

## Koala crisis

The doyen of Australian conservation concerns is in danger of becoming extinct within the next 30 years, one organization has announced, as a result of forest fires, climate change, disease and over-development. Recent surveys have led to estimates that only 43,000 koalas are still living in the wild, compared with 100,000 just six years ago.

The Australia Koala Foundation has said that, if the decline continues, koalas will disappear in the wild by 2040. Deborah Tabart, the charity's chief executive, is urging the Australian government to list the animal as endangered. "I think it will be hard for anyone to walk away from this data. We have a very high level of confidence that it accurately shows a drastic decline."

Nigel Williams



**Worries:** Conservationists are increasingly concerned that koala numbers are declining dramatically. (Photo: Alamy.)

## Q & A

### Raphael Mercier

*Raphael Mercier is a researcher at the Institute Jean-Pierre Bourgin, located at the Versailles node of INRA. He graduated from the University of Paris XI in 2001. After a postdoc at the University of Birmingham UK with Gareth Jones and Chris Franklin, he returned to Versailles, where he got a permanent position in 2003. His entire scientific career has been devoted to the study of meiosis in the model plant Arabidopsis thaliana.*

**What turned you on to biology in the first place?** As far as I remember, I always wanted to be a researcher. As a child at the movies or reading comics, I was always more fascinated by caricatured scientists such as Emmet Brown, The Count of Champagnac or Professor Cuthbert Calculus than by the heroes (Marty McFly, Spiro or Tintin). Although I was raised on a farm, as a child I was not particularly interested by the natural world. It was only at high school, with my first genetics lessons, that I decided I was interested in biology. I was immediately fascinated by classical genetics. Just by looking at the colour of a bug's eyes or the shape of a pea, and thinking a bit, you can decipher the mystery of heredity and construct the map of a chromosome, amazing! Add to that molecular genetics, the ability to read the genetic code and to explain a major trait just because there is an A there instead of a T, and you get a really fascinating area of science. I do not regret that choice, being glad to work in an area of research that has not ceased to be exciting for a century and looking forward to seeing what we will do with the current revolution of deep sequencing.

**How did you decide on your current research topics?** Like many scientists, my current research topic is more the consequence of contingency than of a deliberate choice. I decided early on to work with *Arabidopsis* because, wanting to become a geneticist, working with plants was a natural choice.

Plants have always been at the forefront of the study of heredity. The Mendelian laws of heredity were established from experiments on peas and rediscovered 30 years later in work on a range of plant species. The first demonstration that genetic crossovers are associated with physical recombination of chromosomes was made in maize by McClintock, who also discovered mobile DNA elements. RNA-mediated gene silencing was first discovered in petunia and plants have a central role in deciphering the underlying mechanisms of RNA interference (RNAi) — indeed, it is surprising that a plant scientist was not included among those honoured by the recent Nobel Prize awarded for the discovery of RNAi.

I started my PhD with Georges Pelletier and Christine Horlow who entrusted me with an *Arabidopsis* mutant, *swi1*, that was affected in female gametogenesis. It soon turned out that this mutant had a defect in female meiosis and that the wild-type *SWI1* gene is required for both male and female meiosis. I haven't left the meiosis field since. Meiosis is the fundamental process of heredity in eukaryotes, during which the genetic shuffling occurs that makes each generation different. Given my attraction to genetics, I can hardly imagine a more suited research topic, using genetic approaches to decipher the fundamental process of heredity.

**Do you have a favourite paper?**

There are many wonderful genetic papers, but I would pick up a recent one in my field: the work by T.S. Kitajima *et al.* in Y. Watanabe's group (Nature (2004) 427, 495–497). This paper identifies Shugoshin, a protein that protects sister chromatid cohesion at meiosis, as one of the major features that distinguishes meiosis from mitosis. With a crystalline reasoning they postulated that a protein which is present at meiosis but absent at mitosis must protect Rec8, a component of the molecular glue that holds sister chromatids together at metaphase of meiosis (if expressed in mitosis it does a similar job until it is cleaved to allow sister chromatid segregation). They thus set up a very smart screen, searching for a gene that generates toxicity during mitosis only when

co-expressed with Rec8. In this way, they identified and functionally characterized a protein that protects centromeric Rec8 from degradation during meiosis I, shedding light on a conserved mechanism. Adding to the beauty of the story, they gave to the protein a very nice name, Shugoshin, Japanese for 'guardian spirit'. This work illustrates how a genetic screen, if well thought out, can elegantly solve a biological question. There is no fancy technology or big money, just smart minds.

**What is the best advice you've been given?**

During my PhD I was told, "If you are in a hurry, slow down". This is very good advice. It's much more efficient to sit down and think before running an experiment than to have to redo it several times because of bad design. Will this experiment really answer my question? Am I sure there is no better way to test it? Have I included all the necessary controls? There is nothing more frustrating and time-consuming than to get an exciting result and not be able to undoubtedly conclude because of a missing control. This is equally true for short experiments and for large projects.

**Do you have a scientific hero?**

I could for sure cite one of the extraordinary heroes of genetics such as Mendel, Morgan, Crick or Monod, but I would rather choose someone who opened my eyes to another field — Stephen Jay Gould. Besides his major contribution to the field of evolutionary theory, he is an outstanding story teller. I really enjoyed and learnt a lot by reading his series of anthologies of *Reflections in Natural History* and his book *Wonderful Life* on the re-interpretation of the Cambrian Burgess shale fossils. Gould introduced to me, a reductionist geneticist, concepts such as exaptation, emergence and contingency in evolution, and underlined the dangers of pre-conceptions when doing science. To have a complete view of Gould's vision of evolutionary theory, I would recommend reading of his monumental '*The Structure of Evolutionary Theory*'. It is very long, but well worth the effort. Actually, I have to confess that I read French translation by Marcel Blanc, which is

even longer (2033 pages!) but *quand on aime on ne compte pas*.

**What are the big outstanding questions in your field?**

Actually, the same ones have existed for a century! While our understanding of the mechanism of homologous recombination and chromosome distribution has dramatically increased, especially in the last decade, major questions are unsolved. How do the chromosomes recognize each other? It is still a mystery how chromosome 1 (say) pairs and recombines only with the homologous chromosome 1, and not with chromosome 2, and even more amazingly not with its homeologous chromosome 1 in polyploid species such as wheat. Another fascinating phenomenon is crossover interference, the tendency of a crossover to be some distance from any other, so that multiple crossovers tend to be evenly distributed along a chromosome. Crossover interference has been recognized by early geneticists in the beginning of last century but, almost 100 years later, we hardly have any idea how crossovers 'talk' to each other. The meiosis scientific community is pushing hard to solve these questions, and I bet that, with the combined efforts of scientists working on various experimental model species, we will soon unravel the mystery — hopefully before another century is up! (I would bet, in the next decade.)

**What is your favourite conference?**

I'm a bit monomaniac but the two, alternating bi-annual conferences on meiosis, the Gordon Conference and the EMBO meeting, are just fantastic. They are both of the right size to keep it informal and to allow easy contacts with leaders in the field, who are systemically present. I remember a few years ago, sitting down on the lawn of the Colby-Sawyer College, discussing how to test crossover interference in my *Atmer3* mutant with Frank Stahl. Yes, the Frank Stahl of the famous Stahl and Meselson experiment which proved the semi-conservative replication of DNA, described in every genetic textbook. I was rather impressed. Frank Stahl is also one of the most notable specialists working on crossover interference, and he very kindly

listened to my experiment plans, encouraged me and gave me advice. I have had similar experiences with other big names in the field.

**What is your greatest ambition in research?** To add a little stone to the magnificent edifice of genetics. I would also be happy if some of our findings led to crop improvement, which is a major need for the coming decades. I really enjoy explaining to my parents, who are retired from farming, that working on a weed (*Arabidopsis*) may improve agriculture.

**What do you think about the perception of biotechnology in Europe?** I am quite irritated by the irrationality of the debate which is strongly influenced by fanatics for who “*tout est pour le mieux dans le meilleur des mondes*”, nature being good and everything touched by man being unsafe. Unfortunately, nature is not plain good and for more than 10,000 years, man has selected and modified plant and animal species to produce safe food. Of course we should discuss what to do and not do, but rejecting genetically modified plants as a whole is a big mistake (by the way, meiosis is a huge genetic modification – should we ban it?). I think that agricultural biotechnology, in combination with classical genetics, is one very promising tool to answer the combined need for increased production and preservation of the environment.

While writing, I have just heard that a trial of transgenic grape has just been destroyed by some of these fanatics at the INRA of Colmar, in the east of France. The Colmar experiment, with no commercial purpose, was testing a strategy to protect grapes against a virus transmitted by a nematode, against which the only treatment is barely efficient and very polluting. The experiment plan was discussed, approved and followed by a committee composed of not only scientists, but also winegrowers and associations. This destruction, like the others committed in the last years in France, is simply scandalous and illustrates well the level of the debate.

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## Quick guide

# Stegosaurus

Matthew Cobb

**What is a stegosaur?** Stegosaurus were large, herbivorous quadrupedal dinosaurs with small heads, armoured plates and spines (osteoderms) on their back, shoulders or tail – hence the name meaning ‘roof-’ or ‘tile lizard’. They were at their evolutionary height in the Jurassic, from about 200–145 million years ago (mya). One stegosaurus taxon – once known as *Wuerhosaurus* – is found in the Cretaceous, and survived up to around 125 mya. Relatively few stegosaurus skeletons have been found, most of them incomplete. This may reflect their rarity in the Jurassic ecosystem, or it may be a consequence of taphonomy – the way in which dead organisms are turned into fossils.

**Where are they found?** Stegosaurus fossils have been found on every continent except Antarctica, but fossils might exist there, too. The first stegosaurus was described in 1875 by Richard Owen, the man who invented the term ‘dinosaur’. The decisive discovery was made in the Morrison Formation in Wyoming, by Othniel Charles Marsh, in 1877. Marsh unearthed *Stegosaurus stenops*, the iconic beast with huge bony plates on its back and bony spikes on its

tail. Since then, other genera, such as *Kentrosaurus*, with narrower back plates and sharp, long spines on its shoulders, have been unearthed. The stegosaurus clade appears to be equally distributed around the planet, but most fossils, and the best preserved ones, have been found in North America (Figure 1).

**What were the back plates for?** We don’t know. It is not even certain what position they were in, although most reconstructions show them as vertical, in two alternating or parallel rows. Some paleontologists have suggested they could be moved, but they are generally thought to have been rigid and fixed. It was initially assumed the plates had a defensive function. However, although the outside of the plates was bony, the central area is made up of trabecular (spongy) bone, suggesting that they were not very strong. Furthermore, both the powerful back legs and the head were unprotected. The existence of vascular tubes connecting the plates to the dermis, the presence of clearly visible grooves for blood vessels on the outside of the plates, together with evidence of capillary perforations in the plates, have all led to the suggestion that they played a thermoregulatory role. This conjures up the image of stegosaurus using their plates as giant radiators, to cool down during Jurassic heatwaves, or even of bleary-eyed stegosaurus trudging into the dawn, finding the nearest hill, and standing on a north-south axis to heat themselves up. It is unclear, however,



Figure 1. ‘Sarah’, a young adult *Stegosaurus armatus*.

Discovered in 2003 in Wyoming, in Upper Jurassic rocks (160–145 my old), Sarah is the most complete stegosaurus skeleton ever displayed. The photo shows a cast, as mounted by the Black Hills Institute of Geological Research. Photograph by Urs Möckli, Sauriermuseum Aathal.