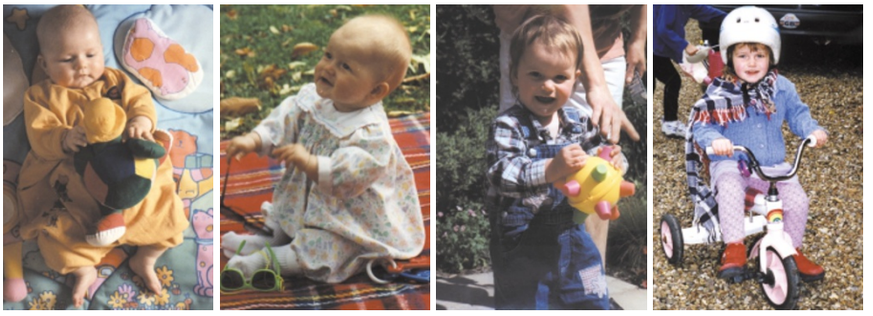
PLANT GENETICS

Developmental milestones



Sophisticated and high-throughput technologies for genetic manipulation are being devised all the time, and can provide rapid insight into gene function. But to realize the full potential of these methods, techniques for phenotyping need to keep pace. Boyes *et al.* report a scheme for phenotyping in *Arabidopsis thaliana* that is thorough, sensitive and high throughput, and that could provide a valuable framework for studying gene function in this plant.

The authors began by formulating a quantitative description of the development of wild-type *Arabidopsis*, covering its complete life cycle. This description has two aspects. First, they defined a series of developmental landmarks (and the times at which they occur), such as "emergence of the cotyledons", "first flower open" and "flowering complete". Second, they collected detailed morphological information as each developmental landmark was reached, such as "number of rosette leaves", "sepal length" and "seed yield". Overall, the authors described 14 developmental landmarks and 52 morphological traits. Importantly, these data can be collected efficiently and cheaply, and the authors also quantified the normal levels of variation for each measurement.

To test whether the collection of these phenotypic data can uncover developmental defects in *Arabidopsis* mutants, the authors looked at five mutants that had previously been described as having only minor or no morphological abnormalities. In each case, clear abnormalities were detected, which provide new information on the role of the corresponding genes in development. The function of *FAE1* (*FATTY ACID ELONGATION 1*), for example, was thought to be confined to the seed, but striking defects in leaf production in the *fae1-1* mutant imply that *FAE1* is also required later in development.

This new scheme for phenotypic analysis provides a sensitive assay for identifying developmental defects in *Arabidopsis* mutants. If adopted more widely it could become a valuable standard, which will allow more robust comparison of the consequences of genetic, as well as environmental, perturbations to *Arabidopsis* development.

Mark Patterson

References and links

ORIGINAL RESEARCH PAPER Boyes, D. C. *et al.* Growth-stage based phenotypic analysis of *Arabidopsis*: a model for high throughput functional genomics in plants. *Plant Cell* **13**, 1499–1510 (2001)

WEB SITE Paradigm Genetics

FISH GENETICS

A colourful catch in medaka

Sun worship might give you a great tan, but it is also behind the increasing incidence of skin cancer, especially among those of northern European descent. As a result, pigmentation biology has come under close scrutiny in recent years, and genetic studies into mouse coat-colour mutants and into human pigmentation disorders have revealed much about the melanin biosynthetic pathway. Now Japanese researchers have discovered a new component of this pathway, surprisingly not in mammals but in a fish — the medaka. This is the first medaka gene to be positionally cloned, and it promises to provide new insights into the biochemical regulation of melanin synthesis, not just in fish but possibly in humans too.

The Japanese have bred an attractive orange-red variety of medaka — which is homozygous for an allele called *b* — for hundreds of years. Melanin formation in *b*-fish is barely visible, except in the eyes (see picture). To positionally clone *b*, Shoji Fukamachi and colleagues mapped it in a backcross derived from two highly polymorphic inbred strains — so polymorphic, in fact, that after mapping only 545 backcross progeny, they were able to narrow down the candidate interval to 40 kb. This region contained two genes, one of which was mutated in seven of eight *B*-locus mutants. No mutations were found in the common *b* allele, but given its tissue-specific effects, this might be because a mutation lies in the gene's upstream regulatory regions.

Importantly, this gene is highly homologous to the human gene *AIM1* (antigen isolated from immunoselected melanoma 1). The medaka and human *AIM* genes, together with a mouse homologue isolated by the authors, are predicted to encode a 12-transmembrane-spanning protein. Because this is a structure common to transporter proteins, Fukamachi *et al.* propose that AIM1 might be located in the melanosomal membrane, where it could transport certain substances required for melanin biosynthesis. No doubt, future fishing trips into the medaka genome are planned — let's hope that they yield as rapid returns as this one.

Jane Alfred

References and links

ORIGINAL RESEARCH PAPER Fukamachi, S. *et al.* Mutations in the gene encoding B, a novel transporter protein, reduce melanin content in medaka. *Nature Genet.* **28**, 381–385 (2001)

WEB SITE Medaka fish web server

A *b*/*b* (top) and a wild-type medaka fish. Courtesy of Shoji Fukamachi, University of Tokyo, Japan.