

Spotlight on...

Gianni Cesareni



Our authors know that, traditionally, papers submitted to *FEBS Letters* are handled by specialized editors who are scientifically active in specific fields. However, some of the journal's editors can comfortably cover several different areas of biology. Gianni Cesareni, Professor of Genetics at the University of Tor Vergata in Rome, Italy, is certainly one of these. "I am a specialist in nothing, but I can talk about anything", he says with a playful smile.

How does this broadness come about?

The main reason, I believe, is that I like to read outside my field. But apart from this, perhaps my interests haven't been very focused over the years. I started out by studying physics at university, but I soon realized that I was more interested in biology. So I did my thesis in biophysics, modeling phage growth in bacteria. Later, I contributed to develop recombinant DNA technology and learned about nematode biology during my postdoc in Cambridge, thanks to stimulating discussions over coffee break with my supervisor, Sidney Brenner. I then moved to the EMBL, in Heidelberg, where I discovered that a small RNA can regulate plasmid replication by pairing with a complementary RNA that primes replication initiation [1]. This was the first demonstration of a biological mechanism regulated by the association of two complementary small RNAs. The characterization of the protein Rop that modulates the association of the two regulatory RNAs led me to the study of its structure and folding [2]. After that, moving back to Italy, I got interested in how the complicated interaction web in the cell governs its physiology.

And where does your research take you now?

It is evident by now that some properties of cell physiology only come to surface with a holistic study. We therefore are now studying protein interactions from a global point of view. To this aim, we have created a database called MINT that collects experimental information about molecular interactions [3]. However, our current view of the protein interaction network is static and does not take into consideration when, where and at what concentration the proteins actually meet and interact in the cell. In order to try to get over this serious limitation, we have developed a tool, called ProtNet, which can simulate the dynamics of protein interactions within the cell [4].

You are now starting an experiment with *FEBS Letters* involving the publication of "Structured Digital Abstracts". What is it about?

Up to now, the MINT database has been implemented by curators who extract protein interaction data from articles published in *FEBS Letters* and some other journals, transforming the information in a computer readable format. However, the amount of information on the interactions between biological entities grows more rapidly than database efforts can keep up with. The risk is that valuable information will be lost in the jungle of scientific literature if it is not systematically stored in databases. In the future, automatic text mining will play an important role in this process of information extraction. However, the text mining strategy is not efficient yet, due to the problem of identifying gene names in scientific text [5] and the vast diversity of expressions used by the authors to say the same thing. We are therefore now asking *FEBS Letters* authors to help in this process by submitting their findings in a structured format, clearly identifying the participating "entities" and their relationships. This information is then used to compile a structured, but human-readable, text, using a controlled vocabulary, to be appended at the end of traditional abstracts. In this way, the information can be easily extracted by a computer without the intervention of a curator. For the first six months the structured abstracts will be an experiment. The results of this experiment will then be offered for discussion in order to formulate a community-accepted proposal to be widely implemented in the scientific publication process.

Why did you choose *FEBS Letters* to launch this project?

There are several reasons. Being a *FEBS Letters* editor makes it easier for me to follow the project. Also, the article on the MINT database (which is, by the way, one of my most cited papers) was first published on *FEBS Letters* [3], and articles from this journal have already been curated by MINT for the past three years. *FEBS Letters* is therefore a natural choice which gives continuity to the project. In addition, the short papers published in *FEBS Letters* are particularly suitable for such an experiment. We have inaugurated the project with a *FEBS Letters* special issue on interaction networks, and the experiment is explained in detail in a minireview within this special issue [6].

What is the advantage for the authors?

The structured abstract will basically increase the visibility of the scientific data, without the risk of misinterpretation. It will mean a little more work for the author, but it is necessary for the sake of science and the scientific community. I am confident that if the experiment is successful, it will encourage a wide community discussion and hopefully stimulate a rewarding revolution in the way we make our results available to the scientific community.

What does Gianni Cesareni do in his spare time, if he has any?

He certainly does, despite the long working hours. I try to defy aging by playing basketball at an amateur level, and by skiing occasionally. I also enjoy gardening.

References

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