The Company of Biologists

FIRST PERSON

First person – Davide Martino Coda

First Person is a series of interviews with the first authors of a selection of papers published in Journal of Cell Science, helping early-career researchers promote themselves alongside their papers. Davide Martino Coda is first author on 'A network of transcription factors governs the dynamics of NODAL/Activin transcriptional responses', published in JCS. Davide Martino is a postdoc in the lab of Johannes Graeff at École Polytechnique Fédérale de Lausanne, Switzerland, investigating epigenetics and transcriptional mechanisms in developmental biology and memory neuroscience.

Davide Martino Coda

How would you explain the main findings of your paper in lay terms?

To allow a complex animal to develop from a small bundle of cells, the cells need to be able to communicate with each other to coordinate their activities. The cells communicate by releasing signals that influence the behaviour of their neighbours by activating proteins called transcription factors. These proteins then change the activity of particular genes in the nucleus by binding to specific places on a structure called chromatin (the structure in which the genes are packaged). One group of signalling molecules is known as the transforming growth factor β superfamily, which is crucial for embryos to develop correctly. We still do not know how the detection of these signals at the surface of the cell leads to changes in the activity of genes inside the nucleus. Two transforming growth factor β signals called Activin and NODAL cause a transcription factor known as SMAD2 to move into the nucleus where it can alter gene activity. Here, we investigated how SMAD2 transmits the NODAL/Activin signal in mouse cancer cells. The experiments showed that SMAD2 can change the activities of genes in multiple ways. SMAD2 can bind to places in the chromatin that are easy to access (which typically contain genes that are already 'switched on'), as well as areas that are difficult to access (which generally contain genes that are 'switched off'). Moreover, by analysing the 'footprint' left on the chromatin by the transcription factors, we identify which of them help SMAD2 to change gene activity at specific times.

Were there any specific challenges associated with this project? If so, how did you overcome them?

Finishing the project was the greatest challenge. At the time when I left the lab to start my postdoc somewhere else, there was still some work to do, both in terms of bioinformatic analyses, as well as biochemistry. On top of the writing, of course! And all of this, in the middle of the pandemic and across different countries. I believe what made it possible was the great dedication to the project of all the team – Dr Harshil Patel for the bioinformatics, Dr Ilaria Gori for the biochemistry and Dr Caroline Hill for the supervision. From a technical point of view, the most difficult part was using the ATAC-seq data for doing transcription factor footprint analysis. It was the first time someone was attempting this approach in the institute, and a consensus on which tools to use for it is still missing in the field.

Reading lots of papers and endless meetings with Dr Harshil Patel enabled us to come up with the solution of using different programs for different questions (Wellington for the novel footprint detection, BagFoot for the temporal analysis of known transcription factor binding).

When doing the research, did you have a particular result or 'eureka' moment that has stuck with you?

Seeing that we were able to validate *in vitro* the transcription factor footprints identified with the bioinformatic analysis was a great eureka moment!

Why did you choose Journal of Cell Science for your paper?

The broad readership and its good reputation were two major factors. On top of it, my supervisor Caroline had recently published another paper from the lab in this journal. Since this previous publishing experience with JCS had been very positive, we decided to send this manuscript too.

Have you had any significant mentors who have helped you beyond supervision in the lab? How was their guidance special?

Beside my supervisor Dr Caroline Hill, who always supported and guided me during the PhD, I am particularly grateful to my colleague Dr Ilaria Gori. Ilaria has a huge experience in molecular biology and it is thanks to her tips and tricks that many experiments worked out. Most importantly, she always knows how to cheer people up and to create a positive working environment!

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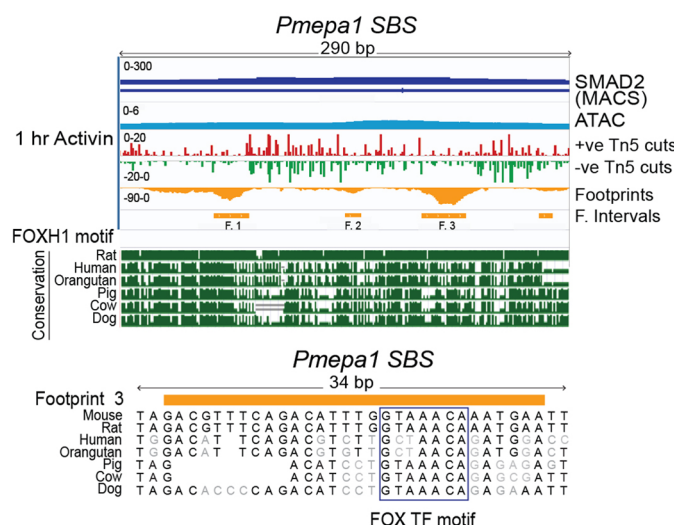
Locus-specific footprint analysis identifies novel cofactors for SMAD binding to closed chromatin at the enhancer of the *Pmepa1* gene.

What motivated you to pursue a career in science, and what have been the most interesting moments on the path that led you to where you are now?

According to my parents, I always had a strong curiosity for nature from a very young age… I think I decided to do science – and biology, in particular – because I wanted to satisfy this personal curiosity towards understanding the mystery that life is. Concerning my career in science, I think the turning point was being accepted into the PhD programme at the Francis Crick Institute. I was coming from a small institute in the north of Italy and I was living close to my hometown. At the Crick, I found myself projected in another dimension: a huge, international institute in the heart of one of the biggest cities on the planet. I believe I would not be the scientist and the person I am now without having gone through such an enriching experience. I will be always grateful to my PhD supervisor Dr Caroline Hill for having given me this opportunity.

Who are your role models in science? Why?

Rita Levi Montalcini was an Italian neuroscientist. She won the Nobel prize in Physiology and Medicine for the discovery of the nerve growth factor. Of Jewish origins, during the 2nd World War Rita was expelled from the University of Torino – the same place where I did my studies – but continued to carry out her experiments by setting up a research lab in her bedroom. To me, she is an extraordinary example of resilience and determination. Thinking about the difficulties she must have been able to overcome as a young Jewish woman scientist helps me to put in perspective the challenges I face in my research.

What's next for you?

Currently, I am very much enjoying doing a postdoc in neuroepigenetics at the Ecole Politechnique Federal de Lausanne (EPFL). It's a completely new field of research for me, and I believe changing field after my PhD helped me to find new motivations to stay in science. My goal for the next years is to complete the postdoc in the best way possible in order to progress in the academia career towards independency. However, if this does not work out, I will do a second postdoc.

Tell us something interesting about yourself that wouldn't be on your CV

I like sailing and alpinism… if I'm not in the lab you will probably find me on the lake or climbing a mountain.

Reference

Coda, D. M., Patel, H., Gori, I., Gaarenstroom, T. E., Song, O.-R., Howell, M. and Hill, C. S. (2022). A network of transcription factors governs the dynamics of NODAL/Activin transcriptional responses. *J. Cell Sci.* **135**, jcs259972. doi:10.1242/jcs.259972