)
3D - Generate populations of structures which satisfy the Hi-C interaction matrices
4D - Compare samples at different time points

Participants can bring- specific biological questions and/or their own 3C-based data to analyze during the course. At the end of the course, participants will be familiar with the TADbit software and will be able to fully analyze Hi-C data. While TADbit software is central in this course, alternative software will be discussed for each part of the analysis.

The **full programme** of the course is available in Annex I.

3.3.3 Feedback

A satisfaction survey focusing specifically on the MuG-related features of the course was distributed to participants (see Annex II). Results of satisfaction survey clearly indicated an interest in attending future MuG-specific trainings (50% attendees (6/14) answered the survey; 60% respondents expressed their interest in further MuG-related training courses.

3.3.4 Lessons learned

This gave a clear message on the need to enhance the benefits of the VRE. This will be possible through the possibility to perform actual **hands-on training on the VRE** once tools are integrated but it is also

considered important to select real biological examples that serve as case studies to feature the whole range of scales and resolutions to participants.

This was taken into account and the above recommendations from instructors were implemented in the first MuG VRE hands-on training in April 2017 (see section 3.4).

3.4 Multi-scale study of 3D Chromatin structure

This course represents the kick-off of hands-on training activities on the MuG VRE and fulfills M18 Milestone MS8 (First Training Workshop)

Fact sheet:

- Type of training event: Hands-on practical
- Course Duration: 2 days
- Number of participants: 18
- Number of instructors: 8

3.4.1 Course purpose, preparation and advertising

The course is one of the 2 Training workshops specifically defined as project Milestones in Annex I of the Description of Action. The course was organized and hosted by EMBL-EBI in their Hinxton facilities.

Different possible formats and contents were evaluated for the first training activity that would focus entirely in MuG tools. Although the availability of an operational version of the VRE was not foreseen until M24, following the advice received from the SAB in the all-hands meeting (November 2016) it became clear that user engagement capacity was very much dependent on our ability to showcase the potential of the VRE to tackle real biological problems as early as possible. Taking the advice from the SAB, the consortium focused on defining a real use-case that could be tackled with a limited number of tools that would be integrated in a Beta version of the VRE. In spite of the strict deadline, the advantages of this option justifies the potential risks that were taken. Only through the tight collaboration between infrastructure developers, tools developers and pilot projects was it possible to offer a hands-on course that allowed delegates to work hands-on with the VRE. The course feedback provides us with very useful insight from external Beta testers.

The workshop was advertised on EMBL-EBI's training portal (https//www.ebi.ac.uk/training) allowing us to reach a broad audience thanks to the high outreach capacity of the EMBL-EBI Training portal. EMBL's course and conference programme welcomed nearly 6500 scientists in 2015 from 90 different countries in 20 conferences and 56 courses.[1]. Additional advertising was made through social media,

[1]EMBL anual report 2015:
https://www.embl.de/aboutus/communication_outreach/publications/annual_report/annual-report-2015.pdf

ELIXIR's training portal and BioExcel CoE website, taking advantage of partner collaborations in both initiatives, as well as MuG's own website and IRB Barcelona website.

3.4.2 Course description

Overview:

This workshop will introduce delegates to the Virtual Research Environment (VRE), created by the Multi-scale complex Genomics project (MuG), to facilitate the analysis and interpretation of the genome. This environment integrates a range of data from genome annotation to 3D folding and DNA flexibility. Recent studies have shown the role that genome organisation can play in gene expression and the VRE has been designed to provide a way of analysing such data. This course will explore how to use the MuG VRE through two case studies; cohesin role in genome organisation in yeast and the proto-oncogene DNA-binding transcription factor Ets1. Both will show how to analyse chromatin structure, model DNA flexibility and protein-DNA interactions.

Audience

The workshop is aimed at both experimental (bench-based) researchers and bioinformaticians; additionally it may be of interest to tool developers who wish to integrate their tools into the VRE.
Participants should have an undergraduate understanding of biology AND have knowledge of genome organisation and the role it can play within the nucleus.

Syllabus, tools and resources

- During this workshop you will learn about:
- The Multi-scale complex Genomics project (MuG)
- The MuG Virtual Research Environment (VRE)
- Nucleosome dynamics
- Hi-C, interaction matrices and TADs (topologically associating domains)
- Protein-DNA interactions

Outcomes

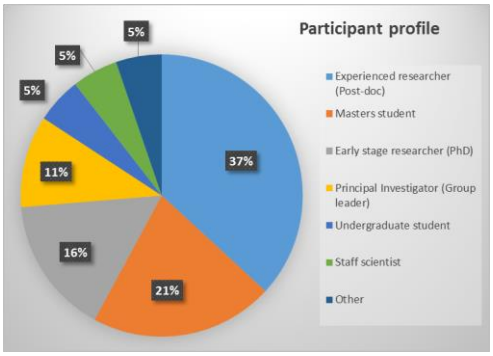
After this workshop you will be able to:

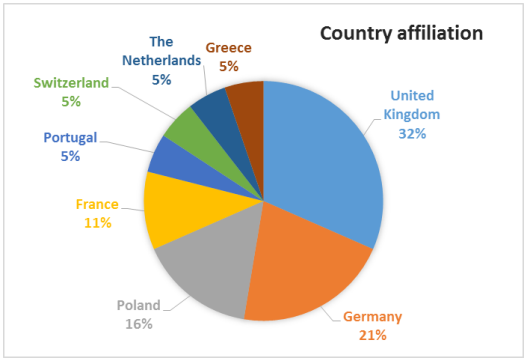
- Navigate the MuG VRE
- Model and analyse a protein-DNA complex at the atomistic scale
- Process Hi-C data sets to produce interaction matrices and TADs
- Apply the MuG VRE to your own data sets

The full course programme is available in Annex I.

3.4.3 Audience description and segmentation

The course draw the attention of a heterogeneous audience both in terms of professional profile/career stage (age implicit) and geographical distribution of participants' country of affiliation (the full list of participants is available in Annex III):





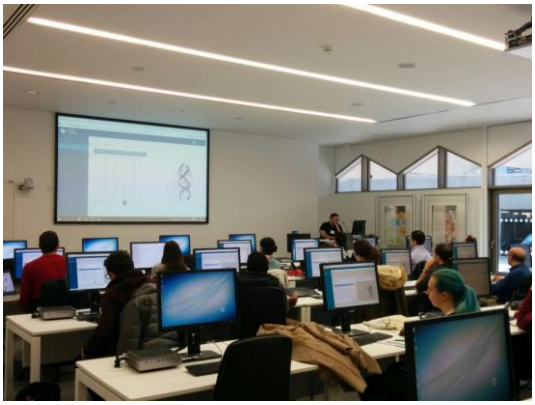
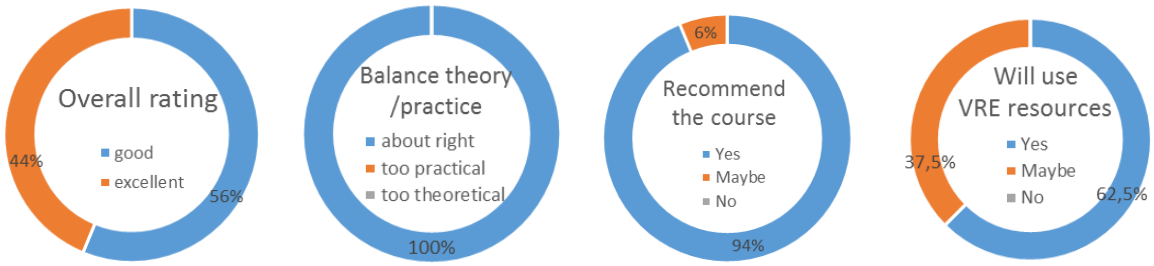


Figure 1: Participants at the course Multi-scale study of 3D Chromatin structure

3.4.4 Feedback analysis

A unified satisfaction survey was prepared in conjunction between EBI and the MuG project (Annex II, section 9.2), in order to compile the feedback from the users on (i) the services and facilities, (ii) the course contents and (iii) the opinion and recommendations of participants about the VRE. The survey that was circulated to participants is shown in Annex II.

The survey was answered by **90%** of the participants (16/18). In addition to rating the course sessions, they provided great feedback and suggestions for the VRE development.



- 16/18 participants answered the survey (90%)
- 16/16 (100%) rated it as good / excellent (average across for EBI courses 2016 was 96%)
- Balance of theoretical and practical content: 100% considered it to be about right.
- To the question “Will you use the resources in future”, 10 and answered Yes and 6 Maybe. Nobody said “No”.
- 15/16 would recommend the course (only 1 “Maybe”)

3.4.5 Lessons learned.

Following the event a meeting was organized with the speakers in order to analyze the feedback and collect a number of recommendations for future courses.

Some recommendations to be taken into account for future editions of MuG VRE training:

- **Candidate segmentation**: Further pre-selection of candidates should be implemented. If career level and/or background expertise are too broad, it is difficult to adapt contents and attend the different participants. Further segmentation and adaptation of the contents to target groups would result in a more positive image of the VRE capabilities for the candidates.
- **Open registration at least 3 months in advance** would facilitate further segmentation and customization of the contents. It would also favor a higher participation of delegates from overseas. We will also try to co-localize the training courses with relevant meetings of the 3D/4D genomics community (e.g. Barcelona BioMed conference on November 2017).
- **Workshop duration:** to address the contents of the tutorial in further depth and better resolve the questions of the participants, a 3-day event might need to be considered for future editions.
- **Further training events:** The success of training activities encourages the MuG consortium to increase the number of originally foreseen training workshops. Collaborations for joint courses with BioExcel CoE , in which EBI, IRB and BSC participate, are already under discussion.
- **The use of the VRE as a training tool for undergraduate students** was proposed by one of the attendees. Teachers are a potentially strong segment not to be underestimated and a unique opportunity for MuG to be adopted massively in a bottom-up manner.

The user's feedback will also be analysed in detail with Pilot Projects and VRE developers in order to define the next steps.

4 MONITORING OF THE DISSEMINATION STRATEGY

4.1 Scientific Publications and data

High impact scientific publications by our partners are a key driver to get potential users to rely on the services offered by the MuG VRE (publication of pilot projects results obtained using the VRE) and for developers to apply for their tools to be offered through MuG. Ten (10) scientific papers have been published by MuG partners in high impact peer-reviewed journals during the first 18 months of the project (

Table 3).

As part of the activities undertaken to ensure the positioning of MuG, and to engage high-profile members of the community up-front, a **position paper** by the MuG consortium on standards in 3D/4D genomics is under preparation.

4.1.1 Consortium publication policy

The internal procedure for the publication of joint results generated in the framework of the MuG project is established in **section 2.1.6.1** of the MuG **Quality Plan (D1.2).** Approval from the consortium is needed for the publication of jointly owned results to ensure that protection and exploitation potential are not jeopardized due to releasing sensitive information (as established in the Grant Agreement – articles 29.1 and 27.1).

4.1.2 H2020 Open Access to publications

In compliance with H2020 **open access policy**, scientific publications are deposited in OpenAIRE-compliant repositories and all partners are committed to publish either in green or golden open access. All partner institutions have agreements with digital repositories that are being used: e.g. Barcelona Tech's institutional repository (UPCommons), the HAL open archive of the Centre pour la Communication scientifique (CCSD), the Digital Repository of the University of Barcelona (UB) or the e-Repositori at Universitat Pompeu Fabra (UPF) have already been used to deposit MuG peer-reviewed publications. A directory of all MuG publications is kept in the project website with links to the repository where the documents can be downloaded.

4.1.3 Open access to data

As a participant in the Open Research Data Pilot, MuG has a DMP in place (Deliverable D4.2) in which the details for data storage in MuG are defined and constraints to comply with IPR policies are established in detail.

Table 3: Publications containing project results (from consortium partners) or making use of MuG VRE features (from MuG community members)

PUBLICATIONS				
Year	**Title**	**Authors**	**Reference**	**DOI**
2016	BIGNASim: a NoSQL database structure and analysis portal for nucleic acids simulation data.	Hospital A, Andrio P, Cugnasco C, Codo L, Becerra Y, Dans PD, Battistini F, Torres J, Goñi R, Orozco M, **Gelpí JL.**	Nucleic Acids Res ;44(D1), D272-8	10.1093/nar/gkv1301
2016	Multiscale Simulation of DNA	Dans PD, Walther J, Gómez H and **Orozco M**	Curr Opin Struct Biol. 37, 29-45	10.1016/j.sbi.2015.11.011
2016	Long-time scale dynamics of the Drew Dickerson Dodecamer	Dans PD, Danilane L, Ivani I, Drsata T, Lankas F, Hospital A, Walter J, Illa R, Battistini F, Gelpi JL, Laverie R and Orozco M	Nucleic Acids Research 44, 4052-66	10.1093/nar/gkw264
2016	Small details matter: the 2'Hydroxyl as a conformational switch in RNA	Darre L, Ivani I, Dans PD, Gómez H, Hospital A and **Orozco M**	J. Am. Chem. Soc. 138 (50), 16355–16363	10.1021/jacs.6b09471
2016	Coordinate redeployment of PRC1 proteins suppresses tumor formation during *Drosophila* development	Loubiere V, Delest A, Thomas A, Bonev B, Schuettengruber B, Sati S, Martinez AM and **Cavalli G**	Nature Genetics 48, 1436–1442	10.1038/ng.3671
2016	Organization and function of the 3D genome	Bonev B and **Cavalli G**	Nature Reviews Genetics 17, 661–678	10.1038/nrg.2016.112
2017	Three-dimensional genome organization and function in *Drosophila*	Schwartz YB and **Cavalli G**	Genetics 205 (1), 5-24	10.1534/genetics.115.185132
2017	The role of unconventional hydrogen bonds in determining BII propensities in B-DNA	Balaceanu A, Pasi M, Dans PD, Hospital A, Lavery R and **Orozco M**	J. Phys. Chem. Lett. 8 (1), 21–28	10.1021/acs.jpclett.6b02451
2017	3D modeling of chromatin structure: is there a way to integrate and reconcile single cell and population experimental data?	Le Dily F, Serra F and **Marti-Renom, M A**	WIREs Computational Molecular Science	(in press)

2017	Stable Polycomb-dependent transgenerational inheritance of chromatin states in *Drosophila*	Ciabrelli F, Comoglio F, Fellous S, Bonev B, Ninova M, Szabo Q, Xuéreb A, klopp Ch, Aravin A, Paro R, Bantignies F and **Cavalli G**	Nature Genetics	10.138/ng.3848

4.2 Scientific conferences and workshops

4.2.1 M1-M18 events

The MuG project partners, and especially their PIs, take part in a great number of events in their respective fields of expertise, providing a unique platform for dissemination of the project worldwide to a large audience.

In summary, MuG has been presented in events targeting the different kinds of audiences identified in our Dissemination strategy:

- Talks/posters at computational biology/bioinformatics conferences
- Posters and talks at 3D genomics conferences /workshops
- Biological data visualization conferences
- EU e-infrastructure events
- Hands-on training on MuG tools and
- Talks at high profile scientific conferences (networking)
- Lectures from MuG partners at workshops/courses

The following map compiles the main dissemination and training events in which MuG partners have contributed between M1-M18. The map is public and will be continuously updated with the new events along the way as they happen. A preview of upcoming 2017 events for which contributions from MuG partners are already confirmed is available in Table 5. The map depicts the broad dissemination potential of the MuG consortium members, which is key for community engagement. Further details on the contributions made by MuG partners in each event can be found in Table 1 and Table 4.

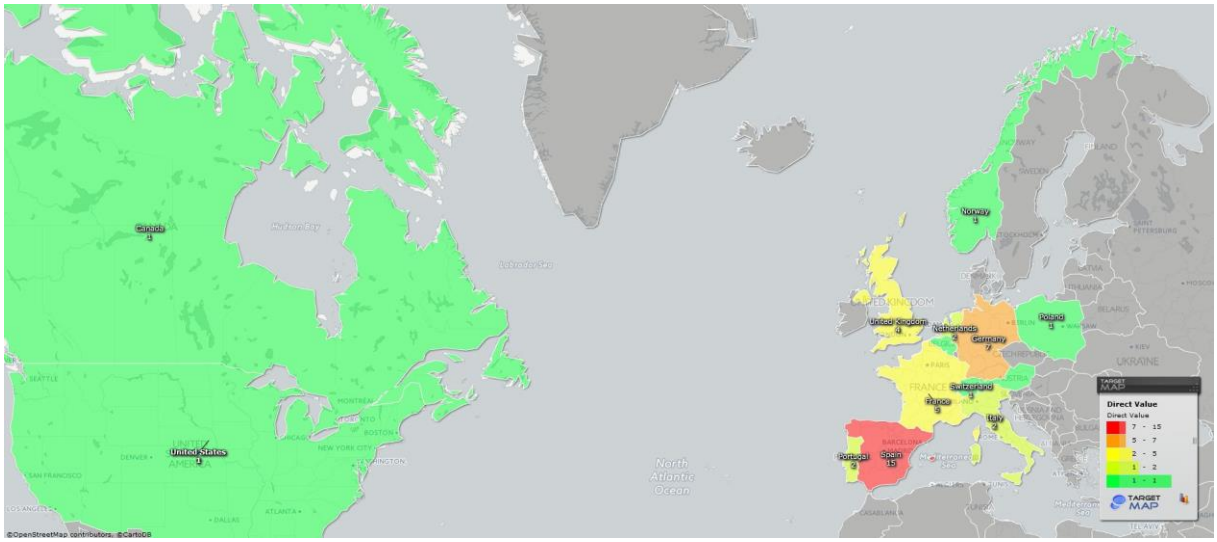


Figure 2: Map with a summary of most important contributions (#events) from the MuG partners between M1 and M18 (updated online: http://www.targetmap.com/viewer.aspx?reportId=52455)

Table 4: Main contributions of the MuG project in workshops and conferences (period 1), targeting the research community users, developers and other relevant stakeholders.

Event title and description	Date	Location	Contributor	Description of contribution
11th e-concertation meeting for European e-infrastructure projects	9/11/2015	European Commission Brussels, Belgium	M. Orozco, A. Montras (IRB Barcelona) J.Ll. Gelpí (BSC)	Participation in discussion groups to explore synergies between e-infra projects.
CECAM Workshop: Models for Protein Dynamics 1976-2016	15/02/2016	CECAM-HQ-EPFL, Lausanne, Switzerland	Modesto Orozco (IRB Barcelona)	"Theoretical investigation of epigenetic 19 signaling"
Ciclo Conferencias Universidad de Murcia	3/3/2016	Facultad de Veterinaria, Universidad de Murcia, Spain	Modesto Orozco (IRB Barcelona)	Invited lecture: "The DNA from the electron to the chromatin"
VizBi2016	9/3/2016	EMBL Heidelberg, Germany.	CNAG-CRG (Mike Goodstadt)	Workshop: "Making Multiscale Make Sense: Seeking Consensus in Biological Visualization"
Joint meeting of the Italian systems biology and epigenetic networks (SYSBIO-EPIGEN joint workshop – Epigenetics and Systems Biology)	11/3/2016	University of Milano – Bicocca (Italy)	Modesto Orozco (IRB)	Invited lecture: "A theoretical view to Epigenetics"
Keystone Symposium: Chromatin and Epigenetics (C2)	20/03/2016	Whistler, British Columbia, Canada	CNRS (Giacomo Cavalli)	"Genome Regulation by Polycomb Proteins, between Epigenetic Inheritance and Dynamic Gene Regulation"
22nd RIMLS PhD Retreat	14/04/2016	Institute for Molecular Life Sciences Veldhoven, NL	Jürgen Walther (IRB Barcelona)	"An in-silico multiscale model of chromatin"
HPC-Leap School on Numerical Analysis and Algorithms at the Exascale	19/4/2016	Aachen, Germany	Modesto Orozco (IRB Barcelona)	Plenary Lecture: "Multi-scale simulation of DNA"
Bioinformatics: Challenges and Opportunities in the Horizon Framework / XIII Symposium on Bioinformatics	10/5/2016	Vera Campus, Universidad Politécnica de Valencia , Spain	IRB (Adam Hospital) BSC (Josep Lluís Gelpí)	Poster presentation: "Multi-scale complex Genomics: exploring the genome beyond sequence"

International Society of Quantum Biology and Pharmacology (ISQBP) president's meeting 2016	19/6/2016	Bergen, Norway	Modesto Orozco (IRB Barcelona)	Invited lecture: "Simulating DNA from the electron to the chromosome"
"Genome Architecture in Space and Time"	20/6/2016	International centre for Theoretical Physics (ICTP) – Trieste (Italy)	Diana Buitrago (IRB Barcelona)	Poster presentation: "Simulation of chromatin structure from epigenetic domains"
Computational Chemistry. Gordon Research Conference – "Theory and Simulation Across Scales in Molecular Science"	24/07/2016	Girona, Spain	Modesto Orozco (IRB Barcelona)	Plenary lecture: "Multiscale simulation of DNA"
EMBL Conference on "Transcription and Chromatin"	27-30/08/2016	Heidelberg, Germany	Giacomo Cavalli (IGH-CNRS)	Talk title: "Polycomb proteins in chromatin regulation and cancer"
III Escuela de Biología Molecular Integrativa. Biología in silico: del modelado molecular a la modelización de sistemas complejos.	29/08/2016	Santander, Spain	Modesto Orozco (IRB Barcelona)	Talk title: "Simulaciones de ácidos nucleicos. Estructura e interacciones"
ECCB 2016: 15th european conference on computational biology	3-7/09/2016	The Hague , The Netherlands	R. Illa (IRB Barcelona), JL Gelpí (BSC)	Poster presentation: "Nucleosome Dynamics portal: a web portal to analyze and visualize Mnase-seq data"
NII Shonan Meeting "Web-based Molecular Graphics"	5/9/2016	Shonan Village Center, Japan	Mike Goodstadt (CNAG-CRG)	Keynote Talk: "This is Not a Noodle: Modeling the Genome in 3D"
MGMS - "Big Data in Biomolecular Systems"	9/9/2016	School of Pharmacy, UCL, London	Charles Laughton (UNOT) Marco Pasi (UNOT)	Talk title: "Multiscale Complex Genomics: the big data challenge"
Dynamics of Genome Structure – ERC Synergy Project "4DGENOME" workshop	22-24/09/2016	Barcelona, Spain	Marc Martí-Renom (CNAG, organizer) Jürgen Walther (IRB Barcelona)	Poster presentation (Jürgen Walther): "A multiscale model of chromatin at bp-level"
Digital Infrastructures for Research 2016	28/09/2016	Krakow, Poland	Modesto Orozco (IRB Barcelona); JL Gelpí (BSC)	Panel (30/09): Virtual research environments for the Open Science Cloud

SFB 716 colloquium - lecture series	20/10/2016	Institute for Computational Physics, Univ. Stuttgart, Germany	Modesto Orozco (IRB Barcelona)	*Invited lecture:* "Simulating DNA from the electron to the chromosome"
Architecture and plasticity of the cell nucleus	29/11/2016	Paris, France	Satish Sati (IGH-CNRS) Giacomo Cavalli (IGH-CNRS)	*Poster presentation:* "Multi-scale complex Genomics: exploring the genome beyond sequence"
Conferences of the Chemistry PhD programme at University of Barcelona	14/12/2016	Barcelona, Spain	Modesto Orozco (IRB Barcelona)	Conference: "Simulating DNA, from the electron to the chromosome"
CECAM Workshop: challenges across large-scale biomolecular and polymer simulations	21-24/02/2017	Vienna, Austria	Modesto Orozco (invited speaker); Antonija Kuzmanic; Jürgen Walther (IRB Barcelona)	Invited talk by Modesto Orozco: "Advances and challenges in the simulation of DNA"
SFB International Symposium on coupling and modification of proteins	27/03/2017	Freiburg, Germany	Giacomo Cavalli (IGH-CNRS)	Talk title: 3D Genome organization and epigenetic regulation by Polycomb proteins
Multiscale Modeling and Experimental Approaches to Genome Organization	2/04/2017	Les Houches, France	Jürgen Walther (IRB Barcelona)	Talk by Jürgen Walther: "Introducing a multiscale model of chromatin at bp-level"
Abcam conference "Chromatin and Epigenetics: From Mechanism to Function	5/04/2017	München, Germany	Giacomo Cavalli (IGH-CNRS)	Talk by Giacomo Cavalli "Polycomb proteins and 3D epigenetic regulation of development"

Table 5: Future Dissemination opportunities already confirmed for 2017

Event title and description	Date	Location	Contributor	Description of contribution
EBDMA 2017 - 1st Workshop on the Integration of Extreme Scale Computing and Big Data Management and Analytics	14/05/2017	Madrid, Spain	Rosa Badia (BSC)	Keynote speaker "Task-based programming model as an alternative for Big Data and Analytics"

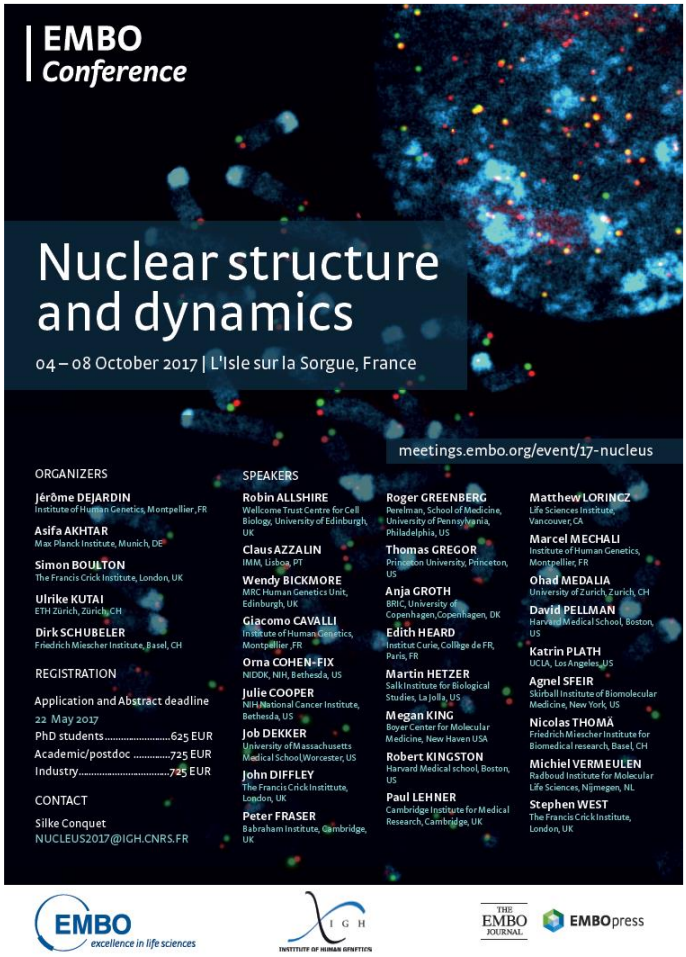
PRACE days 17: HPC for innovation. When Science meets industry. PRACE scientific and industrial conference	16/05/2017	Barcelona, Spain	Jürgen Walther (IRB Barcelona)	Talk (title to be confirmed)
iNEXT 2nd Annual Users meeting Workshop on "Contemporary Trends - Conformational Dynamics at Atomic resolution"	23/05/2017	Brno, czech republic	Modesto Orozco (IRB Barcelona)	Talk title: "Exploring protein dynamics in the postgenomic era"
ELIXIR Innovation and SME Forum: Genomics, Bioinformatics and health – Public private partnerships in open data	6-7/06/2017	Barcelona, Spain	Josep Ll. Gelpí (BSC)	ELIXIR (organizer)
EuroVis 2017: EuroGraphics conference on Visualization	12-16/06/2017	Barcelona, Spain	Mike Goodstadt (CNAG-CRG)	To be confirmed
EMBO Conference Series on Nuclear Structure and Dynamics 2017	4-8/10/2017	L'isle sur la Sorgue, France	Giacomo Cavalli (confirmed speaker)	Talk title to be confirmed Further MuG contributions under discussion
Barcelona BioMed conference Multidimensional genomics: the 3D/4D organization of chromatin.	13-15/11/2017	IEC, Barcelona, Spain	Organized by M. Orozco (IRB), M. Martí-Renom (CNAG), G. Cavalli (CNRS)	Contributions from partners to be defined. Co-localized hands-on training under preparation (see training section)

4.2.2 Upcoming events

The present year 2017 contains some key target events and milestones not to be missed to enhance MuG community engagement.

EMBO Conference: Nuclear structure and dynamics (4th -8th October 2017)

http://meetings.embo.org/event/17-nucleus



This EMBO Conference covers chromosome structure and organization, epigenetic modifications, chromatin remodelling and reprogramming, silent chromatin, genome stability and telomere biology, replication and repair, nuclear RNA, systems biology of genome functions and nuclear compartments. This is the seventh meeting of a series of conferences that is celebrated every two years and is a key meeting point in Europe for the 3D/4D genomics community.

The meeting will constitute a unique dissemination platform to attract the MuG end-user community by presenting results obtained using MuG tools and making the VRE benefits known to potential end users.

The 2017 edition will take place between 4th -8th October at l'Isle sur la Sorgue, France. Giacomo Cavalli (IGH-CNRS), MuG partner and lead user of the MuG VRE, is a key note speaker at the conference.

Barcelona BioMed conference. Multidimensional genomics:the 3D/4D organization of chromatin (13th -15th November 2017)

https://www.irbbarcelona.org/en/events/multidimensional-genomics-the-3d4d-organization-of-chromatin

Organized by IRB Barcelona with the support of BBVA Foundation, this BioMed conference is chaired by MuG PIs Modesto Orozco (Project coordinator), Marc Martí-Renom and Giacomo Cavalli. The conference will verse around the relevance of the 3D organization of chromatin, covering both theoretical and experimental features. The conference will constitute a key dissemination platform for the MuG VRE benefits among the end-user community. A co-localized training event is being organized. The foreseen format for the event is a reduced version of the successful VRE hands-on course (section 3.4).

Genomics is moving from a static monodimensional picture to a time-dependent 3D structure. Chromatin is not any more a magic word used to represent a portion of the cell absorbing more colorant than the rest. Chromatin is now a plastic supramolecular structure composed of DNA and protein whose conformation regulates accessibility of the genes to the protein machinery that regulate their function. Nothing of the activity of the cell can be understood without considering the time-dependent three dimensional structure of chromatin.

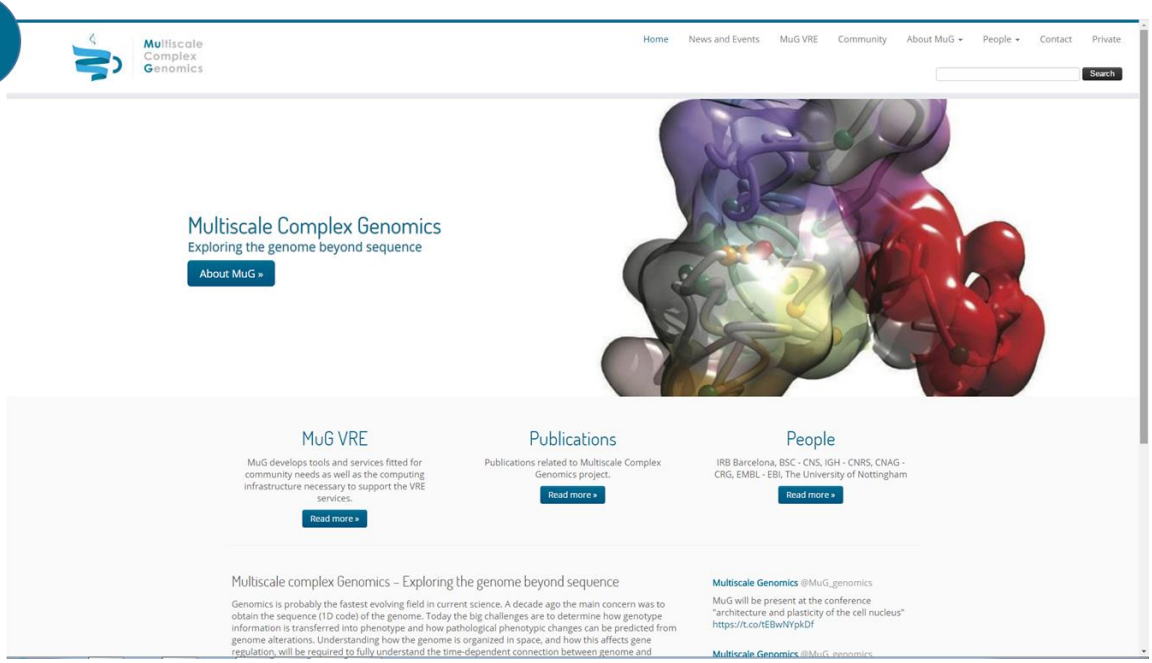
The BioMed conference will be a forum to meet many of the most distinguished scientists in the field. We will learn from the basic physical principles governing the deformation of DNA to the last advances in the experimental techniques providing information on chromatin structure, from the nucleosome to the entire chromatin fiber. We will learn from how chromatin structure is regulated by specific cellular system, and how in turn, chromatin structure modulates the entire cellular live.

4.3 Project website

The design and contents of the MuG website (http://multiscalegenomics.eu) were fully upgraded in May 2016. From the home page, the user gets direct access to the VRE. The VRE portal is designed with a view to future sustainability, providing access to the MuG VRE compute platform, which provides access to community-tailored applications and workflows as well as to other services offered by the VRE (relevant news and events in the 3D/4D genomics field, publications, information on MuG tools, user support/discussion forum. On the other hand, the MuG project website, compiles publications containing MuG acknowledgements, project-related news and events, etc. Both websites are hosted and maintained by IRB Barcelona and BSC.

MuG project website

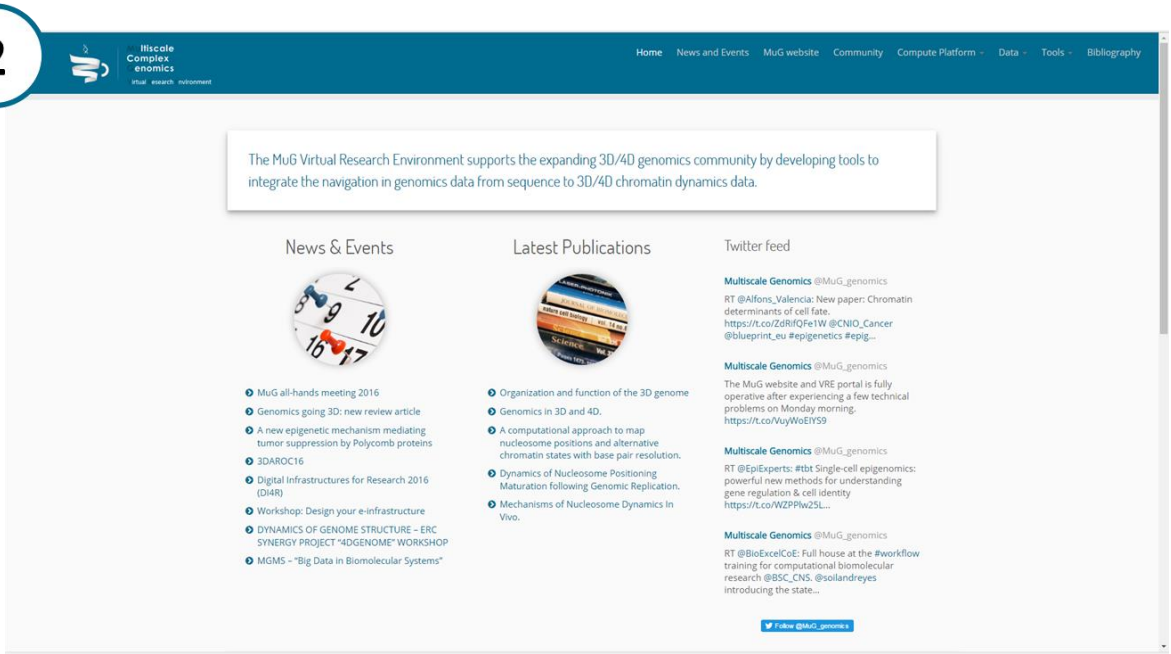
1



MuG VRE portal

The MuG VRE portal provides different services that address the interest of the 3D/D genomics community. Access to the compute platform for end-users is obtained upon registration.

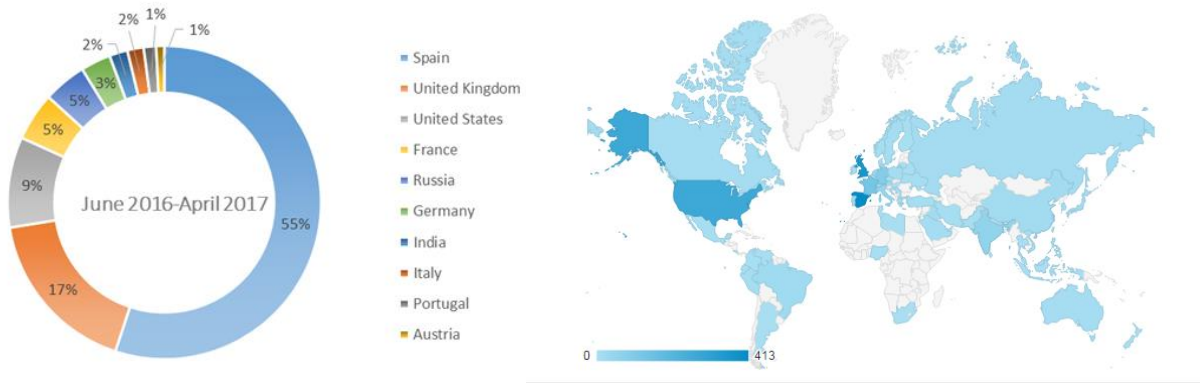
2



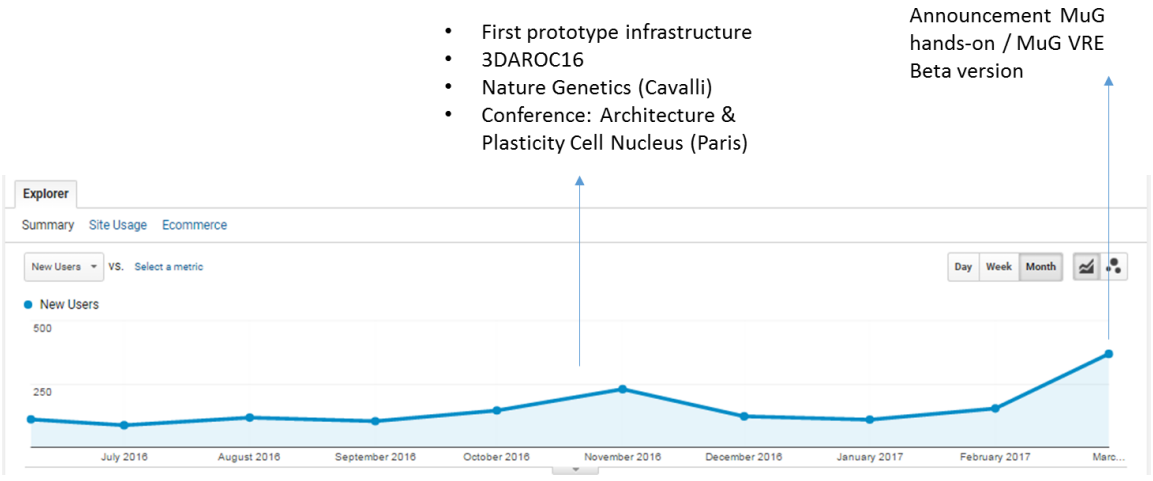
4.3.1 *Traffic monitoring*

Both the VRE and MuG project websites traffic is being monitored through Google Analytics. The increase in traffic is proportionate with the new features becoming available to the community. We have found that training events, as well as publications from our pilot projects are the most efficient to draw the attention of the MuG user community.

The MuG website has received the visits from a total number of **1762** new users from **68** countries, with an average of **150 new users /month**. The following figure depicts the top 10 countries with most visitors since traffic monitoring was implemented in late May 2016.



The progress of the website traffic can be tightly correlated to the VRE and pilot project activities. The highest traffic on the website can clearly be correlated with some key events and publications.



4.4 MuG community registered members

The aim of the MuG community is to create the foundations for a 3D genomics hub. In the short term, the community has been conceived as an interest group whose members get the latest MuG updates and are allowed to interact with users, developers and other stakeholders (a forum in Discourse is operative to comply with the functions of user support for the VRE and discussion forum for the community)

So far **40 members have registered their interest** in the MuG community. Some of them have expressed their interest in becoming involved more actively in the VRE definition or in offering their tools (developers) through the MuG VRE.

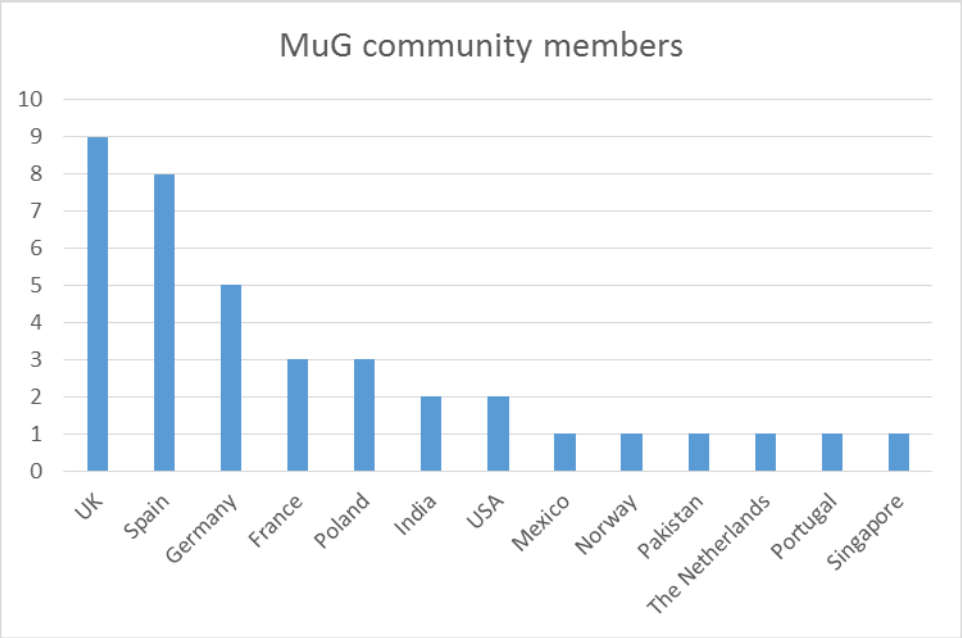


Figure 3: Number of MuG community registered members by 20th April 2017 by country.

4.5 Analysis of social media

Social media are important to target all different kinds of stakeholders that may have an interest in MuG. Twitter (@MuG_genomics) targets a wider community and a LinkedIn group is in place to handle, most importantly, interest from industrial stakeholders and public sector.

4.5.1 Twitter @MuG_genomics

Social media are an increasingly relevant tool in user engagement.

The @MuG_genomics twitter profile counts with **98 followers** by 20th April 2017 (M18). An analysis of the organic audience of the twitter account (i.e. the audience engaging with the account's tweets) reveals the following audience composition:

In terms of demographics, the highest engagement (**55%**) comes from the age segment between 25 and 34 years old. In terms of geographical distribution, the highest engagement figures come from the USA, Spain, the UK and Germany (which together amount **69%** of the organic audience) followed by France, Italy, Canada, the Netherlands, Belgium and Switzerland.

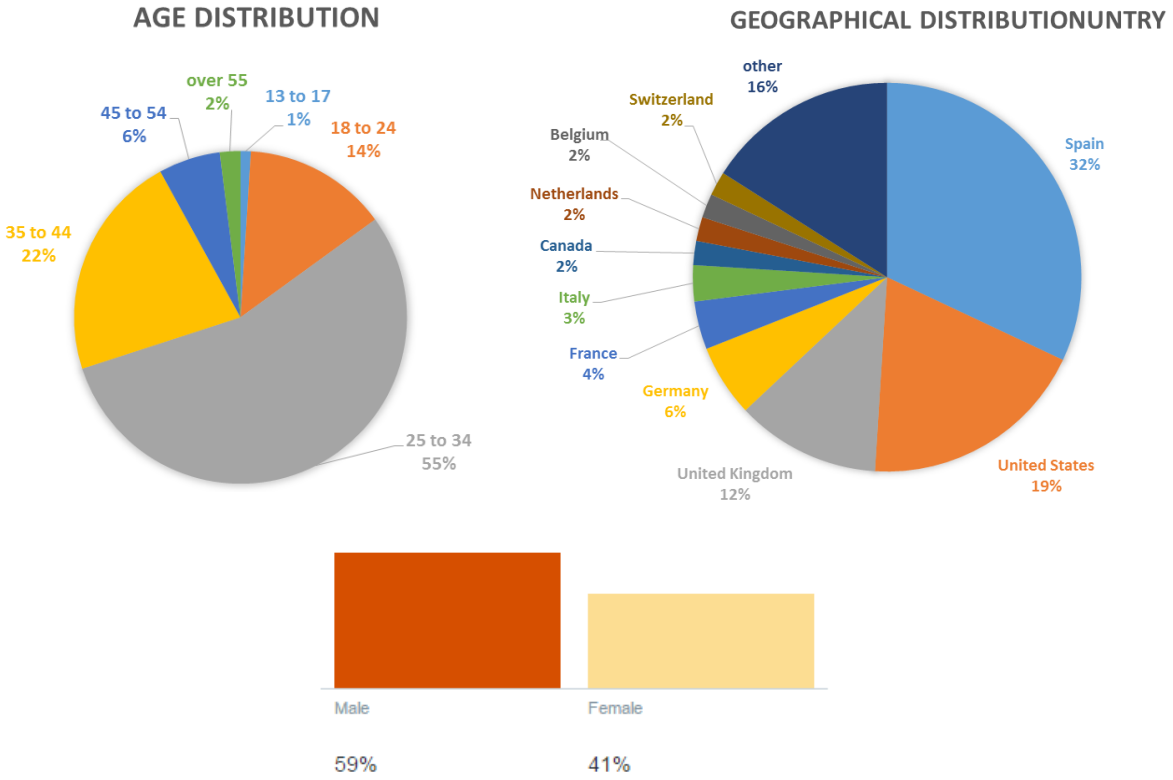


Figure 4: Demographic information of the organic audience engaging with the @MuG_genomics Twitter activity (January 2016- 19th April 2017)

The tweets that led to the highest engagement numbers were those related to high-impact peer-reviewed publications by MuG partners and those informing about training activities or software releases by the VRE, which are matched by an increase in the visits to the MuG VRE portal.

4.5.2 Linked In Multi-scale Genomics group

https://www.linkedin.com/groups/8572323

A group has recently been created with the purpose to handle, mostly, interest from industry stakeholders and direct it to the MuG VRE site. The group is being used as a channel to make available project related information and progress to a wider audience that might not usually engage with other media such as Twitter.

5 KNOWLEDGE MANAGEMENT

As described in Deliverable 2.3, data, including both genomic experimental data and post-processed data, is a key asset of the MuG project. MuG has a Data Management Plan in place (Deliverable D4.2). The DMP will be monitored and updated as necessary based on ongoing discussions with pilot projects generating data.

In order to assist the consortium in the management of Intellectual Property, the partners have sought the assistance from an external consultant. Different candidates have been contacted and at M18 we are in the process of discussing the project needs with them in order to select the most suitable company.

The subcontractor will provide professional advice, reviewing results generated by the project in order to identify any transferability potential before publication, licensing of results, inclusion of third party tools on the VRE, etc.

6 KEY PERFORMANCE INDICATORS

The success, in terms of reaching the target communities, of dissemination and training activities as well as the feedback received from participants, allows us to measure the performance of the project.

6.1 KPIs, metrics and timing

Specific KPIs for the monitoring of the impact of the project directly related to WP2 were defined in D2.3.

Deviations and revised KPIs:

The status at M18 and the explanation of incurred deviations are described in Table 6.

Where necessary, additional KPIs have been added that will measure the performance in terms of registered users / members of the community.

- **Social Media** – YouTube targets are considered to have been overestimated. The suitability of YouTube at this stage is reconsidered and other media such as Twitter are found to be more instrumental to reach the community. The use of YouTube for the time being will be further exploited at a later stage with Demo activities once the VRE is fully operative.
- **Project website:** Original KPIs defined in D2.3 were not measurable enough. Explanations are provided based on the original (non-quantitative) metrics. For future revisions, additional KPIs have been added (KPI7, 8, 9), which are based on incremental traffic on the website (KPI7), registered members of the community (KPI8) and registered VRE users (KPI9). The latter will start to apply once a stable version of the VRE is available (end 2017).

Table 6: Revision of KPIs at M18 (April 2017)

	KPI and metrics description	Metrics description	Target 2016	Target 2017 (cumulative)	Revision M18	
1	Interest of companies to collaborate with MuG.	Number of contacts established with industry: (Pharma, Biotech, Instrument vendors)	1	3		Interest from some companies has been registered through social media (Twitter followers, Newsletter subscribers) although no agreements have been formalized. A longer period of Beta operation of the VRE is needed to generate real interest from the industry. Only when scientific publications have made an impact and more academia users generate data will the industry pick up on the innovations. At present, the twitter account receives a few shares and followers from industry who monitor our activity.
2	Presence in the media	Number of published news reports.	5	15	*3 press releases *Estimated > 15 news reports based on media uptake abovementioned releases	3 press releases have been issued by April 2017 with good uptake by media. Estimated number of news reports based on them exceeds 15. **(2016): 2 press releases (CNRS + IRB) – see Annex IV** News reports mentioning MuG and its potential impact **(see D2.3**). SPECIALIZED MEDIA: International, online: 1.FierceBiotech (Dec 15) /2. Labtimes (Jan16) // Spain , online: 3. Medicineonline GENERAL MEDIA: Spain: 4. La Vanguardia/ 5. CulturaRSC; News reports on G. Cavalli publication: ~5 news reports **(2017): 1 press release by April 2017 – see Annex IV** Media uptake of the press release not yet measured. Estimated to be >10 news reports (examples in Annex IV)

3	Scientific publications	Number of publications in top-ranked scientific journals	3	6		**10** publications by April 2017
4	**Presence in International congresses**	**Number of events where MuG results are presented**	**5**	**10**		**19** international conferences/workshops with direct contributions by MuG Partners by April 2017.
5	Attendees in training workshops	Number of attendees in two workshops (2017 and 2018). A significant increase is expected due to (i) dissemination plan, (ii) quality of VRE services.	0	30		**35** in MuG-organized courses >**159** in trainings about MuG tools and technology. (see section 3.2 above for more information on training events)
6	Project website functionality and performance	• Implemented new features • Frequence of updates • Cross links to and from other websites in the field. • Google analytics statistics				Qualitative targets established have been achieved. Additional KPIs have been added (7-9) with more quantifiable metrics for future evaluation.
7	Website traffic	• Number new visitors/month MuG websites		250	(New KPI)	
8	Registered VRE members			30	(New KPI)	
9	Registered members MuG community / Newsletter	Signed up members of MuG community + Newsletter		50	(New KPI)	**35** (April 2017)
10		Twitter followers	50	100		**98** (April 2017)

	Impact on social media					
		YouTube (No videos /No followers)	2/10	10/50		Reformulated (see above)
		Linked In	0	30		**14** (April 2017)
11	Generation of commercial prototype projects	No. commercial prototype projects	0	0		A contract with a consultancy company is being negotiated to assist in exploitation matters. To be revised in November 2017.
12	Candidate technologies for IPR protection	Number of evaluated technologies Number of protected technologies	0 0	1 0		A contract with a consultancy company is being negotiated for assistance in identifying protectable assets. To be revised in November 2017.

The reported deviations from the targets have allowed us to identify some of the points in which we are weaker in terms of engagement.

The KPIs in which MuG has shown lower performance are those related to communication to the general public and involvement from industry. On the other hand, interest from academia is growing fast. Although a higher involvement from the early stages of development would be desirable, the progressive growth of the interest in the community seems to indicate that, as further results from lead users are published and data begin to be available, interest will continue to increase and be extended to other stakeholders. Actions have been planned for the second half of 2017, including an enhancement of the messages on the website to enhance the message to other stakeholders beyond academia.

7 CONCLUSIONS

- The **MuG training programme** has kicked-off with great results. Training activities organized by partners have progressively incorporated the MuG concept with very good reception. The first hands-on workshop on MuG VRE-integrated tools took place in April 2017 at EBI in Hinxton, with extremely positive feedback from delegates. Feedback obtained from the course will be very valuable not only for fine-tuning of the organization and contents of future training courses. Participants also provided very valuable feedback on their view of the VRE, which will be very useful for MuG VRE developers. The heterogeneous composition of the audience (both in terms of career level and scientific/technical background) will be of much use to improve the dissemination strategy and achieve a broader impact.
- **Dissemination** efforts made by all partners have contributed to a progressive increase in the web visits and community engagement is progressively increasing. Dissemination among end-users who are in need of the developed tools is the most important at the early stages of the project. High-profile publications by MuG pilot projects as well as the release of new MuG tools, together with training activities, are the key drivers for community engagement. Dissemination activities targeting industry stakeholders will be enhanced at a later stage, when a stable version of the VRE has been fully tested.

8 ANNEX I: PROGRAMMES MuG TRAINING WORKSHOPS

8.1 3DAROC16: 3C-based data analysis and 3D reconstruction of chromatin folding

Mon, Oct 10th	Day #1
09:30 - 10:00	Welcome and introductions
10:00 - 11:00	Overview on structure determination
11:00 - 11:30	Coffee Break
11:30 - 12:30	3D modeling of genomes and genomic domains
12:30 - 14:00	Lunch Break
14:00 - 15:00	Introduction to Linux and Python: the Jupyter notebook
15:00 - 16:00	Next Generation Sequencing (NGS) and data handling
16:00 - 16:30	Tea Break
16:30 - 18:00	From raw data to Hi-C contact matrices

Tue, Oct 11th	Day #2
09:30 - 11:00	Morning wrap-up: what have we done so far? Chromatin structure and Hi-C data
11:00 - 11:30	Coffee Break
11:30 - 12:30	Integrative modeling applied to chromatin
12:30 - 14:00	Lunch Break
14:00 - 16:00	Biological applications (I)
16:00 - 16:30	Tea Break
16:30 - 18:00	Hi-C contact matrices: filtering and normalization
Wed, Oct 12th	**Day #3**
09:30 - 11:00	Morning wrap-up: what have we done so far? Biological applications (II)
11:00 - 11:30	Coffee Break
11:30 - 12:30	Compartment detection and analysis
12:30 - 14:00	Lunch Break
14:00 - 16:00	Topologically Associated Domains detection and analysis
16:00 - 16:30	Tea Break
16:30 - 18:00	Comparison between experiments

Thu, Oct 13th	Day #4
09:30 - 11:00	Morning wrap-up: what have we done so far? Biological applications (III)
11:00 - 11:30	Coffee Break
11:30 - 12:30	3D Modeling of real Hi-C data with TADbit (I)
12:30 - 14:00	Lunch Break
14:00 - 16:00	3D Modeling of real Hi-C data with TADbit (II)
16:00 - 16:30	Tea Break
16:30 - 18:00	Analysis of the results
Fri, Oct 14th	**Day #5**
09:30 - 11:00	Morning wrap-up: what have we done so far? Multiscale Genomics: From genomes to structures (Description)
11:00 - 11:30	Coffee Break
11:30 - 12:30	Coarse-Grained DNA and Chromatin Dynamics (Description)
12:30 - 14:00	Lunch Break
14:00 - 16:00	Nucleosome positioning and Nucleosome Dynamics (Description)
16:00 - 16:30	Tea Break
16:30 - 18:00	Final wrap-up session

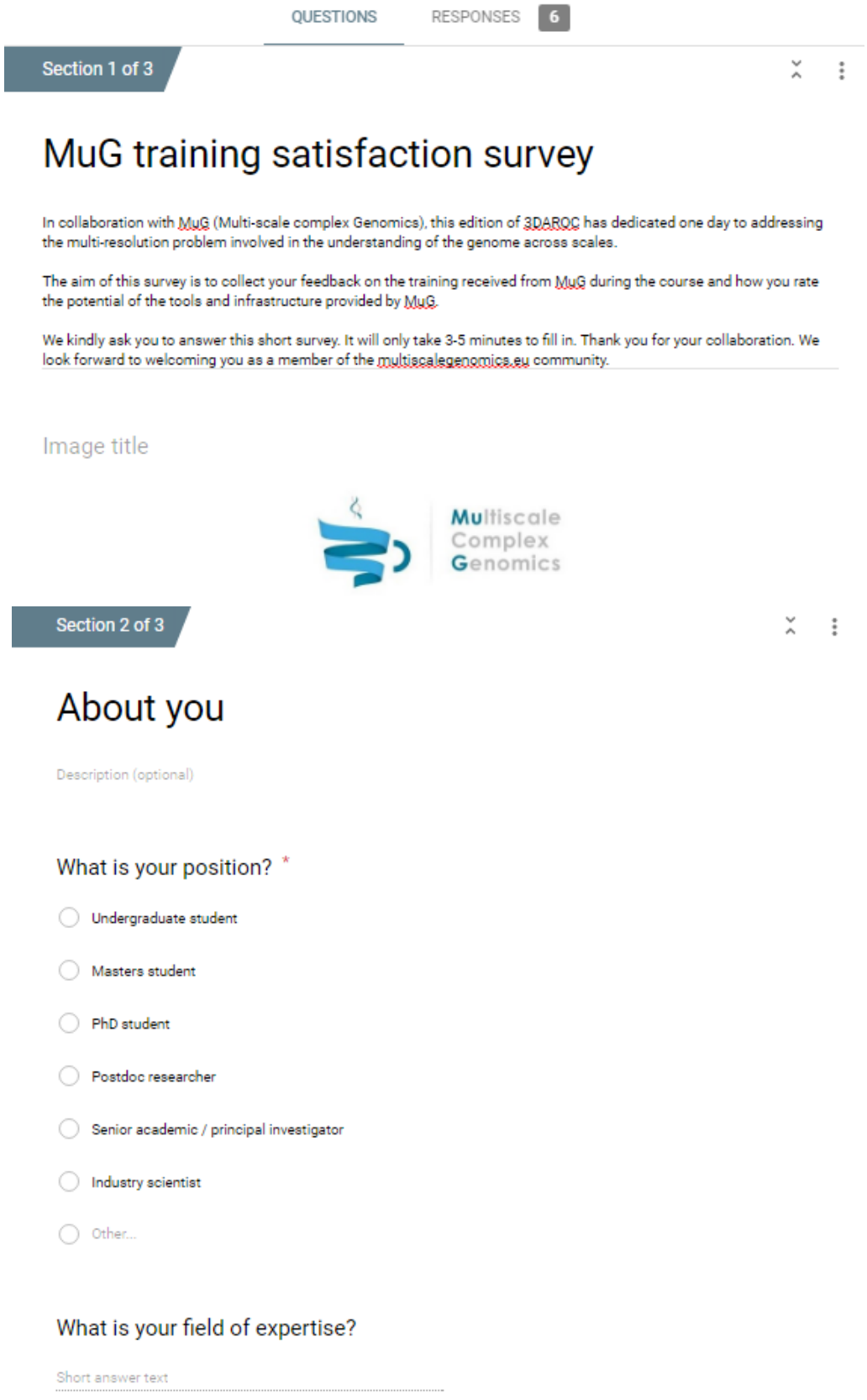
8.2 Multi-scale study of 3D Chromatin structure

Time	Topic	Trainer
Day 1 - 10th April 2017		
09:30	Registration and tea/coffee	
09:50 - 10:00	Welcome to EMBL-EBI	Andy Yates
10:00 - 10:30	MuG and participants Introduction	Modesto Orozco
10:30 - 11:30	Presentation of Nucleosome Dynamics	Ricard Illa /Federica Battistini
11:30 - 12:00	Tea/coffee break	
12:00 - 13:00	User case : Nucleosome dynamics at cohesin binding sites throughout the cell cycle in yeast	Ricard Illa /Federica Battistini
13:00 - 14:00	Lunch	
14:00 - 15:30	Coarse grained model of DNA; Build and analyze a sequence of interest.	Jürgen Walther
15:30 - 16:00	Tea/coffee break	
16:00 - 17:00	Coarse grained model of Chromatin; Generation and analysis of chromatin fiber structures	Jürgen Walther
17:15	Bus back to Cambridge Train Station	

Day 2 - 11th April 2017		
09:00 - 10:30	Presentation of Protein-DNA and protein-protein docking tools.	Brian Jiménez
10:30 - 11:00	Tea/coffee break	
11:00 - 12:30	Protein-DNA interactions, DNA flexibility and binding specificity.	Marco Pasi / Federica Battistini
12:30 - 13:30	Lunch	
13:30 - 15:00	Presentation of TADbit : Generation of Hi-C interaction matrices from Hi-C data	François Serra
15:00 - 15:30	Tea/coffee break	
15:30 - 17:00	Generation of populations of structures that satisfy the Hi-C interaction matrices and Visualization of 3D models with TADkit	François Serra
17:00 - 17:30	Course wrap up and feedback	Andy Yates
17:30	Course end	

9 ANNEX II: SATISFACTION SURVEY FORMS MuG TRAINING EVENTS

9.1 3DAROC16: 3C-based data analysis and 3D reconstruction of chromatin folding



QUESTIONS RESPONSES 6

Section 1 of 3

MuG training satisfaction survey

In collaboration with MuG (Multi-scale complex Genomics), this edition of 3DAROC has dedicated one day to addressing the multi-resolution problem involved in the understanding of the genome across scales.

The aim of this survey is to collect your feedback on the training received from MuG during the course and how you rate the potential of the tools and infrastructure provided by MuG.

We kindly ask you to answer this short survey. It will only take 3-5 minutes to fill in. Thank you for your collaboration. We look forward to welcoming you as a member of the multiscalegenomics.eu community.

Image title

Multiscale Complex Genomics

Section 2 of 3

About you

Description (optional)

What is your position? *

- Undergraduate student
- Masters student
- PhD student
- Postdoc researcher
- Senior academic / principal investigator
- Industry scientist
- Other...

What is your field of expertise?

Short answer text

Section 3 of 3

Your feedback about MuG

Your feedback as a future user of the MuG Virtual Research Environment is very important to us. Your answers will help us design future training events and learn about your user requirements.

Had you heard about MuG before attending this course? *

- ○ Yes
- ○ No

Can you rate your overall level of satisfaction with the Friday sessions? *

- ○ Very satisfied
- ○ Satisfied
- ○ Neutral
- ○ Dissatisfied
- ○ Very dissatisfied

Which features offered by the MuG portal are more interesting for you? *

- ☐ Source for the latest news around the 3D/4D genomics community
- ☐ Multidisciplinary hub to interact with other 3D/4D genomics community members
- ☐ Multi-resolution browser
- ☐ Integrated analysis tools and execution of analysis workflows
- ☐ Common data repository, compatible with other repositories and with personal workspace
- ☐ Other...

Would you be interested in attending a hands-on course focused on the use of the different features of the MuG Virtual Research Environment portal? *

- Yes
- No

Do you have any further comments or suggestions for future MuG trainings?

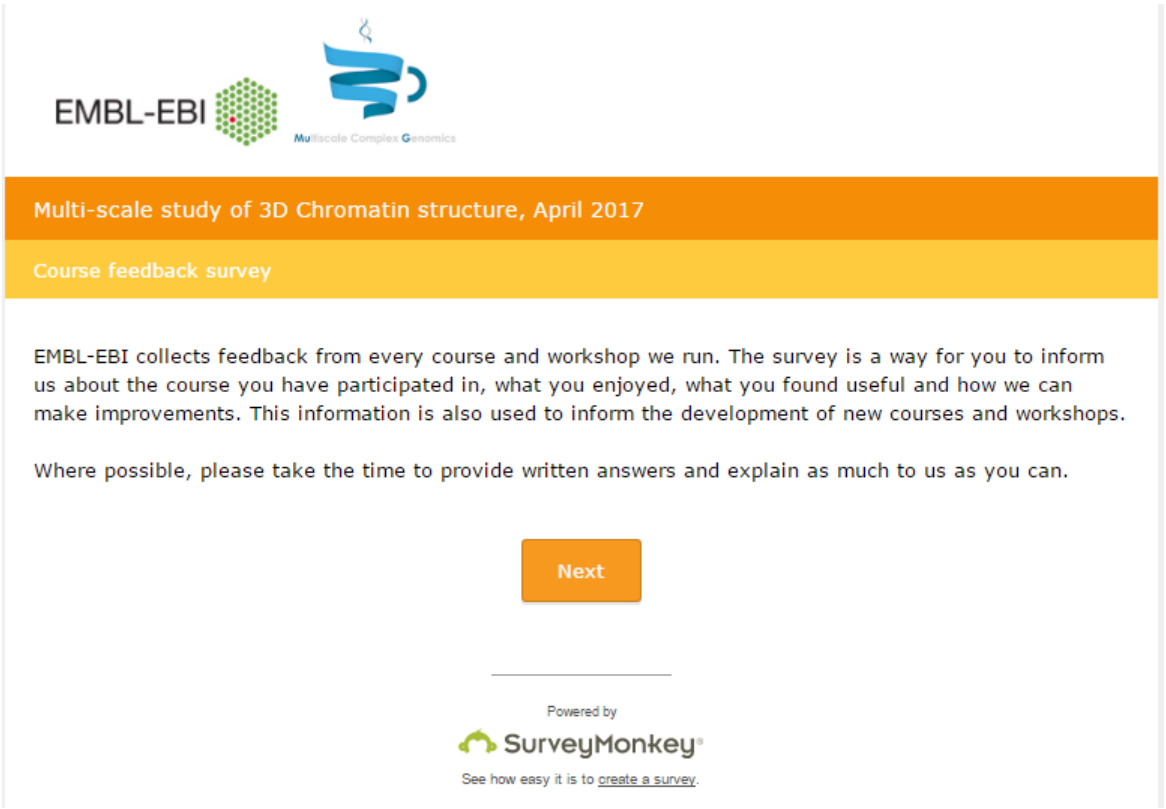
Long answer text

Do you have any suggestions for the MuG portal developers?

Long answer text

9.2 Multi-scale study of 3D Chromatin structure

The following survey, integrating questions related to satisfaction with the facilities and organization as well as additional questions designed to collect the recommendations from participants, as external Beta testers of the VRE:



EMBL-EBI

Multiscale Complex Genomics

Multi-scale study of 3D Chromatin structure, April 2017

About you

This section asks for a few personal details.

We may want to contact you about future EMBL-EBI courses and to gather long-term feedback.

You do not need to provide these details if you do not want to. EMBL-EBI will not use your personal details for any purpose other than that stated above. We will not pass your details to any third party.

1. Name

2. Email

3. May we contact you by email in future to take part in user research activities ?

- ◯ Yes
- ◯ No

4. Would you like to be added to the MuG community database?

- ◯ Yes
- ◯ No

Prev Next

EMBL-EBI

Multiscale Complex Genomics

Multi-scale study of 3D Chromatin structure, April 2017

Course content

This section asks for your thoughts on the content and delivery of the course.

* **5. Please tell us your overall rating for the entire course.**

◯ Poor ◯ Satisfactory ◯ Average ◯ Good ◯ Excellent

* **6. Please rate each section of the course.**

	Did not attend	Poor	Satisfactory	Average	Good	Excellent
Nucleosome dynamics and use case application	◯	◯	◯	◯	◯	◯
Coarse grained model of DNA	◯	◯	◯	◯	◯	◯
Coarse grained model of Chromatin	◯	◯	◯	◯	◯	◯
Protein-DNA interactions, DNA flexibility and binding specificity	◯	◯	◯	◯	◯	◯
TADbit - Generation of Hi-C interaction matrices from Hi-C data	◯	◯	◯	◯	◯	◯
Generation of populations of structures that satisfy the Hi-C interactions matrices and visualisation of 3D models with TADkit	◯	◯	◯	◯	◯	◯

Comments

* **7. What was the best part of the course?**

* **8. What was the worst part of the course?**

* **9. The balance of theoretical and practical content across the course was**

- ◯ Too practical
- ◯ About right
- ◯ Too theoretical

* **10. Have you used the resources covered in the course before?**

- ◯ Unaware of them
- ◯ Used other service
- ◯ Occasionally
- ◯ Frequently

Other (please specify)

* **11. Will you use the tools/resources covered in the course in your future work?**

- ◯ Yes
- ◯ No
- ◯ Maybe

Comments

12. Which features offered by the MuG portal are of most interest to you?

- ☐ Source for the latest news around the 3D/4D genomics community
- ☐ Multidisciplinary hub to interact with other 3D/4D genomics community members (forum, etc.)
- ☐ Integrated analysis tools and execution of analysis workflows
- ☐ Common data repository, compatible with other repositories and with personal workspace
- ☐ Multi-resolution browser
- ☐ Training and user support
- ☐ Other (please specify)

* **13. Would you recommend this course?**

○ Yes ○ No ○ Maybe

Comments

* **14. What would be your suggestions for MuG developers to improve the VRE functionality according to your needs as a user? Are you missing any features?**

Prev Next

EMBL-EBI Multiscale Complex Genomics

Multi-scale study of 3D Chromatin structure, April 2017

Course logistics

This section asks for your thoughts on the organisation of the course.

* **15. The overall course organisation (including: registration, accommodation, EMBL-EBI assistance) was:**

○ Poor ○ Satisfactory ○ Average ○ Good ○ Excellent

Comments

* **16. The catering provided during the course was:**

○ Poor ○ Satisfactory ○ Average ○ Good ○ Excellent

Comments

* **17. The accommodation you stayed in during the course was:**

○ Poor ○ Satisfactory ○ Average ○ Good ○ Excellent

Comments

Prev Next

Multi-scale study of 3D Chromatin structure, April 2017

18. Any other comments on either EMBL-EBI training courses or suggestions for future MuG training courses?

Prev Next

10 ANNEX III: List of participants Multi-scale study of 3D chromatin structure

Name	Last Name	Institution	Country	Position
Stephen	Farr	University of Cambridge	United Kingdom	Masters Student
Sivapalan	Chelvaniththilan	Department of Physics, University of Cambridge	United Kingdom	Early Stage Researcher (PhD)
Hans-Wilhelm	Nützmann	John Innes Centre	Germany	Experienced Researcher (Post Doc)
Luis Mariano	Polo	University of Sussex	United Kingdom	Experienced Researcher (Post Doc)
Hanna	Kranas	University of Warsaw	Poland	Masters Student
Christian	Häring	EMBL Heidelberg	Germany	Principal Investigator (Group Leader)
Karolina	Sienkiewicz	University of Warsaw	Poland	Masters Student
Jennifer	Tan	University of Lausanne	Switzerland	Experienced Researcher (Post Doc)
Steven	Wingett	The Babraham Institute	United Kingdom	Other
NIDHIBEN	PATEL	Centre of Recherché Interdisciplinaire	France	Masters Student
Jyotsana Jewel	Parmar	Institut Pasteur	France	Experienced Researcher (Post Doc)
Joana	Teixeira	IBMC - institute for molecular and cell biology	Portugal	Early Stage Researcher (PhD)
Ali	Imam	Erasmus Medical Center	The Netherlands	Staff Scientist
Aleksander	Jankowski	EMBL Heidelberg	Germany	Experienced Researcher (Post Doc)
Eleni	Katsantoni	Biomedical Research Foundation, Academy of Athens	Greece	Principal Investigator (Group Leader)
Ekaterina	Zabolotnaya	Pharmacology Department, University of Cambridge	Germany	Early Stage Researcher (PhD)
Paulo	Amaral	University of Cambridge	United Kingdom	Experienced Researcher (Post Doc)
Namshik	Han	University of Cambridge	United Kingdom	Experienced Researcher (Post Doc)
Piotr	Sliwa	University of Warsaw	Poland	Undergraduate Student

11 ANNEX IV: Press releases and media uptake

11.1 IGH-CNRS: Publication Nature Genetics 2016

A new epigenetic mechanism mediating tumor suppression by Polycomb proteins

The Cavalli lab (Institute of Human Genetics, Montpellier) shows that a complex of Polycomb group proteins has a tumor suppressor activity that depends on its specific binding to hundreds of genes involved in the control of proliferation, cell signaling and polarity. This activity was discovered in *Drosophila*, but the same chromosomal binding pattern is observed in differentiated human cells, suggesting that this phenomenon might be conserved in some human tumors. This study, published in the journal Nature Genetics, opens new perspectives in the field of carcinogenesis.

Polycomb Group proteins (PcG) are evolutionarily conserved epigenetic factors originally discovered in the fruit fly Drosophila melanogaster as repressors of homeotic gene expression. The canonical view is that PcG proteins exert their function via the sequential action of two protein complex called PRC2 and PRC1 that maintain the cellular memory of transcriptional repression throughout development.

Nevertheless, PcG proteins are also involved in many other biological functions, such as the renewal of stem cells and cancer processes. The Cavalli lab had previously shown that mutations in the gene *polyhomeotic*, a Polycomb group gene, could induce neoplastic cancers in flies. This tumor suppressor function involved the repression of the Notch signaling pathway. This link between Polycomb and Notch, a major oncogene, paved the way to a systematic analysis of mutations in different PcG genes. The present study reveals that only mutations affecting PRC1 members lead to tumorigenesis, whereas mutations affecting PRC2 do not affect cell proliferation (see Figure). This result thus calls for a revision of the mainstream view that in which PRC2 and PRC2 function in a collaborative and sequential manner to repress their target genes.

In order to get insights in this phenomenon, the team, led by Anne-Marie Martinez and Giacomo Cavalli, performed a comparative analysis of the genome-wide distribution of PRC1 complex members during development. This work revealed that, between the embryonic and larval stages, a massive wave of PRC1 recruitment, independent of the action of PRC2, brings PRC1 at hundreds of target genes involved in the control of proliferation, cell polarity and signaling. These genes (called "Neo PRC1", see Figure) become overexpressed in larvae mutant for PRC1 subunit, whereas they are unaffected by PRC2 mutations.

This study shows that a major physiological role of PRC1 is actually to fine tune, both temporally and spatially, the expression of genes whose deregulation leads to tumor formation. This dynamic redeployment of PRC1 during development seems to evolutionarily conserved. While in human stem cells the PRC1 complex co-localizes with its cognate H3K27me3 epigenetic mark that depends on PRC2 function, in differentiated cells PRC1 gets recruited to a large group of active, H3K27me3 depleted genes that control cell proliferation and signaling , similar to what occurs in *Drosophila* larvae. Future studies in *Drosophila* and humans should allow to elucidate this phenomenon and potentially lead to diagnostic and therapeutic applications in carcinogenesis.

Reference:
Massive Coordinate redeployment of PRC1 proteins suppresses tumor formation during *Drosophila* development.
Vincent Loubière, Anna Delest, Aubin Thomas, Boyan Bonev, Bernd Schuettengruber, Satish Sati, Anne-Marie Martinez and Giacomo Cavalli.
Nature Genetics (2016), doi:10.1038/ng.3671
PMID: 27643538 - https://www.ncbi.nlm.nih.gov/pubmed/27643538

Corresponding authors:

Giacomo Cavalli
Institute of Human Genetics
CNRS UPR1142- University of Montpellier, 141, rue de la Cardonille, 34396 Montpellier
Giacomo.Cavalli@igh.cnrs.fr

Anne-Marie Martinez
Institute of Human Genetics
CNRS UPR1142- University of Montpellier, 141, rue de la Cardonille, 34396 Montpellier
Anne-Marie.Martinez@igh.cnrs.fr

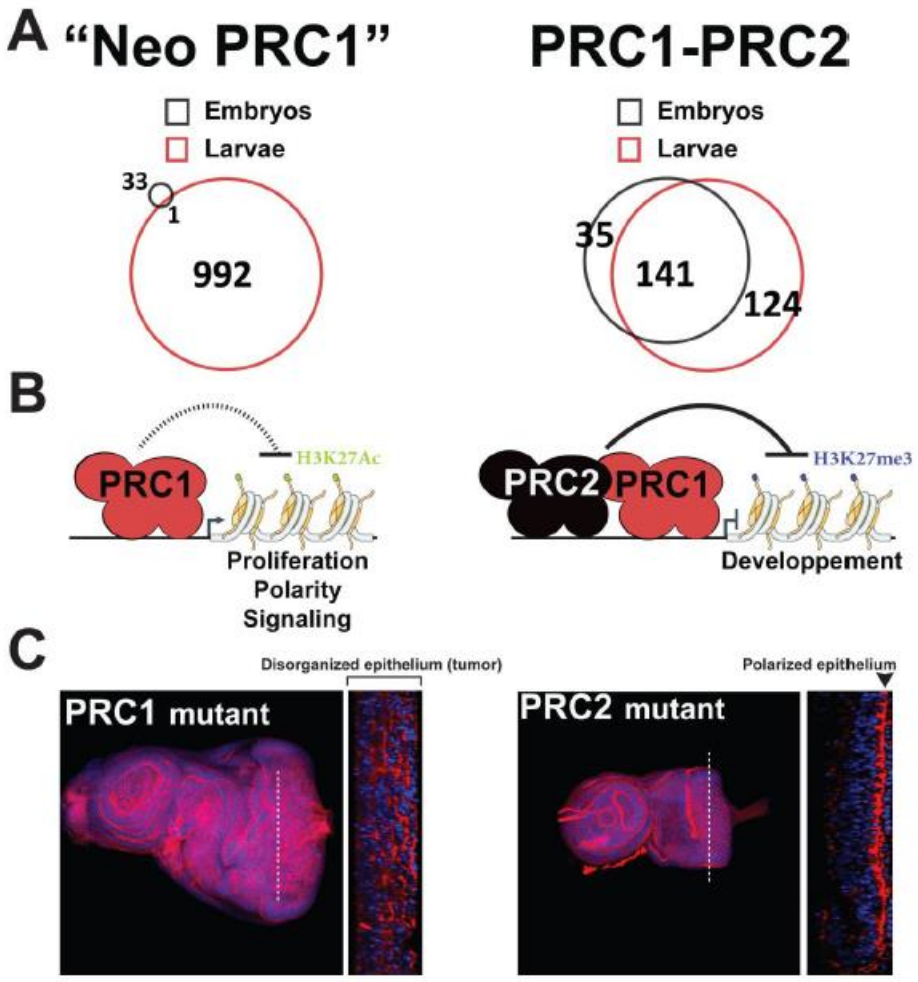
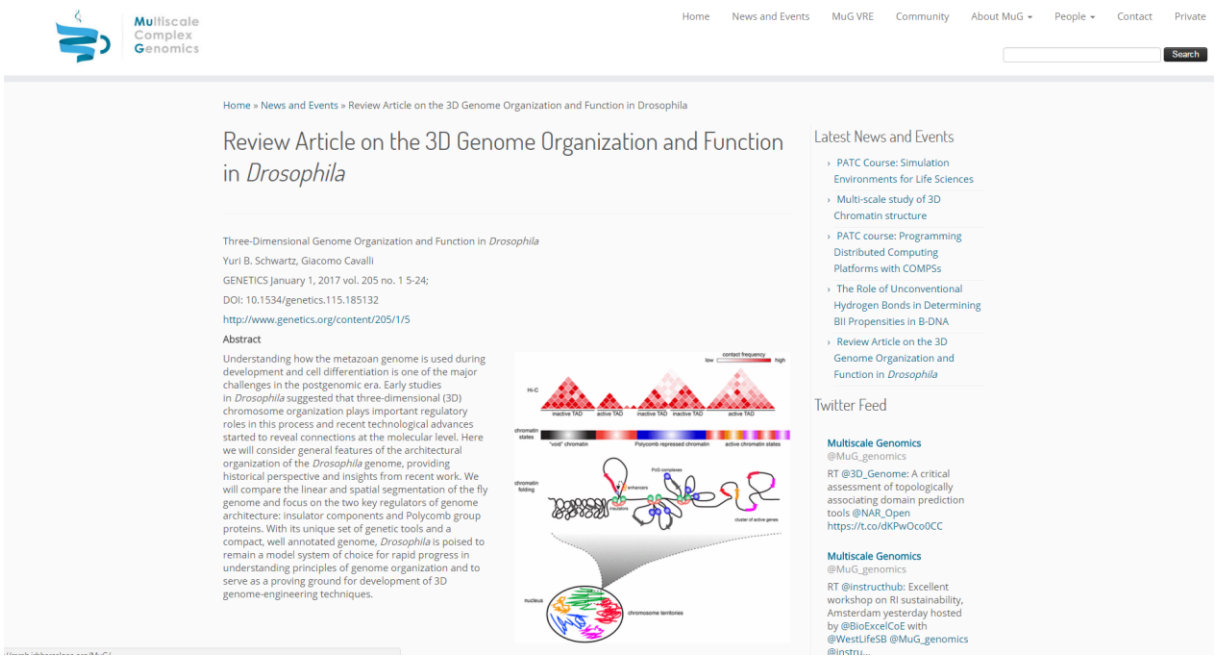


Figure: The PRC1 Polycomb complex is recruited independently from the enzymatic function of the second Polycomb complex, called PRC2, on a large group of target genes (called « Neo PRC1 ») that are deregulated during tumorigenesis.
A- Venn diagrams showing the number of Neo PRC1 target genes (left) versus canonical target genes bound by both complexes and possessing the PRC2-specific H3K27me3 mark (right), during embryo (black) and larval (red) stages. B- Illustrative scheme showing the defining molecular features of « Neo PRC1 » or PRC1-PRC2 (canonical) target genes. The main molecular functions of the two classes are shown below the cartoon. C- *Drosophila* epithelial tissues stained in blue to show cell nuclei and in red to show tissue polarity. The dashed line indicates the area in which orthogonal planes are shown at the right hand side of the main panels. Figure courtesy of Vincent Loubière.

News feature on the MuG project website about the publication:



Press uptake examples:

1. http://www.techno-science.net/?onglet=news&news=15533

Vie et Terre

Posté par Adrien le Lundi 26/09/2016 à 00:00

Un mécanisme épigénétique à l'origine d'une activité anti-tumorale

drosophile protéines groupe Polycomb

L'équipe de Giacomo Cavalli à l'Institut de Génétique Humaine, démontre chez la drosophile qu'un complexe de protéines du groupe Polycomb, un répresseur épigénétique de l'expression génique, exerce une fonction anti-tumorale en se fixant spécifiquement à des centaines de gènes impliqués dans le contrôle de la prolifération ainsi que dans la signalisation et la polarité cellulaires. Cette fixation massive est également observée dans des cellules humaines différenciées. Cette étude, publiée dans la revue *Nature Genetics*, ouvre de nouvelles perspectives dans le domaine de la cancérogenèse.

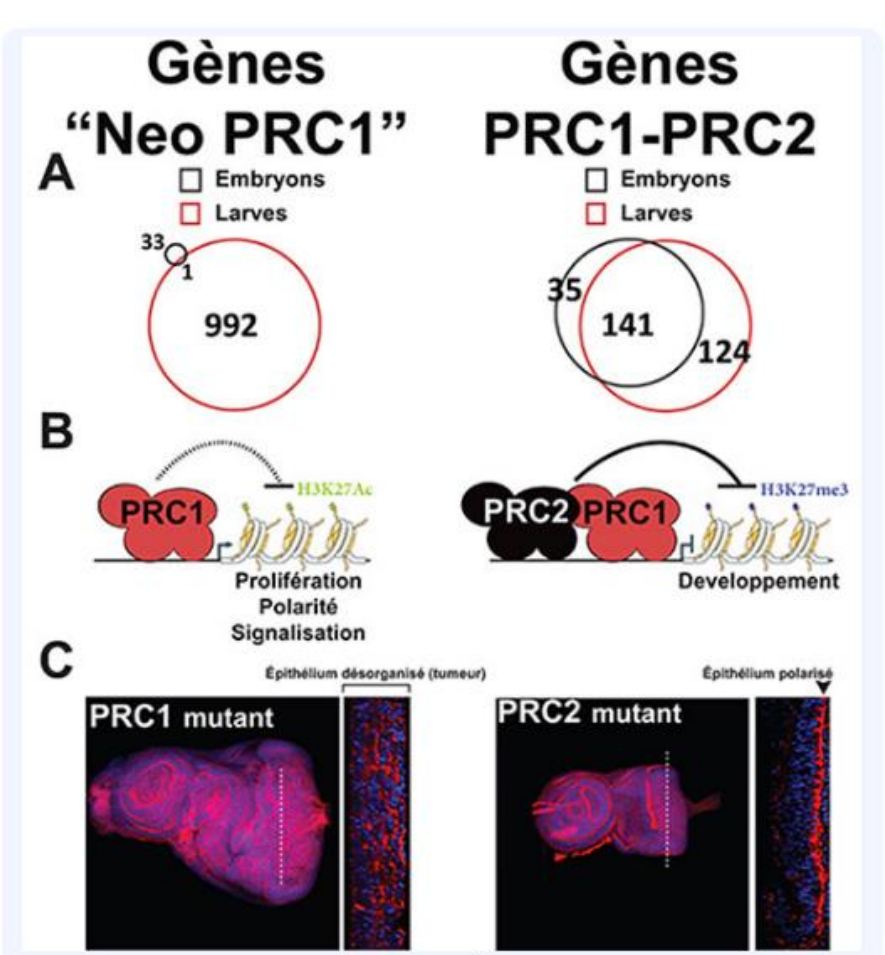


Figure: Le complexe PRC1 est recruté au cours du développement, sans le complexe PRC2, sur un ensemble de gènes ("Neo PRC1") dont la dérégulation transcriptionnelle participe à la formation de

11.2 IGH-CNRS: Nature Genetics April 2017

PRESS RELEASE | PARIS | APRIL 24, 2017

We are more than our DNA: Discovering a new mechanism of epigenetic inheritance

Giacomo Cavalli's team at the Institute of Human Genetics (University of Montpellier / CNRS), in collaboration with the French National Institute for Agricultural Research (INRA),[1] has demonstrated the existence of transgenerational epigenetic inheritance[2] (TEI) among *Drosophila* fruit flies. By temporarily modifying the function of Polycomb Group (PcG) proteins—which play an essential role in development—the researchers obtained fruit fly lines having the same DNA sequence but different eye colors. An example of epigenetic inheritance, this color diversity reflects varying degrees of heritable, but reversible, gene repression by PcG proteins. It is observed in both transgenic and wild-type lines and can be modified by environmental conditions such as ambient temperature. The scientists' work is published in *Nature Genetics* (Monday, April 24, 2017).

Same DNA, different color. Researchers have obtained drosophila *epilines*—that is, genetically identical lineages with distinct epigenetic characteristics—with white, yellow, and red eyes respectively. They achieved this by transiently disturbing interactions between target genes and PcG proteins, which are complexes involved in the repression of several genes governing development. Cavalli and his team at the Institute of Human Genetics (University of Montpellier / CNRS) are the first to show that regulation of gene position can lead to transgenerational inheritance.

DNA is not the only medium for communicating information necessary for cell function. Cell processes are also determined by the chemical labeling (or *marks*) and specific spatial organization of our genomes, which are *epigenetic* characteristics—that is, nongenetic but nonetheless inheritable traits. Epigenetic marks include modifications of histones, the proteins around which DNA is wound. PcG proteins, on the other hand, play a regulatory role by affecting 3D chromosomal configuration, which establishes certain interactions between genes in the cell nucleus. The position of a gene at any given moment determines whether it is active or repressed.

Through temporary disruption of these interactions, the scientists were able to produce *Drosophila* epilines characterized by different levels of PcG-dependent gene repression or activation. They verified that these epilines were indeed *isogenic*, or genetically identical, by sequencing the genome of each. Despite their identical DNA, the integrity of epilines—and the unique phenotypic characteristics they program—can be

[1] Researchers from the Centre de Biologie pour la Gestion des Populations in Montpellier and the Toulouse branch of the Division of Applied Mathematics and Informatics (MIAT).
[2] Epigenetics is the study of changes in genetic expression that do not involve modification of DNA sequences but may still be passed on through cellular division. Unlike mutations altering DNA sequences, epigenetic modifications are reversible.

www.cnrs.fr

maintained across generations. But this phenomenon is reversible. Crosses between drosophilas with over- or underexpressed genes and others having no such modifications to gene activity "reset" eye color without altering the DNA sequence, thus demonstrating the epigenetic nature of this inheritance.

The researchers then showed that new environmental conditions, such as a different ambient temperature,[3] can affect the expression of epigenetic information over several generations, but they do not erase this information. Such transient effects of environmental factors to which earlier generations were exposed on the expression of characteristics in their progeny illustrate the unique, pliable nature of this epigenetic mechanism. By conducting "microcosm" experiments that recreated natural environmental conditions, the researchers—working with INRA—confirmed that epigenetic inheritance in *Drosophila* can be maintained in the wild.

Giacomo Cavalli's crew has therefore proven the existence of Polycomb-mediated stable transgenerational epigenetic inheritance dependent on 3D chromosomal structure. Their findings offer new horizons for biomedical science. They suggest that epigenetics could partly solve the mystery of "missing heritability"—that is, the absence of any apparent link between genetic makeup and certain normal hereditary traits and diseases.

Three drosophila epilines are shown. All share the same DNA sequence, but each has a unique eye color caused by transient perturbation of their epigenetic state. This perturbation alters levels of Polycomb-mediated repression of the eye color gene.
© Filippo Ciabrelli

[3] Like other insects, drosophilas cannot establish a constant internal temperature independent of environmental conditions.

www.cnrs.fr

© Elisa Cavalli

Reference:

Ciabrelli F, Comoglio F, Fellous S, Bonev B, Ninova M, Szabo Q, Xuereb A, Klopp C, Aravin A, Paro R, Bantignies F, Cavalli G. Stable Polycomb-dependent transgenerational inheritance of chromatin states in *Drosophila*. Nat. Genet. 2017 Apr 24. doi:10.1038/ng.3848.

Contact:

CNRS researchers | Giacomo Cavalli | **T (+33) (0)4 34 35 99 70** | giacomo.cavalli@igh.cnrs.fr
Frédéric Bantignies | **T (+33) (0)4 34 35 99 97** | frederic.bantignies@igh.cnrs.fr

CNRS press officer | Anne-Sophie Boutaud | **T (+33) (0)1 44 96 46 06** | anne-sophie.boutaud@cnrs.fr

Press release in France (News Press)

http://www.newspress.fr/communique_302459_641_RSS-FR-TS-67.aspx

CNRS - Centre National de Recherche Scientifique - 25/04/2017 12:20:00

L'équipe de Giacomo Cavalli, à l'Institut de génétique humaine de Montpellier (Université de Montpellier/CNRS), en collaboration avec l'Inra1, démontre chez la drosophile l'existence d'une hérédité épigénétique2 transgénérationnelle. En modifiant de façon transitoire la fonction des protéines du groupe Polycomb, dont l'activité est essentielle au cours du développement, ils ont obtenu des lignées de drosophile porteuses de la même séquence d'ADN mais caractérisées par des yeux de couleurs différentes. Ces différences dépendent d'un degré variable de répression par les protéines Polycomb qui est hérité de façon stable mais réversible. Cette hérédité épigénétique s'applique aussi bien à des lignées transgéniques qu'à des lignées naturelles et peut être modifiée par des changements de conditions environnementales, comme la température ambiante. Ces résultats sont publiés dans la revue Nature Genetics, le 24 avril 2017.

Elles ont toutes le même ADN mais des caractères bien différents : des chercheurs ont obtenu des lignées de drosophiles aux yeux blancs, jaunes ou rouges, en perturbant de façon transitoire des interactions entre des gènes cibles des protéines Polycomb, des complexes protéiques impliqués dans la répression de nombreux gènes, notamment des gènes de développement.

Les informations nécessaires au fonctionnement des cellules ne sont pas toutes portées par le matériel génétique. D'autres paramètres, transmis de façon héréditaire mais non codés par les gènes d'un individu, pilotent la vie des cellules. Ces facteurs dits épigénétiques sont un étiquetage chimique et une organisation spatiale bien définie de notre génome. Ils correspondent en particulier aux modifications des histones, les protéines autour desquelles l'ADN s'enroule. Les protéines du groupe Polycomb, elles, sont impliquées dans la définition de l'architecture tridimensionnelle des chromosomes, qu'elles régulent en établissant des interactions entre gènes dans l'espace 3D du noyau cellulaire. Or, selon la position d'un gène à un moment donné, son expression sera activée ou réprimée.

En perturbant de façon transitoire ces interactions, les chercheurs ont pu établir des lignées de drosophiles caractérisées par des niveaux différentiels de répression ou d'activation génique dépendant des Polycomb. Les chercheurs ont séquencé le génome entier de chaque lignée de drosophiles, afin de vérifier que leur ADN soit bien identique. Malgré l'identité de leurs séquences d'ADN, ces lignées peuvent être maintenues indéfiniment et transmettent fidèlement leurs différences phénotypiques une fois établies. Ce phénomène peut être réversible : en croisant ces individus aux gènes surexprimés ou sous exprimés avec des drosophiles n'ayant pas de modifications, il est possible d'induire un retour à la normal de la couleur des yeux sans changer la séquence d'ADN, ce qui démontre le caractère épigénétique de cette forme d'héritage.

Les chercheurs ont ensuite pu montrer que la modification des conditions environnementales, notamment la température ambiante3, peut affecter l'expression de l'information épigénétique sur plusieurs générations, sans pour autant effacer sa transmission. Cette influence transitoire de l'environnement dans lequel ont vécu les générations précédentes sur l'expression des traits des insectes confère à ce mécanisme épigénétique des propriétés évolutives uniques. La pertinence du phénomène dans la nature a de plus été confirmée par des études en microcosme menées en collaboration avec l'Inra.

L'équipe de Giacomo Cavalli démontre ainsi l'existence d'un héritage épigénétique transgénérationnel stable, dépendant de la structure tridimensionnelle des chromosomes et régulé par les facteurs Polycomb. Ces résultats ouvrent de nouvelles perspectives pour les sciences biomédicales. Ils suggèrent notamment que l'épigénétique pourrait expliquer en partie le mystère de « l'hérédité manquante », c'est-à-dire l'incapacité de trouver les causes génétiques de certains caractères héréditaires normaux ainsi que de nombreuses pathologies humaines.

AGENCE
NEWS

Press uptake examples:

1. https://phys.org/news/2017-04-mechanism-epigenetic-inheritance.html

This website uses cookies to ensure you get the best experience on our website. More info

PHYS.ORG Nanotechnology Physics Earth Astronomy & Space Technology Chemistry Biology Other Sciences

search

Home » Biology » Biotechnology » April 26, 2017

Discovering a new mechanism of epigenetic inheritance

April 26, 2017

Discovering a new mechanism of epigenetic inheritance

Three drosophila epilines are shown. All share the same DNA sequence, but each has a unique eye color caused by transient perturbation of their epigenetic state. This perturbation alters levels of Polycomb-mediated repression of the eye color gene. Credit: Filippo Ciabrelli

Giacomo Cavalli's team at the Institute of Human Genetics (University of Montpellier / CNRS), in collaboration with the French National Institute for Agricultural Research (INRA), has demonstrated the existence of transgenerational epigenetic inheritance (TEI) among Drosophila fruit flies. By temporarily modifying the function of Polycomb Group (PcG) proteins—which play an essential role in development—the researchers obtained fruit fly lines having the same DNA sequence but different eye colors. An example of epigenetic inheritance, this color diversity reflects varying degrees of heritable, but reversible, gene repression by PcG proteins. It is observed in both transgenic and wild-type lines and can be modified by environmental conditions such as ambient temperature. The scientists' work is published in *Nature Genetics*.

Drosophila Micro-Injection - & Genetic Services
$200/Construct, High Success Rate. Ship Transformants/Balanced Lines!
thebestgene.com

Same DNA, different color. Researchers have obtained drosophila epilines—that is, genetically identical lineages with distinct epigenetic characteristics—with white, yellow, and red eyes respectively. They achieved this by transiently disturbing interactions between target genes and PcG proteins, which are complexes involved in the repression of several genes governing development. Cavalli and his team at the Institute of Human Genetics (University of Montpellier / CNRS) are the first to show that regulation of gene position can lead to transgenerational inheritance.

DNA is not the only medium for communicating information necessary for cell function. Cell processes are also determined by the chemical labeling (or marks) and specific spatial organization of our genomes, which are epigenetic characteristics—that is, nongenetic but nonetheless inheritable traits. Epigenetic marks include modifications of histones, the proteins around which DNA is wound. PcG proteins, on the other hand, play a regulatory role by affecting 3-D chromosomal configuration, which establishes certain interactions between genes in the cell nucleus. The position of a gene at any given moment determines whether it is active or repressed.

Through temporary disruption of these interactions, the scientists were able to produce Drosophila epilines characterized by different levels of PcG-dependent gene repression or activation. They verified that these epilines were indeed isogenic, or genetically identical, by sequencing the genome of each. Despite their identical DNA, the integrity of epilines—and the unique phenotypic characteristics they program—can be maintained across generations. But this phenomenon is reversible. Crosses between drosophilas with over- or underexpressed genes and others having no such modifications to gene activity "reset" eye color without altering the DNA sequence, thus demonstrating the epigenetic nature of this inheritance.

The researchers then showed that new environmental conditions, such as a different ambient temperature, can affect the expression of epigenetic information over several generations, but they do not erase this information. Such transient effects of environmental factors to which earlier generations were exposed on the expression of characteristics in their progeny illustrate the unique, pliable nature of this epigenetic mechanism. By conducting "microcosm" experiments that recreated natural environmental conditions, the

See what you've been missing with RNAscope® ISH technology
ACD a biotechne brand
Learn more

Featured Last comments Popular

Caterpillar found to eat shopping bags, suggesting biodegradable solution to plastic pollution Apr 24, 2017 7

Cassini, Voyager missions suggest new picture of Sun's interaction with galaxy Apr 24, 2017 10

Scientist invents way to trigger artificial photosynthesis to clean air Apr 25, 2017 0

Gut bacteria tell the brain what animals should eat Apr 25, 2017 2

The Radiohead ant: A new species of 'silky' ant grows fungus gardens for food Apr 24, 2017 0

more »

Phys.org
Follow +1
+ 132,316

Phys.org on facebook
Like 1.3M people like this.

researchers—working with INRA—confirmed that epigenetic inheritance in Drosophila can be maintained in the wild.

Giacomo Cavalli's crew has therefore proven the existence of Polycomb-mediated stable transgenerational epigenetic inheritance dependent on 3-D chromosomal structure. Their findings offer new horizons for biomedical science. They suggest that epigenetics could partly solve the mystery of "missing heritability"—that is, the absence of any apparent link between genetic makeup and certain normal hereditary traits and diseases.

Explore further: Biological mechanism passes on long-term epigenetic 'memories'

More information: Filippo Ciabrelli et al. Stable Polycomb-dependent transgenerational inheritance of chromatin states in Drosophila, *Nature Genetics* (2017). **DOI: 10.1038/ng.3848**

Journal reference: Nature Genetics

Provided by: CNRS

Related Stories

Biological mechanism passes on long-term epigenetic 'memories' March 28, 2016
According to epigenetics—the study of inheritable changes in gene expression not directly coded in our DNA—our life experiences may be passed on to our children and our children's children. Studies on survivors of traumatic ...

Revolutionary new view on heritability in plants February 11, 2014
Complex heritable traits are not only determined by changes in the DNA sequence. Scientists from the University of Groningen Bioinformatics Centre, together with their French colleagues, have shown that epigenetic marks can ...

A new principle for epigenetic changes discovered January 23, 2017
In a new study, researchers at Uppsala University have found

Recommended for you

Mysterious drop in prized bait worms threatens a way of life April 27, 2017
Dan Harrington makes his living unearthing marine worms by hacking away at mudflats with a tool that resembles the business end of an old steel rake.

Barley genome sequenced April 26, 2017
Looking for a better beer or single malt Scotch whiskey? A team of researchers at the University of California, Riverside may have you covered. They are among a group of 77 scientists worldwide who have sequenced the complete ...

Researchers identify genes that help trout find their way home April 26, 2017
In the spring when water temperatures start to rise, rainbow trout that have spent several years at sea traveling hundreds of miles

User comments

Please sign in to add a comment. Registration is free, and takes less than a minute. Read more

email

password

Sign in

Click here to reset your password.
Sign in to get notified via email when new comments are made.

2. http://www.techno-science.net/?onglet=news&news=16225

3. http://www.scoop.it/t/entomonews

12 ANNEX V: MuG Poster

A MuG poster was developed which has been shown in different events in which MuG has been present. The poster describes the main innovations offered by the MuG VRE to the 3D/4D genomics community.