

Dispatches

Genomics: An Inordinate Fondness for Beetles

Beetles are reckoned to make up about one quarter of animal species. Now, the first genome of a beetle — the red flour beetle *Tribolium castaneum*, a pest and developmental model system alike — has been sequenced.

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The great British biologist J.B.S. Haldane is said to have replied to a cleric who asked him what the study of living creatures could tell us about the nature of their presumed creator: He has an “inordinate fondness for beetles”. And it’s true, this creator must have spent a fair part of the fifth day of creation making beetles: other animal groups may hold records in terms of the number of individuals (nematodes) or biomass (ants), but beetles are by far the winners when the number of species is considered. More than 350,000 species of beetle have been described [1], which means that about one in four of all described animal species is a beetle. But there is also a second lesson, as at the same time beetles are — a few oddities aside — remarkably uniform in their morphology, which may perhaps be attributed to a certain forgivable laziness on the part of the creator.

Beetles are an amazing example of an evolutionary radiation. This radiation began 285 million years ago [2] and led to astonishing diversity, for instance in body size — the largest beetle is 17 cm long and the heaviest one weighs in at close to 100 grams, while the smallest species are well below 1 mm in size [1]. Key to this success may have been the most distinctive feature shared by all but a few beetles: the hardened forewings (elytra) that cover the hindwings used for flying. These protective wings may have allowed the beetles to pursue a mainly crawling lifestyle, much like the second great insect success, the ants — delicate, exposed wings could get terribly in the way when you want to crawl under a leaf or dig for food. While ants have reserved the ability to take-off only for certain castes during certain times, the hardened elytra endowed beetles with an ability to fly when needed — an almost classical best-of-both-worlds solution [1].

Given all the beetles’ success, it was about time that the genome of a member of this strikingly successful group was sequenced. The chosen species whose genome sequence was described recently [3] is the red flour beetle *Tribolium castaneum*, an economically very relevant pest species. *Tribolium* has been well characterised using classical genetics and more recently has become a model system for comparative developmental biology.

A Flourishing Beetle

Tribolium, a member of the family Tenebrionidae and often colloquially referred to as ‘bran bugs’ (Figure 1), are a significant pest wherever processed grain products are in abundance. *Tribolium* has a generation time of 3–8 weeks depending on temperature and can reproduce for a long time [4]. These features make *Tribolium* an ideal lab animal and it thus became an early and important model of classical genetics, in particular population genetics. *Tribolium* is cosmopolitan, and it is not clear where it originated. Strikingly, it is not known what *Tribolium* ate before flour was invented about 10,000 years ago. There is some reason to believe, based on morphology as well as on the feeding ecology of some of *Tribolium*’s closer relatives, that the ancestors of the flour beetle were living under the bark of dying trees feeding on decaying plant materials [4].

At an estimated 160 mb, the euchromatic genome of *Tribolium* is about one third bigger than that of *Drosophila*. Also in terms of gene number, *Tribolium* currently scores higher, with an estimated 16,404 genes, but this may well be due to technical differences in gene prediction between the two systems [3,5]. What is more noteworthy is that, by and large, *Tribolium* seems to be ‘less derived’ than some of the other insects for which the genomes have been sequenced, in particular the fly and the

mosquito. It has been known that insects in general, and especially the lineage leading to *Drosophila*, have undergone accelerated evolution [6], and this was confirmed when a molecular phylogeny was constructed using the newly available data from *Tribolium*. Overall, *Tribolium* shares more genes with humans than the Dipterans do. *Tribolium* researchers will surely be tempted to use this finding to argue that their organism is ‘more ancestral’, ‘more representative’ or simply ‘less weird’ than *Drosophila*.

Indeed, *Tribolium* is by many tokens a better representative of insect embryonic development than the mother of all model organisms, *Drosophila melanogaster*. *Drosophila* represents the so-called ‘long-germ’ mode of development, which means essentially that the early embryo anlage fills up the entire length of the egg, and that all body segments will form from this anlage in a more or less simultaneous manner. In *Drosophila*, segment formation occurs while the embryonic cells are still in direct cytoplasmic contact with one another, which allows for diffusion of the intracellular regulatory factors that orchestrate early development. *Tribolium* embryos, like those of most insects, however, follow the



Figure 1. Beetle in the bran.

An adult *Tribolium castaneum* on an oat flake. The status of this beetle as both a pest and a model organism should make its recently sequenced genome of interest to a wide range of scientists. (Photograph: Gregor Bucher).

‘short-germ’ mode: they form simultaneously only the segments of head and thorax, while the remaining segments are added sequentially from a growth zone at the posterior of the embryo. Moreover, most of *Tribolium* embryogenesis takes place in an environment of separated cells, making direct diffusion of transcription factors unlikely [7]. This raised the obvious question of whether developmental patterning mechanisms are conserved between these two types of insect embryo.

So far, this question has mainly been approached by isolating homologues of *Drosophila* developmental genes from *Tribolium* and comparing their expression and function. This revealed that — despite all the differences in egg and embryo architecture — the principal logic of early developmental patterning is very similar: the subdivision of the embryo into increasingly smaller areas and the transition from the broad individual domains of gap gene expression to the repetitive expression patterns of pair-rule and segment-polarity genes appears to take place in *Tribolium* as well (e.g. [8,9]), even though it had been implicitly assumed that gap genes might operate effectively only in a non-cellularised environment. Of course, expression patterns and regulatory relationships can differ considerably between *Tribolium* and *Drosophila* [10], but to what extent such differences are due to evolutionary drift or reflect an adaptation of the patterning system to the short- versus long-germ mode of development is not clear at present.

In parallel, a less-biased approach was taken by the analysis of developmental mutants in *Tribolium* [11]. The most striking example of those is perhaps a deficiency that removes most of *Tribolium*’s Hox cluster [12]. This is only possible because *Tribolium*, unlike flies, has kept an unsplit Hox gene cluster. The mutant larvae display a striking phenotype in which the anterior–posterior identity of all segments is transformed, such that all body segments bear antennae instead of the appropriate appendage or lack thereof. In general, the mutant collection offers the possibility of studying *Tribolium* development, as it were, ‘from scratch’, i.e. without the bias of comparison to *Drosophila* genes, and it also allows the study of the development of structures,

such as the larval leg and head, which in fly larvae are not or only poorly developed [13]. With the genome at hand now, identifying the genes underlying these mutants has just gotten considerably easier.

But what does the genome sequence tell us straight away about *Tribolium* development? Unsurprisingly, very little. Almost all of the genes implicated in embryonic development of *Drosophila* are also present in *Tribolium* and this holds in much the same way for most of the signalling pathways that are used across all animals [3]. As expected from previous futile searches, there really is no *bicoid* orthologue in *Tribolium*. Instead, the function of *bicoid* in setting up the pattern in the anterior of the embryo, well established from work on *Drosophila*, appears to have been taken over by the homeodomain transcription factor Otd, which forms an anterior gradient in *Tribolium* and works in synergy with Hunchback to specify head and thorax in the beetle [14]. *Tribolium* larvae show thoracic legs and a well-formed head with mouth appendages, while the *Drosophila* larvae are legless and their head segments are folded inwards [7]. The genome analysis shows that a large fraction of vertebrate head patterning genes are also present in *Tribolium* and expressed in the right time and place to suggest a conserved role. Likewise, a number of genes involved in *Drosophila* adult leg patterning are present and expressed in the larval legs [3]. Here, the genome will prove particularly valuable for identifying the dozens of appendage mutants that have been isolated in *Tribolium* [15]. Thus, as so often with genomic analyses, the sequence is not so much offering a direct insight into the biology of a particular process. Instead, it provides a starting point and a resource for investigating these problems (much against the grain of the current systems-biology trend) on a gene-by-gene basis.

A Fondness for Flour

In terms of biological insight offered, the genome sequence scores quite well with those aspects of the genome that relate in one way or another to *Tribolium*’s ‘pestness’. *Tribolium* is known to be readily adaptable and develop resistance to a number of insecticides [13]. Indeed, the *Tribolium* genome reveals a notable expansion of

subfamilies of the cytochrome P450 proteins, which are involved in detoxification and are frequently evolutionary targets of selection for insecticide resistance. Likewise, the beetles’ inordinate fondness for flour may have left traces in the genome: the number of so-called C1 peptidases has greatly expanded in the *Tribolium* genome. This is indicative of their grainy diet and the need to overcome certain defence mechanisms within the grain that often involve protease inhibitors. In addition, the *Tribolium* genome, unlike that of other insects, contains a vasopressin-like neuropeptide gene and its putative receptor. This hormone system is key for regulating water retention in the kidneys of mammals, leading the authors to speculate about a possible involvement of this system in *Tribolium*’s striking ability to obviate the need to drink and to live essentially on its metabolic water alone [3].

Perhaps the most surprising finding of the genome analysis is the large number of genes for receptors of taste and smell found in *Tribolium* as opposed to other insect genomes. The beetle genome features 265 odorant receptor genes (*D. melanogaster*: 60; *Anopheles*: 79; honeybee: 170) and 220 gustatory receptor genes (*D. melanogaster*: 60; *Anopheles*: 52; honeybee: 10) [16–18]. Most of these fall into subfamilies that are so far only known from *Tribolium* and in the case of the odorant receptors there is a clear indication that a large fraction of them arose from tandem duplications after the beetles split from the other insect lineages.

At first sight, this rich molecular chemosensation equipment seems to be at odds with the beetle’s rather monotonous feeding habits, which are nowadays directed towards a relatively uncomplex diet. The fact that only a few chemoreceptor genes are undergoing molecular decay, known as pseudogenisation, suggests that the receptor repertoire is also maintained under the presumably only recently acquired lifestyle as a pest. But there are several ways of conceptualising the need for good chemosensation. For one, *Tribolium* might be in need of good chemosensation in order to be able to recognise and evade the intricate defence mechanisms with which many plants defend their grains, i.e. their offspring. This may also explain why *Tribolium* is so good at evading

insecticide attacks. Alternatively, the good chemical sense might be a means of sensory compensation. *Tribolium* are adapted to fairly low light environments, which is reflected in their comparatively small eyes and also at the genome level by the fact that they possess only two opsin genes as opposed to three in most other insects. Thus, improved chemosensation may make up for the lack of optical sensory input due to the cryptic environment of this species.

It may be naïve to expect revolutionary insights into the biological peculiarities of a species from its genome sequence alone, but the genome sequence can in a sense help to refocus on the species itself. It may thus be seen as a reminder of how some problems that naturally have to be studied as isolated phenomena might interact and inform each other. The genome might thus help to focus on the species itself as a product of evolution, whose traces can be read from the genome. Only much further work — now able to draw on the resource of the *Tribolium* genome sequence — will reveal whether the genome holds an explanation for why evolution was so fond of beetles.

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Animal Locomotion: A New Spin on Bat Flight

Biologists and engineers have long struggled to understand the hovering flight of insects, birds, and bats. The enormous diversity of these groups would suggest they fly using a variety of mechanisms, but a new study shows that hovering bats use the same aerodynamic mechanisms as do moths and other insects.

Michael Dickinson

Active flight has evolved within just four taxa in the history of life: insects, pterosaurs, birds and bats. The ecological advantages of flight are manifest in the extraordinary success of these groups. Insects, birds, and bats include about 10^6 , 10^4 and 10^3 species, respectively — together, the vast majority of described animal species on the planet. Even the ill-fated pterosaurs exhibited a diversity comparable to that of modern birds [1], with species ranging in size from sparrows to small aircraft. In addition to

powerful muscles and an adequate control system, active flight requires aerodynamically effective wings [2]. Because of the multiple origins of flight, wings have long served as textbook examples of evolutionary homology and convergence. The wings of pterosaurs, birds and bats are homologous because they all originated from tetrapod forelimbs, whereas the wings of insects — probably derived from tiny dorsal extensions of the legs [3] — are convergent analogs. In comparing animal wings, it is possible to consider not only morphology and phylogeny,

but also the aerodynamic mechanisms by which they work. A recent study of bats [4] suggests that hovering insects, birds and bats may use physical mechanisms that are more similar than previously supposed, and in doing so illustrates how common physical laws can drive distantly related creatures to similar solutions.

A coherent understanding of animal aerodynamics has been long coming, largely because the principles that explain how fixed-wing aircraft work are not sufficient to explain the flapping flight of birds, bats, and insects. Of the three, the forward flight of birds is the easiest to explain, because their wings function to some degree as do those of an airplane. If you place a bird wing in a wind tunnel, the forces one measures are usually sufficient to explain how flapping birds offset their body weight and fly forward through the air. This is not to say that bird flight is fully understood [5], but at least it makes sense in the context of conventional aerodynamics.