

- [ScienceWatch Home](#)
- [Inside This Month...](#)
- [Interviews](#)

- Featured Interviews
- Author Commentaries
- Institutional Interviews
- Journal Interviews
- Podcasts

Analyses

- Featured Analyses
- What's Hot In...
- Special Topics

Data & Rankings

- Sci-Bytes
- Fast Breaking Papers
- New Hot Papers
- Emerging Research Fronts
- Fast Moving Fronts
- Corporate Research Fronts
- Research Front Maps
- Current Classics
- Top Topics
- Rising Stars
- New Entrants
- Country Profiles

About Science Watch

- Methodology
- Archives
- Contact Us
- RSS Feeds



Interviews

Analyses

Data & Rankings

Special Topics : Epigenetics : Fred Berger & Pauline Jullien Interview - Special Topic of Epigenetics

AUTHOR COMMENTARIES - From Special Topics

Epigenetics - March 2009

Interview Date: May 2009



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Fred Berger & Pauline Jullien

From the Special Topic of Epigenetics

One of the core papers in the Arabidopsis thaliana DNA Methylation Research Front Map, which is a part of our Special Topic on Epigenetics, is "Maintenance of DNA methylation during the Arabidopsis life cycle is essential for parental imprinting," (Jullien PE, et al., Plant Cell 18[6]: 1360-72, June 2006). In Essential Science IndicatorsSM from Thomson Reuters, this paper has 44 citations to its credit up to December 31, 2008.

In this interview, ScienceWatch.com talks with two of the paper's authors, Dr. Frederic Berger, who is the Senior Principal Investigator, and Dr. Pauline Jullien, who was the major contributor to this study. Both authors work at Temasek Lifesciences Laboratory, which is an affiliate of the National University of Singapore and Nanyang Technological University.

Below, they talk about the paper and its significance for the research community.

SW: Would you please describe the significance of your paper and why it is highly cited?

At the time the paper was published only two genes had been reported for their monoparental expression (imprinting) in plants. In this paper, we identified *FERTILIZATION INDEPENDENT SEED 2 (FIS2)* as a third imprinted gene in the model plant *Arabidopsis*. More importantly, our study clearly showed that the maintenance DNA methyltransferase MET1 is responsible for silencing of the paternal allele of *FIS2* during the vegetative life cycle, male gametogenesis, and development of the endosperm, the extra-embryonic tissues where imprinting takes place in plants. Thus, in this study we described the whole cycle of imprinting in plants for the first time.

SW: How did you become involved in this research, and were there any particular successes or obstacles that stand out?

Our original main research interest was to study endosperm development. Amongst mutants affecting endosperm development, *fis2* mutations (originally identified by A. Chaudhury) affected endosperm development when inherited from the mother. This suggested that *FIS2* expression was restricted to the maternal allele. The lack of typical signature for targets of DNA methylation on *FIS2* was problematic for identification of the cis-element responsible for imprinting, and our collaborator Tetsu Kinoshita helped to solve this problem. This study caused a major shift in the research orientation of our team, which

became focused on investigations of imprinted gene regulation in the endosperm.

SW: Where do you see your research and the broader field leading in the future?

One of the current aims of our research is to dissect how imprinted gene expression is established. We want to understand how two alleles with identical DNA sequences can be differentially marked by epigenetic modification, which, in turn, results in imprinted gene expression. This takes place during male and female gametogenesis, and we have recently shown that the Retinoblastoma pathway plays an essential role in maternal activation of DNA methylation dependent imprinting genes (Jullien PE, *et al.*, Retinoblastoma and its binding partner MSI1 control imprinting in *Arabidopsis*," *PLoS Biology* 6[8]: 1693-1705, August 2008). One of the broader directions of the field will be to identify new imprinted genes in *Arabidopsis* in order to draw general conclusions.

What are the implications of your work for this field?

Two years ago, in parallel with the identification of imprinting of *FIS2*, we showed that maternally expressed imprinted genes could be also controlled by a different silencing mechanism dependent on histone methylation by Polycomb group activity (Jullien PE, *et al.*, "Polycomb group complexes self-regulate imprinting of the polycomb group gene *MEDEA* in *Arabidopsis*," *Current Biology* 16[5]: 486-92, 7 March 2006). This identification also led to the understanding of a negative feed-loop involving the Polycomb Group gene *FIS2*. Both DNA and histone methylation are also essential for imprinting of genes in mammals and our results pointed to a convergent evolution of imprinting mechanisms.

Work in our team and in the teams of T. Kinoshita and R. Fischer has shown that epigenetic marks establishment during gametogenesis is critical for imprint establishment for genes regulated by DNA methylation. The same principle probably holds true for imprinting genes dependent on histone methylation, and the mechanisms involved in the dynamics of these epigenetic marks now needs to be addressed. We hope that the concerted efforts of researchers will lead in the near future to a general view of imprinting mechanisms in plants. This will provide the basis for longer-term major questions pertaining to the biological significance of imprinting and how this remarkable epigenetic mechanism evolved. ▀

Frederic Berger and Pauline Jullien
Developmental Biology Program
Temasek Lifesciences Laboratory
Republic of Singapore

Fred Berger & Pauline Jullien's current most-cited paper in *Essential Science Indicators*, with 44 cites:

Jullien PE *et al.*, "Maintenance of DNA methylation during the *Arabidopsis* life cycle is essential for parental imprinting," *Plant Cell* 18(6): 1360-72, June 2006. Source: *Essential Science Indicators* from Thomson Reuters.

KEYWORDS: DNA METHYLATION, ARABIDOPSIS THALIANA, MONOPARENTAL EXPRESSION, IMPRINTING, PLANTS, ENDOSPERM DEVELOPMENT, GENE REGULATION, IMPRINTED GENE EXPRESSION, GAMETOGENESIS, GENE SILENCING, EPIGENETIC MARKS.



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Lead author
Pauline Jullien

"We want to understand how two alleles with identical DNA sequences can be differentially marked by epigenetic modification, which, in turn, results in imprinted gene expression."

[back to top](#)

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