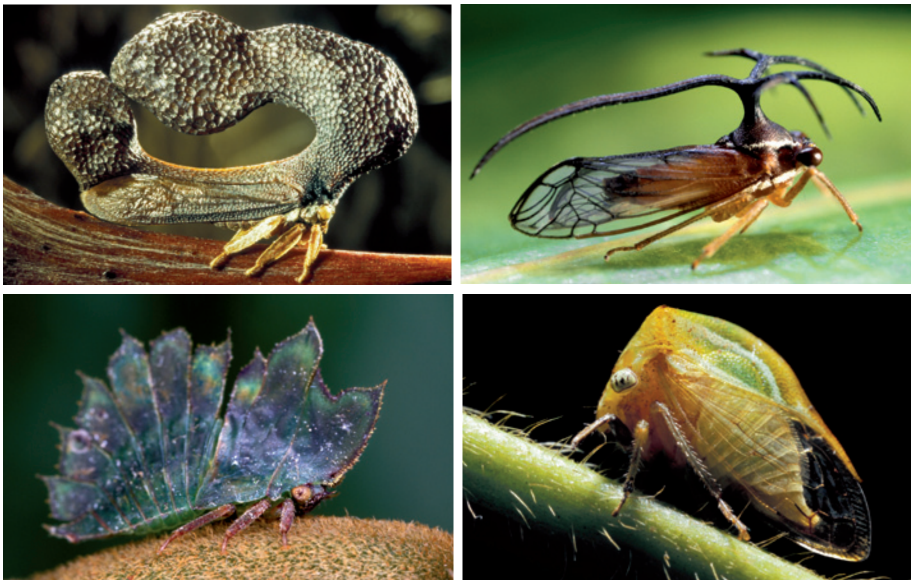
NEWS & VIEWS

EVOLUTIONARY BIOLOGY

The origins of novelty

Treehoppers produce highly diverse structures called helmets. To do so they seem to have exploited the genetic potential, long inhibited in other winged insects, to develop wings on a particular anatomical segment. SEE LETTER P.83

ARMIN P. MOCZEK



P. LANDMANN/SPL

Figure 1 | The exuberance of treehopper helmets. Clockwise from top left: *Cladonota benitezi*; *Umbelligerus peruviensis*; *Nassunia binotata*; and a nymph of a *Cymbomorpha* species. Helmets are generally thought to aid in camouflage by disrupting the animal's shape and outline, or by mimicking thorns, animal droppings or aggressive ants and wasps. Further examples are shown on the cover of this issue, and in Figure 1 of Prud'homme and colleagues' paper[1].

Understanding the origin of complex traits is among the most enduring puzzles in evolutionary biology. On the one hand, evolution operates within a framework of descent with modification — everything new must come from something old. On the other hand, structures such as the eye, the wing and the turtle's shell stand out because they lack obvious correspondence to the old. On page 83 of this issue, Prud'homme *et al.*[1] address this puzzle by connecting a complex and highly diverse trait — the helmet of membracid treehoppers — to its origins in both development and evolution.

Treehoppers are insects that would resemble miniature cicadas were it not for the presence of the helmet (Fig. 1). This structure appears to reside on top of the animal's thorax, and extends dorsally, and in remarkably varied ways, to mimic thorns, animal droppings or aggressive ants. Entomologists joke that some treehoppers use their helmets to send signals to their home planet, so other-worldly is their appearance.

Helmets have been interpreted as an extension of the pronotum, the dorsal portion of the first segment of the three-segmented thorax shared by all insects[2]. The thorax is a defining feature of insects, bearing a pair of legs on each of its three segments and, in most insect orders, a pair of wings on the second and third segments (but not on the first, the prothorax). We have long known from fossil evidence that insects arrived at this organization following a period of progressive loss of wings or wing-like appendages from all abdominal segments, as well as from the first thoracic segment[3] (Fig. 2). More recently, developmental studies have shown that this loss has been achieved through the evolution of inhibitory mechanisms that prevent the formation of wings in inappropriate segments. For instance, one of the many functions of a gene called *Sex combs reduced* (*Scr*) is to mediate the inhibition of wing formation in the first thoracic segment of insects[4], including the order Hemiptera, to which treehoppers belong[5].

Enter the treehopper *Publilia modesta* and its helmet. Through careful analysis of this structure's anatomy, placement and attachment to the thorax, Prud'homme *et al.*[1] discovered that the helmet may not be a mere extension of the pronotum. Instead, it is attached bilaterally to the thorax by paired articulations reminiscent of joints, much like regular wings. Moreover, when they examined its early developmental stages, the authors found that the helmet forms from paired buds — again, much like wings. The expanding buds subsequently fuse along the midline, creating the continuous helmet. Study of the expression of one gene, *nubbin,* normally specific to insect wing development, and two genes specific to appendage formation in general, provided additional evidence that helmet development may rely on developmental mechanisms involved in the formation of wings.

Combined, these observations suggested that treehoppers evolved a way to develop a wing-like structure using a developmental program shared by traditional wings, but in a place in which wing development is typically inhibited in modern winged insects. Prud'homme and colleagues' investigation of *Scr* revealed that the gene is still expressed in the prothorax of treehoppers and is able to repress wing formation when transformed into *Scr*-deficient fruit flies. This implies that wing development in the first thoracic segment of treehoppers was not made possible simply by the loss of the inhibitory ability of *Scr*, but through some unknown mechanisms operating downstream.

The study by Prud'homme *et al.*[1] is noteworthy for several reasons. First, it illustrates how, to this day, careful developmental observations can set the stage for startling discoveries. Generations of entomologists have studied treehopper diversity, but research into development has a way of revealing evolution hidden from the study of adults. Second, as with so many studies, it raises as many questions as it answers. Although the morphological observations provide strong evidence that the helmet is a modified wing, the developmental genetic data are modest and correlational: expression patterns can suggest, but not prove, function. And the mechanisms that permit wing-like development in the

Figure 2 | A wing-bearing first thoracic segment. As shown in this line drawing of a fossil of an extinct species (*Stenodyctya lobata*), expression of the wing-development program in the first thoracic segment (arrow) was common in early insects. In extant winged insects, wings are borne only on the second and third thoracic segments, with wing development on the first segment being suppressed. Prud'homme *et al.*[1] provide evidence that treehoppers have overcome such suppression to produce their helmets. (Drawing reproduced from Fig. 6.17 of ref. 3.)

presence of *Scr* repression remain to be discovered. Nevertheless, these findings provide a valuable starting point for framing future enquiries into the origin and diversification of the treehoppers' 'third pair of wings'.

Finally, and most importantly, the work[1] illustrates how novelty can arise from ancestral developmental potential — how developmental abilities can be lost or silenced over millions of years, only to be redeployed to contribute to the evolution of a complex and beautiful appendage. ■

Armin P. Moczek *is in the Department of Biology, Indiana University, Bloomington, Indiana 47405, and at the National Center for Evolutionary Synthesis (NESCent), Durham, North Carolina 27705, USA.*
e-mail: armin@indiana.edu

1. Prud'homme, B. *et al. Nature* **473,** 83–86 (2011).
2. Stegmann, U. E. *J. Morphol.* **238,** 157–178 (1998).
3. Grimaldi, D. & Engel, M. S. *Evolution of the Insects* (Cambridge Univ. Press, 2005).
4. Carroll, S. B., Weatherbee, S. D. & Langeland, J. A. *Nature* **375,** 58–61 (1995).
5. Chesebro, J., Hrycaj, S., Mahfooz, N. & Popadić, A. *Dev. Biol.* **329,** 142–151 (2009).

BIOCHEMISTRY

Life imitates art

The biosynthetic route to a naturally occurring insecticide, spinosyn A, has been established. One of the enzymes involved might catalyse a reaction that, although widely used by chemists, has proved elusive in nature. SEE LETTER P.109

WENDY L. KELLY

The Diels–Alder reaction is a powerful instrument in the synthetic organic chemist's toolkit[1]. A variant of '[4+2] cycloaddition' reactions, the Diels–Alder reaction forges two carbon–carbon single bonds in the process of making a cyclohexene ring — a six-membered carbon ring possessing a carbon–carbon double bond. A biochemical equivalent of this process has been invoked as a crucial step in the biosynthesis of many naturally occurring molecules, but the roster of enzymes that clearly catalyse transformations consistent with the Diels–Alder reaction has been limited. What's more, the enzymes on that list mediate sequences of reactions, of which the putative Diels–Alder reaction is just one, thereby confusing efforts to study biological cycloadditions.

On page 109 of this issue, Kim *et al.*[2] identify an enzyme whose sole function is to catalyse the formation of a cyclohexene, a process consistent with a Diels–Alder reaction. This transformation, along with the others detailed in the authors' report, is a critical step in the biosynthesis of spinosyn A, a commercially useful and environmentally friendly insecticide.

Spinosyn A belongs to the polyketide family of natural products, and is produced by fermentation of the bacterium *Saccharopolyspora spinosa*[3]. The molecular backbone of spinosyn A is a complex framework: a large 'lactone' ring is fused to a highly unusual system called a perhydro-*as*-indacene, which consists of three smaller rings (Fig. 1a). During the biosynthesis of spinosyn A, a polyketide synthase enzyme assembles the molecule's carbon backbone, initially generating a single large ring (a macrocycle). Later in the synthesis, the macrocycle is converted into the multi-ring system and glycosyltransferase enzymes attach carbohydrate groups to the macrocyclic scaffold.

Although a [4+2] cycloaddition has been proposed as a key step in the installation of spinosyn A's fused-ring system, the exact point at which this occurs was uncertain. It was suggested that the system is generated when a series of carbon–carbon bonds form as bridges across a macrocyclic intermediate consisting of only one ring. This proposal was strengthened by the discovery that SpnJ — an enzyme involved in spinosyn A biosynthesis — uses an unbridged macrocyclic precursor of spinosyn A as its substrate[4,5]. Bridge-forming reactions must therefore occur after the macrocycle has been formed. The bridge-forming process could follow at least two paths, which would differ according to whether the proposed [4+2] cycloaddition precedes or follows formation of the bridge between positions 3 and 14 of spinosyn A (Fig. 1a shows how the atoms in spinosyn A are numbered).

Kim *et al.*[2] now reveal the full sequence of reactions that proceed from an unbridged macrocyclic intermediate to the characteristic fused-ring system of spinosyn A. They find that a [4+2] cycloaddition reaction, catalysed

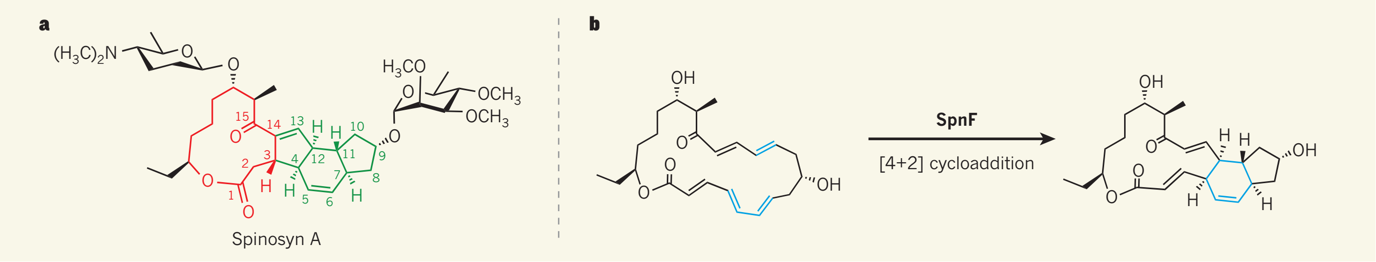


Figure 1 | The biosynthesis of spinosyn A. **a**, Kim *et al.*[2] have worked out the biosynthetic pathway for spinosyn A, a naturally occurring insecticide. The core structure contains a macrocyclic lactone (red) fused to a perhydro-*as*-indacene system (green). Part of the numbering system used to identify the atoms in the molecule is shown. **b**, A [4+2] cycloaddition reaction catalysed by the enzyme SpnF is a key step in the formation of the perhydro-*as*-indacene. The reacting parts of the starting material, and the cyclohexene ring formed in the product, are highlighted in blue.