IN BRIEF

EVO–DEVO

Microevolutionary analysis of the nematode genus *Pristionchus* indicates a recent evolution of redundant developmental mechanisms during vulva formation.

Srinivasan, J. *et al. Evol. Dev.* **3**, 229–240 (2001)

Studying closely related species or subpopulations can help to uncover mutations that are important for phenotypic variation. Here, 13 lab strains of the nematode genus *Pristionchus* were divided into four different species on the basis of mating experiments and genetic sequence comparisons, and then molecular variation between strains was studied. As morphologically distinct strains were identical at tested polymorphic loci (using amplified fragment length polymorphism analysis), developmental differences might rely only on a small number of genetic changes.

MICROBIAL GENOMICS

Evolutionary genomics of *Staphylococcus aureus*: insights into the origin of methicillin-resistant strains and the toxic shock syndrome epidemic.

Fitzgerald, J. R. *et al. Proc. Natl Acad. Sci. USA* **98**, 8821–8826 (2001)

Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*.

Tettelin, H. *et al. Science* **293**, 498–506 (2001)

Comparative genomic studies of microorganisms are providing new information on the origins and variation of important human pathogens. Fitzgerald *et al.* used genomic microarrays to compare the genomes of 36 clinical isolates of *Staphylococcus aureus* with varying pathogenicity. They found substantial genomic variation and showed that a 1970's epidemic of toxic shock syndrome could not have been caused by the rapid spread of a hypervirulent strain of *S. aureus*, resolving a long-standing controversy in this field. With the completion of the genome sequence of *Streptococcus pneumoniae*, by Tettelin and colleagues, similar work can now be carried out on this pathogen. Indeed, a comparison with two clinical isolates reveals striking variation in genes likely to be involved in pathogenesis.

TECHNOLOGY

Diphtheria toxin receptor-mediated conditional and targeted cell ablation in transgenic mice.

Saito, M. *et al. Nature Biotechnol.* **19**, 746–750 (2001)

Saito *et al.* have used a transgenic approach to ablating cells by introducing into mice a transgene that encodes a human diphtheria toxin (DT) receptor driven by a liver-specific promoter. The hepatocytes of transgenic mice exposed to DT undergo damage in a dose-dependent manner, leading to hepatitis. This approach could be used to ablate other cell types in DT-insensitive animals for studies of human disease and tissue regeneration.

DEVELOPMENTAL BIOLOGY

BMP de-livers

Inductive signalling between mesenchyme and epithelium is a common feature in organogenesis, and hepatogenesis is no exception. It has been known for some time that fibroblast growth factor (FGF) signals produced by the cardiac mesoderm (CM) induce liver formation in the anterior gut. Now Rossi and colleagues show that liver specification also requires a bone morphogenetic protein (BMP) signal that comes from septum transversum (ST) mesenchyme, which contributes to the epicardium and the diaphragm. Together with the FGF signals from the CM, this signal specifies which part of the anterior gut endoderm becomes the liver.

Classical transplantation studies established that the CM was necessary and sufficient for early hepatogenesis. Equipped with a new, ST-specific marker, Rossi *et al.* realized that ST cells are frequently present in CM explants because of the tight association between these tissues. This raised the possibility that they too could function in early hepatogenesis.

To investigate this further, the authors analysed the ST mesenchyme in a $Bmp4^{LacZ}$ mouse in which *LacZ* disrupts *Bmp4*. Expression of *LacZ* was strong in the ST, and early hepatogenesis was severely retarded in $Bmp4^{LacZ}$ homozygous mice. A more severe liver phenotype only became apparent when exogenous noggin — a general BMP antagonist — was added, indicating that other members of the BMP family, also expressed in the ST, are required for hepatogenesis and might compensate for the loss of Bmp4 in the $Bmp4^{LacZ}$ mice. They also noticed that the expression of albumin — an early liver-specific gene — was absent when the BMPs were blocked by noggin and that the FGF signal from the CM could not substitute for the BMP-induced albumin expression.

Rossi *et al.* also concluded that, by inducing liver development, the BMP signal from the ST and the FGF signal from the CM indirectly prevent pancreatic development. This is because in the presence of the BMP signal, which leads to albumin induction, expression of *Pdx1* — an early pancreatic marker — is lost. Conversely, in the absence of the BMP signal, albumin is not induced, but *Pdx1* is expressed.

Furthermore, the authors showed that the BMP signal is, at least in part, mediated by the Gata4 transcription factor.

The molecules behind the mesodermal induction signals required for the development of the different organs that arise from the gut endoderm gradually begin to reveal their identities. Thanks to Rossi and colleagues, hepatogenesis can now be added to the list of other developmental processes that involve the combined action of BMP and FGF signals.

Magdalena Skipper

References and links

ORIGINAL RESEARCH PAPER Rossi, J. M. *et al.* Distinct mesodermal signals, including BMPs from the septum transversum mesenchyme, are required in combination for hepatogenesis from the endoderm. *Genes Dev.* **15**, 1998–2009 (2001)

WEB SITE Ken Zaret's lab