

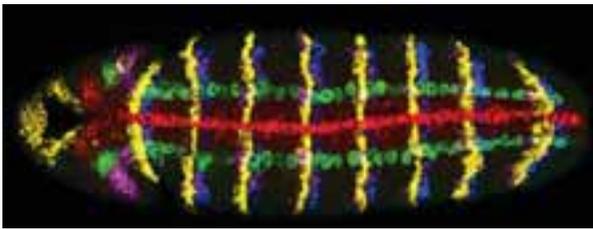
Evolutionary developmental
biology (evo-devo)

New Models, Please

The amalgamation of developmental and evolutionary biology, called evolutionary development (evo-devo), revealed a wealth of new data on how animal and plant forms are made and how they evolved. More, new model organisms promise new insights. However, how does one choose the right ones for research?

Xenopus, the chick, the mouse, the zebrafish, *Drosophila*, *Caenorhabditis elegans* and *Arabidopsis thaliana* are the classic representatives of higher organisms in life sciences, ranging from genomics via physiology to developmental research. These models also dominate evo-devo, the science of understanding evolution via the comparative analysis of early animal or plant development. In the past 15 or so years the “big six” animal models did a good job for evo-devo.

To begin with research on myriads of flies followed by mice, worms, frogs and chicks revealed that the development of body parts such as limbs, wings, eyes or hearts, though very different in structure among animals, is governed by the same genes in different animals. The animals



The analysis of the expression of homoeotic genes opened the door to evo-devo research.

share a common “tool kit”, common “master genes” that guide their development and the formation of their bodies. That insight, at the same time, was a breakthrough for understanding how body structures evolved during evolution – how fins were modified into limbs, how mouthparts, claws, swimming and feeding appendages, wings and – in the case of plants – how flowers or trichomes have evolved.

Now that genome sequences of these model organisms as well as from many other species are available and new high throughput technologies have been developed, lots of new data are rapidly being collected. Certainly people also expect

a wealth of new insights about how biological diversity was and is still formed.

However, missing is the very basis for evo-devo studies – more model animals and plants. This year Ronald Jenner and Matthew Wills at the University of Bath (UK) lobbied in *Nature Review Genetics* for new model organisms for evo-devo research.

“The choice of new model organisms has not been optimal”, write Jenner and Wills. It’s true, the “big six” model organisms have been chosen because they are easy to keep in the laboratory, select and breed – and because it was assumed that biological phenomena uncovered in them could be transferred to humans. While these arguments generally turned out to be correct and useful in the context of developmental research, the benefits to evo-devo as a subject are limited.

Limited?? Those six were very true treasure troves, allowing for one of the most fascinating discoveries in recent biology, the identification of homoeotic genes that form body plans and body parts in animals (and plants – see page 20). Their analysis finally led to the discovery of some law-like generalities of development and evolution. However, flies, mice, frogs, worms, zebrafish and chicks cover only 3 of more than 35 phyla of animals. “By far not enough,” says Jenner adding in the same breath that simply selecting new model animals by maximising phylogenetic spread, or by plugging holes in the phylogenetic tree is not the best option of choice.

How to choose a model organism?

In times of spare money and spare time one should give some thoughts to how to choose a new evo-devo model. Those who are familiar with the history of biology know that it can take umpteen years of

work to fully exploit a new model system, giving scientists a hard time. On top of everything, such model (re)search results appear if at all in only a few publications that are not likely to attract a great deal of attention. Basic research on new creatures typically doesn’t get you to the top of citation lists, it doesn’t grab overwhelming attention of colleagues and editors – leaving us with the sobering question: How can one develop new evo-devo models and which animals or plants should one choose?

Questions count

Jenner and Wills suggest that an organism is picked by its suitability to answer a specific evo-devo question. “Maximising phylogenetic spread is good to show diversity but it doesn’t necessarily lead to new general insights about evolution,” says Jenner. This position is supported by other evo-devo scientists, as for example Frietson Galis (Leiden University, The Netherlands) who heads the brand new European Society for Evolutionary Developmental Biology (EED). She says, “I fully support Jenner and Wills. However, I also think that we put too much emphasis on model systems. We should not forget that we need to study biodiversity.” Scrupling that focusing on model organisms limits the scope of science. She says that, “for any question raised one should choose a suitable subject, irrespective of whether it is a model system or not. It’s really important that science managers understand that we need to do research not only on model systems.”

Armin Moczek from the Indiana Molecular Biology Institute who is working with the horned dung beetle of the genus *Onthophagus*, stated, “The choice of model systems should primarily be motivated by the exact question(s) one is trying to answer, and not all questions require particular phylogenetic considerations. For example, many people would argue that some of



the greatest frontiers in evolutionary biology include the following three issues: (i) the origin of life, (ii) the origin of multicellularity, and (iii) the origin of major evolutionary novelties. I would argue that to address issues (i) + (ii) phylogenetics is critical, for (iii) it is largely irrelevant.”

Also Milan Milinkovitch and Athanasia Tzika argue in a recently published paper (Escaping the Mouse Trap, *J. Exp. Zool.* 2007, 308B, 337-346) that “the phylogenetic-distance criterion is limited by at least two parameters: (i) the rate of phenotypic transformation is highly variable among lineages and (ii) variation worth investigation exists at multiple phylogenetic levels.”

The genome pipeline is full

Can it be true? Is phylogenetics really not so relevant for the analysis of evolutionary novelties as generally thought? Scientists often assume that the position in the evolutionary tree correlates with basal or more advanced developmental stages, respectively. Accordingly, among species that descend from the same common ancestor

those are designated as basal that are separated from this ancestor by the smallest number of speciation events. That’s the reason why biologists chose the zebrafish as a “canonical vertebrate” – the common ancestor of all vertebrates was a fish.

However, what is the zebrafish a model for? For chordates, for vertebrates, for bony fish, for ray-finned fish, for teleost fish or for the family Cyprinidae? “The answer heavily depends on what characters one is interested in,” argue Milinkovitch and Tzika. They are right.

One should keep that in mind when sequencing the genomes of representatives of possibly the deepest nodes of major clades like the South American opossum (*Monodelphis domestica*), the African elephant (*Loxodonta africana*), the European common shrew (*Sorex araneus*), the European hedgehog (*Erinaceus europeus*), the guinea pig (*Cavia porcellus*) and the nine-banded armadillo (*Dasypus novemcinctus*).

The choice of these species for future evo-devo research was made on the assumption that each of these species represents a

non-overlapping subset of mammalian phylogenetic and morphological diversity. Also, the Plant Genome Comparative Sequencing Program (PGCSP) funded by the American National Science Foundation looks out for “key nodes or groups of plants in the Tree of Life that would enable researchers to answer specific biological questions relevant to the goals of the PGRP”

The problem of true novelties

However, the correlation of putative key nodes and the evolution of genome sequence leading to evolutionary novelties isn’t stringent. Speciation can be accompanied with increased evolutionary change and vice versa, evolutionary change can occur without speciation. Simplicity must not be ancestral, it can also be the result of a subsequent reduction of the body plan. As Jenner says, “Just because an organism has sprung from the base of the evolutionary tree this does not make it more primitive or representative. Knowledge of phylogenetic position is essential for studying the origins of novelties which is an important

goal of evo-devo studies.” In fact, nobody can predict which of the species is the least modified in the evolutionary tree or which one is closest to the origin of a novelty. “For example, the snake-like body has evolved multiple times independently in squamate reptiles. Is there a most primitive snake-like animal?” explains Jenner,

Therefore, you can be sure that calling your attention to a specific animal or plant because you think that it will answer specific evo-devo questions leads to a certain, if not heavy, bias and insight into the general laws of development may be limited. That outspoken critique is made often. “[Model organisms] are all somehow a little odd and not mainstream. [...] If we want to understand evolution through Evo-Devo studies we need to look at a broad range of species

because we can't build out an evolutionary pathway by looking at extreme organisms,” said Janet Rossant (Hospital for Sick Children, Toronto) in an interview with *Nature Review Genetics*. To be honest, there's no other way. One can study the development of wings and winglessness only in insects, the development of limbs only in tetrapods. Anyway, Jenner doesn't judge bias to be a big problem. “Bias is just another word for focus”, he says.

A strong voice for evo-devo

Bias, phylogenetic spread – can we really predict what experimental animal or plant may ultimately prove a special evo-devo concept or provide us with the most informative answers? Didn't scientific breakthroughs often come from unexpect-

ed places? Galis doesn't want to give any specific advice concerning the criteria for how to choose a model system. Jenner says that one should not develop new models from scratch but “perhaps search the literature for appropriate organisms that scientists from other disciplines have already worked on”.

Whatever you choose as a new organism, evo-devo is about comparing species or taxa so there's no other way than working with more than a handful of animals or plants. Also, given the importance of better understanding the basic mechanisms underlying biological diversity, evo-devoists should play an energetic, proactive role in the scientific community when it comes to singling out new model species.

KARIN HOLLRICHER

Candidates on the Catwalk

For a while now, the impressive horns of beetles of the genus *Onthophagus* (1) have been challenging any audacious scientists to figure out just how those head satellites evolved. Yet, evo-devo research on these beetles commenced only recently. Armin Moczek from the Indiana Molecular Biology Institute wrote in an email, “If you define evo-devo more narrowly as evolutionary developmental genetics, then horned beetles are a much more recent phenomenon.”

An ideal new model animal for evo-devo research could be the water flea *Daphnia pulex* (2), suggests Ronald Jenner. The tiny freshwater crustacean has been the subject of ecological, evolutionary and toxicological studies for decades. Five years ago, the *Daphnia* Genomics Consortium started to develop genomic tools; the *D. pulex* genome is currently being annotated. Its distantly related congener *D. magna* is also on board; a sequencing project is on its starting block. Studying close relatives – so-called satellite species – allows insights into micro-evolution.

The choice of the starlet sea anemone *Nematostella vectensis* (3) as a model for evo-devo was motivated by the remarkable amenability to laboratory manipulation. That has already made it a productive system for exploring cnidarian development and a proliferation of molecular and genomic tools, including the currently ongoing *Nematostella* genome.

For studying segmentation and body patterning, Nipam Patel, from the Center for Integrative Genomics (University of Berkeley), has a new crustacean in his lab known as *Parhyale hawaiiensis* (4). As he reports, embryos of the easy-and-quick-to-grow animal survive injections; transposon-induced mutagenesis and RNAi also seem to work.

A research team led by Bernie Degnan (University of Queensland, Australia) focuses on the sea sponge *Amphimedon queenslandica* (5). This animal belonging to the earliest metazoans has no Hox genes

that in flies, worms, mice, elephants and even humans are responsible for the head-tail-axis. Body-organising functions are governed by NK-homeobox-like genes.

Mathieu Joron (University of Edinburgh) is promoting *Heliconius* (6) butterflies as promising models for studying micro-evolution, especially for investigating the adaptive changes of colour-patterns on the wings. Studying *Heliconius* species could shed light onto the mechanisms underlying colour-pattern changes and the longstanding question whether adaptive convergence between unrelated species is driven by natural selection or occasional phenotypic leaps facilitated by conserved developmental pathways.

Yet another group of interesting evo-devo candidates are *cichlid fish* (7). Hundreds of extremely young and genetically almost identical, though phenotypically diverse, species offer a kind of “natural experiment” and can be seen as “natural mutants”. Work on the development and evolution of colorational differences, that play an important role in sexual selection and speciation, as well as evo-devo studies on tooth shape difference, that are crucial for trophic adaptations, are ongoing in several labs around the world. Also, work on the evolution of *swordtail*

fishes' swords, which are in fact modified caudal fins and which have arisen through sexual selection, should not be forgotten. Genomic resources exist and a genome project is in the planning stage.

Platynereis dumerilii (8), a marine annelid exhibiting many ancient features in its lifestyle, anatomy, development and gene inventory could also become a new evo-devo model. Though there are a mere 41 entries in PubMed documents about this tiny animal, the oldest dating from 1951, recent work in Detlev Arendt's lab (EMBL, Heidelberg, Germany) raises hope that *P. dumerilii* will serve us with an answer to the question: How did the central nervous system come into existence?





Quillwort



Columbine

Evo-devo in plant research

“Ten years behind”

For a long time evo-devo research seemed to be a true animal topic. However, plants have a lot to offer to the field.

“Several books on evo-devo have been written completely ignoring plants,” complains Günter Theissen, an expert in the development of flowers at the Department of Genetics at the University in Jena (Germany). He says, “The way large parts of the evo-devo community confine research to animals thus ignoring plants is sub-optimal, perhaps even provocative.”

What are the reasons why green evo-devo seems to be largely ignored? Theissen, “The first reason is of a historical nature. Homeotic genes regulating the development and morphogenesis of living organisms were first identified in animals. The discovery of those genes established the basis for the emerging field of evo-devo. However, later homeotic genes were also identified in plants, *i.e.* MADS box genes that regulate the development of flowers. These genes have not, however, reached the same level of popularity as Hox-genes, the most famous subgroup of homeobox genes in animals that are missing completely in plants.

Plants do not get the “press”

The second reason is money. The strong connection to well-funded biomedicine has dramatically boosted research on animals and at the same time boosted animal evo-devo. Therefore, it’s not really surprising that many plant evo-devo researchers complain that their science is lagging ten years or so behind animal evo-devo.”

However, Saray Wyatt from the Environmental and Plant Biology Department at the Ohio University in Athens (USA) is not so sure. She wrote in an e-mail, “Certainly, plants do not get the “press” that animals do but there are some distinct advantages. One example is that because of the way plants grow, unlike animals, one fossil can provide numerous developmental stages of the plant life cycle. Thus it may be easier for us to use palaeontology to provide a context for evolutionary pattern (evolution of structure/transformational series) that can be combined with information about genetic developmental regulation to formulate a hypothesis.”

Until now, plant scientists focused mainly on plants like *Arabidopsis*, maize, snapdragon and, in more recent years, rice. Research in those model organisms has uncovered genes that organise and control morphogenesis of roots, shoots, leaves and flowers. However, those plants have not been chosen for their phylogenetic relation to each other. That’s why new model plants are urgently needed to elaborate the evolution of developmental mechanisms and their genetic basis, regardless of the fact that the plant kingdom doesn’t offer as many phylogenetic groups as the animal kingdom.

A geneticist’s nightmare

The group of land plants is comprised of mosses, lycophytes, ferns, gymnosperms and angiosperms only. Gymnosperms are a geneticist’s nightmare. Those plants are without exception woody plants. They need some 10 or 20 years growth to reach a reproductive stadium, plus a lot of space and there are no protocols for efficient mutagenesis. Also, ferns do not provide good genetic model plants. “We have tried to work with *Ceratopteris* for several years but we gave up,” says Theissen.

Perhaps the most interesting question of plant evo-devo is how did the floral structures of angiosperms develop from gymnosperm reproductive cones? Most research on this issue has been done on *Arabidopsis* and *Antirrhinum* resulting in the identification and function of MADS box genes.

Not the foggiest notion on how ...

“Orchids are fascinating plant models for the analysis of flower evolution,” adds Theissen. Those fragile, monocotyledonous plants develop zygomorphic flowers that co-evolved with their pollinators in a way that originated about 30,000 different species. Besides orchids, basal flowering plants such as water lilies and the bush *Amborella trichopoda*, probably the most ancient taxon of flowering plants, are promoted as interesting model plants. Also Poppy (*Papaver*), Gerbera and Columbine (*Aquilegia*) are discussed as new floral evo-devo models.

Yet, Columbine not only raises interest because of its enormous flower variability and unusual floral organs, the staminodia, but also because of its rapid adaptive radiation that the some 70 species of this genus have undergone. Growing in coastal forests as well as in deserts and in the mountains, Columbine species show an enormous flexibility and adaptiveness. The plant was put forward for genome sequencing in the US.

Wyatt would like to put forward Isoetes (*Isoetaceae*), also known as Quillworts. She argues that Quillworts “is perhaps the most important of all vascular plants to develop as a model organism. It represents the most distant living sister group to flowering plants. It evolved nearly everything that is found in flowering plants independently (and first) and therefore allows us to test hypotheses of the genetic basis for development and to differentiate among hypotheses of homology at the developmental and structural levels. As the only living representative of a developmental programme that produced a vast array of mature morphologies, Isoetes may possess the developmental programmes needed to produce many of those morphologies.”

... higher plants evolved from mosses

Yet another challenge for plant evo-devo is to provide a better understanding of the alternation of generations in land plants. All land plants pass through a generation change: The haploid gametophyte and the diploid sporophyte. In mosses the gametophyte dominates plant life, whereas for flowering plants (angiosperms) the sporophyte comprises almost all of their lifetime. Only pollen and embryo sacs are the gametophytic structures of those higher plants. Scientists haven’t the foggiest notion yet on how the transition from moss-like ancestors to higher land plants has taken place. To illuminate that secret one needs appropriate plant species of different taxa, certainly including the moss *Physcomitrella* as an important model system.

Obviously, concepts and ideas enough to finally keep up with animal evo-devo.

KARIN HOLLRICHER



Elliot Meyerowitz (l.), Christopher Somerville (r.)
and *Arabidopsis*

A talk with Elliot Meyerowitz and Christopher Somerville (USA)

“We had to fight some pretty hard battles”

Elliot Meyerowitz and Christopher Somerville, two pioneers of *Arabidopsis* research, talk about the advantages of having a model organism; science funding; help from James Watson; and European concerns about “green genetics”.

In recent decades, molecular biology seems to be driven almost completely by research on animal model organisms such as Drosophila, the mouse or C. elegans. What is driving plant research?

Elliot Meyerowitz: Well, we should not forget that most of our central notions in molecular biology stem from research on plants. These began with the cell, discovered by Thomas Hooke in the 17th century, the cell nucleus by Robert Brown and the gene by Gregor Mendel. Also many other things were first discovered in plants in the late 20th Century. Just a few years ago, RNA interference was found in plants ...

...but the Nobel Prize 2006 was awarded to Andrew Fire and Craig C. Mello for discovering it in C. elegans, an animal model organism. Do you have an explanation for the fact that most of the attention goes into research on animal model systems?

Christopher Somerville: It is not only the attention. Only about one percent of investigator-initiated, peer-reviewed funding for biological research in the U.S. goes to plant research.

Why is that?

Meyerowitz: My explanation is that most research and funding is organised around illness and that leads research away from plants towards animal systems of diseases. In the USA we have the National Institutes of Health, but in fact only one of the institutes studies health, all the others study the absence of health. That is why most of the money goes into animal research: because it seems to be more relevant. Probably we learn as much from plants.

Somerville: There is another explanation to explain why the resources are allocated to animal research and not to plant research. In the developed world, many peo-

ple face all these diseases, but only a few are hungry. Though actually, one of the largest health problems in the world is a plant problem: the problem of iron nutrition. Nearly a billion people are starving for iron. That is their main medical problem, because if you are dependent on rice, it will remove iron from your diet causing anaemia and other major health problems.

Meyerowitz: There are of course a few researchers who are studying iron-metabolism. They are paid to do it, because of haemochromatosis, a rare disease found only in Europeans and their descendants, where there is an accumulation of iron. All the study is concentrated on this rare group of people who accumulate too much iron overlooking the real problem which is people who have too little iron. It is as simple as that: modern research is not directed towards the problems of the developing world.

To what degree is business, i.e. the pharmaceutical industry, influencing the allocation of resources towards biomedical research?

Meyerowitz: I would not overdo the influence of business in this – at least compared to politics. In the United States the National Institutes of Health are the most important funding body and they are very much a creature of Congress. All the congressmen have their individual concerns, which reflect the concerns of their constituents. What are the constituents worried about? Getting a disease! They are not really interested in a general understanding of health or of nature.

Don't the big agro-industrial and energy companies have an interest in plant research and sponsor it?

Somerville: Their impact is tiny compared to the pharmaceutical industry in biomedicine. Up to now they haven't had

“Most research and funding is organised around illness and that leads research away from plants towards animal systems of diseases.”

much positive influence on research. That may change. Shell and BP are starting to invest large amounts to broaden energy research. I feel very optimistic about what these companies might do in the future in terms of supporting research. This is desperately needed.



You both began your careers in different fields – Drosophila and E. coli – before you became pioneers of Arabidopsis research 25 years ago. How did you move into this new field of research?

Meyerowitz: I have been interested in plants for a very long time. When I was a graduate student, I went to the plant seminars. However, the sophistication of *Drosophila* genetics was so much greater than that of any plant. Nevertheless, I was reading about *Arabidopsis* because it seemed so much like *Drosophila* in terms of its classical genetics. Though once my own laboratory was started at Caltech, I had a graduate student who was also very interested in plants and we obtained some *Arabidopsis* seeds from his uncle. The shift was modest. I continued to work on *Arabidopsis* and on *Drosophila* for another ten years but by 1991 the last person working on flies had left my lab.

Somerville: My story was a bit simpler. I married a plant breeder and she was very unhappy because so little of modern science was being applied to plant improvement. We could see at that time that the cloning of genes was going to become important in plant improvement. We recognized that we could make a lot more progress if we settled on a good model organism. As a result *Arabidopsis* has become the model organism in plant genetics.

Why this plant and not another one?

Meyerowitz: We independently settled on *Arabidopsis* because preliminary experiments by George Redei and others indicated that it had the kinds of properties that were desirable in a model plant. In particular,

it was small, easy to grow, self-fertile, diploid, and rapid cycling. It was also closely related to many of the most important food plants in the world. We initially began communicating about technical issues such as how to carry out basic genetic studies with *Arabidopsis* but, upon the discovery that we

had common values and goals, we soon began working together to encourage development in the field.

How was that received?

Somerville: Plant biology at that time was driven by two things: one was botany, which was the study of diversity and the other was agriculture. Therefore we had a lot of resistance in the beginning. They didn't understand what we were doing. We had to fight some pretty hard battles to get people to understand that it would be much easier to solve problems when we could work on a model. We facilitated the research from the very start by creating a stock-centre, where the seeds, the DNA and other things were made freely available.

Meyerowitz: The whole concept of a model organism was pretty new in plant biology at that time. The first thing that we did was measure the genome. It was known that it would be small, because it already had been shown that it was radiation resistant and that is proportional to the size of the genome. We both created tools that allowed other labs to do things they had never done before. The long-term goal of having the model organism was to focus a lot of people on a single experimental system.

Somerville: Today, we have 13,000 people working with *Arabidopsis*. That maybe more people than the number doing research on *Drosophila*. There is also more literature and many more papers.

In 2000 you and others completed the sequencing of Arabidopsis, the first fully-sequenced plant.. How did you do that?

Somerville: In the late eighties we started talking about sequencing the whole genome, first of all technically. At that time we were struggling to do relatively small amounts of sequences. In our labs we were only doing a few thousands of these pairs. However, in sequencing the whole genome we were talking about 130 million base-pairs! We knew it would cost hundreds of millions of dollars and no investment in plant biology had ever been made remotely like that. It was very ambitious and to begin with we started publishing brochures, calling for this project.

Meyerowitz: Finally, for sequencing the genome we managed to get about \$ 75 million. That is a lot of money for a plant biologist but for a medical scientist it would just be a huge grant. To us though it seemed like a lot.

Somerville: At that time that was a huge amount of money. James Watson was very helpful back in those days.

In what respect?

Somerville: In 1989, Elliot and I went to a meeting at the National Science Foundation convened by Watson. He had a fundamental idea, which influenced both of us, that is: if you don't ask for a lot of money you are never going to get it. He told us physicists come up with a single idea such as the space station then they go to Congress and ask for billions of dollars. Also, he said that it could be easier to get that than to get a million dollars for a smaller project. So he forced us to come up with a really big project that is easy to understand and for which we could get a lot of money.

Meyerowitz: Watson is a very smart guy and understands the politics of science very well – which we didn't.

Somerville: We were educated by a master. I also remember walking back to the hotel after the meeting and asking him, "Why did you support our project at the NSF?" His answer was, "I don't care about plants at all but we are going to figure out the human genome and to do that, we need a lot of information from different sources. Maybe plants will have a few genes that will help us to understand the human genome." However we also went on to get a lot of money in another way.

Which way was that?

Somerville: We started publishing papers that were of higher quality in journals such as *Nature* and *Science*. Doing that attracted people to our field, because young scientists like to see that their work can be

placed in the great journals. That in turn allowed them to get funded, based on the quality of their discoveries. Then funding agencies started allocating resources to this research. That is probably the biggest way we created money: we improved the quality of our research.

But as you said, you do not seem to receive very much money...

Meyerowitz: My own lab has always been very modestly funded and we just go from year to year. I was always interested in attracting people not money but if you have high quality young people: that makes it an exciting field. There is the top-down way of funding and the bottom-up of these great programmes like the sequencing project. However, there is also a level where politics stops and science continues. At least in the US system you have to have peer-reviewed grants and the peers choose the exciting work.

Somerville: In this context, one has to understand that US-American science is very different to European science. If we were Europeans, we would have organized one of these big EC programmes.

Meyerowitz: We would have built an institute, in which hundreds of students would still be there with greying hair and would be doing the same poor jobs they did when they were eighteen. If you want to catalyse information up, you need to understand catalysis. You can have a lab up

to a certain size, but if you cast the people out to start their own lab, you are working catalytically. Our idea was to empower individuals to do the research then let them go out and catalyse new areas.

Somerville: We didn't really build that. No big consortium programmes. We did not create an *Arabidopsis* society or an *Arabidopsis* Journal. We tried to build that in the existing structure, which is a kind of American attitude. Here in Europe everything is so hierarchically organized.

To come back to Arabidopsis, how do you see the current state of affairs? What do you now know about it?

Somerville: Now, with this huge community of people working on *Arabidopsis*, we can say that we have a broad understanding of the organism. We know fundamentally what all the genes do and how that integrates into the overall dynamic process. There is so much progress on so many fronts that you can observe how diverse processes integrate together. We predictably use that knowledge to make changes in the plant.

How much of the genetic structure can you actually change? Aren't you limited to a small number of genes?

Meyerowitz: Well, we are managing up to eight already. We are getting better and better at predicting effects when we change genes. Anything more than three genes can't be done in your head anymore. You need a computer model. If you understand the interactions and the feedback-mechanisms you can map that out in an explicit mathematical description of the processes. There are two possibilities here: We can learn how plants work or we can learn how naïve we are. Either way it is going to be great fun!

What are the possible applications of your basic research?

Meyerowitz: There are two sorts of issues. One is that the population of the world is expanding and the land for crops is decreasing rather quickly in some places. Soon, a lot of people won't have enough food

to eat. That is not a distribution problem. What can we do about that? We need plants that don't need as much fertilizer, plants that resist insects and bacteria. Fifty percent of all the food that is grown is lost either

pre- or post-harvest and there is much information that has been generated in *Arabidopsis* that is directly applicable.

Somerville: There are two other major problems: that is, energy and CO₂-accumulation. I am an advocate of using biofuels. We are definitely going to improve the productivity of certain plant species and then modify the composition of the tissues we use in biofuels. In the future, we are going to make plants with modified lignins that allow the plants to be more easily broken down into fuels.

This all means new genetically modified plants. What do you think of the European resistance to GMO and "green biotechnology" in general?

Meyerowitz: From an American point of view this is a religion. In the United States most of the people don't believe that evolution occurs, that is our religious problem. In Europe, the problem is that you have a concept of nature that doesn't align very well with the facts, that is: there is something better about agriculture that your grandparents did although they were starving. I don't know how to explain that.

Somerville: I think that the Europeans also have been misled by organisations such as Greenpeace. They have been using biotechnology to force a political confrontation that might have social good. Such confrontations certainly have their benefits and I am not really opposed to that. Scientists, however, are poorly qualified to participate in political confrontations, because they feel constrained by the limitation of facts. So we always lose.

But what about the shrinking diversity in crop plants such as rice because of monocultures?

Somerville: There is a certain danger in that. Corporations do shrink diversity. A good example is McDonalds. Half of the potatoes in the world are Russett Burbank because that is what McDonalds likes. Mechanised agriculture demands that. It is not clear that genetic engineering has any effect on diversity, but globalisation and corporatisation probably do have negative effects.

INTERVIEW: KLAUS TASCHWER



Elliot Meyerowitz, 55, is currently George W. Beadle Professor of Biology and Chair at the California Institute of Technology, Division of Biology.



Christopher Somerville, 59, born in Canada, is Director of the Carnegie Institution, Department of Plant Biology, and Professor of Biological Sciences at Stanford University.