Evolution: *oskar* Reveals Missing Link in Co-optive Evolution

The *oskar* gene is critical for germ plasm formation and reproduction in higher insects. A recent study reports that *oskar* has more ancient roots than previously thought, indicating it was co-opted for its reproductive role in higher insects.

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Evolutionary developmental biology has made it abundantly clear that to a large degree natural selection works with what already exists, exploiting ancestral traits, such as genes, organs, and morphological structures, for new uses or the generation of novel traits [1–4]. Elegant examples abound in nature; the gene *Distal-less*, which originally evolved to specify limb development [5,6], has been exploited by natural selection to pattern eyespots on butterfly wings [7], jaws in vertebrates [6], and to transform male water strider antennae into grasping structures for sexual conflict [8]. This process, which is most often called 'co-option', is considered by many to be a fundamental principle in evolution biology [4,9,10]. Indeed, the degree to which evolutionary paths are shaped by constraints, biases, or opportunities, depends on the nature of the substrates available for co-option [11]. Despite its importance, several gaps remain in our knowledge of the mechanisms through which co-option occurs [2]. An article by Ewen-Campen and colleagues [12] recently published in *Current Biology* provides insight into the evolutionary mechanisms of co-option.

Before delving into Ewen-Campen and colleagues, [12] discovery, I will turn back just a few pages in the history of evolutionary thought to Stephen Jay Gould and Elisabeth Vrba's classic 1982 paper *Exaptation-a missing term in the science of form* [11]. Gould and Vrba [11] presciently recognized the importance of co-option in the evolutionary process and made several conceptual advances that remain relevant for understanding the evolutionary mechanisms of co-option. Unfortunately these advances were largely lost in translation between Gould and Vrba's [11] complicated terminology and polemics of adaptationism. They introduced the term 'exaptation' to describe the process of co-option, and argued that

exaptation is not limited to ancestral traits that had originally evolved for other uses, but can also occur through non-adaptive traits or 'nonaptations' that are non-adaptive by-products with no current function. These non-adaptive traits, which represent a potential substrate for co-option, may be the missing link in co-optive evolution; "Exaptations that began as nonaptations represent the missing concept. They are not covered by the principle of preaptation, for they were not adaptations in ancestors. They truly have no name, and concepts without names cannot be properly incorporated in thought" [11]. In a recent review, True and Carroll [2]

speculated that the co-option of non-functional gene expression domains may underlie the widespread and repeated co-option of the highly conserved developmental regulatory genes known as the 'genetic toolkit'. However, we still lack clear examples of co-option of non-functional variation in gene expression domains.

Ewen-Campen and colleagues' [12] study provides us with an example in insects of how developmental novelties can arise from the co-option of non-functional gene expression domains. Germ cells transfer heritable information and develop through two different modes in animals [13]. Germ cells in crickets, like those of all basally branching insects, are specified by 'induction'; inductive signals from a group of somatic cells that cause neighbouring cells to adopt a germ cell fate [12,13] (Figure 1). By contrast, germ cells in the majority of higher insects, like flies, are specified by 'germ plasm'; a region of the cytoplasm localized to the posterior pole during oogenesis that is capable of producing
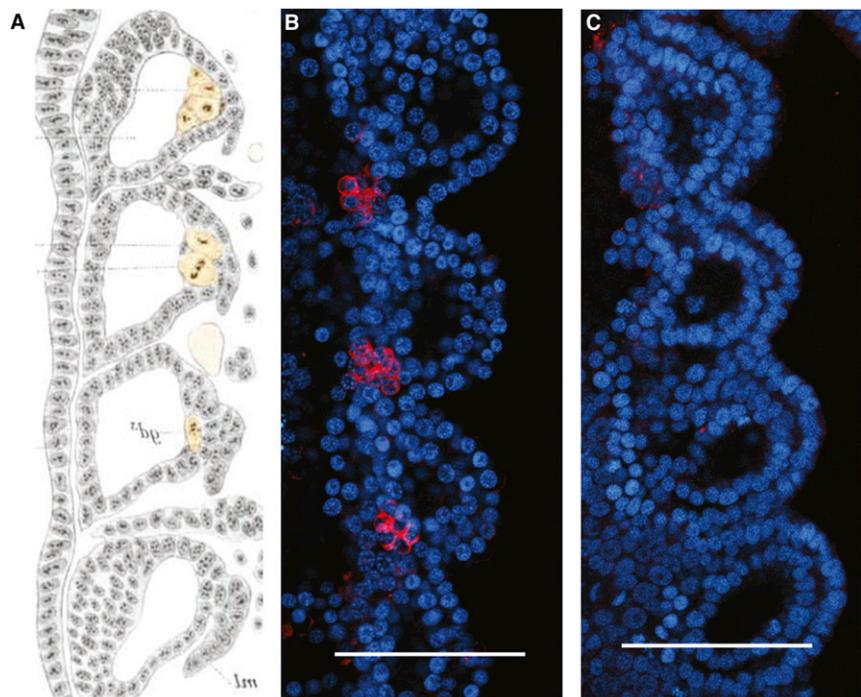

Figure 1. *oskar* expression in germ cells of the cricket *Gryllus bimaculatus*.
(A) William Morton Wheeler (1865–1937), generally known for his pioneering work on ant taxonomy and evolution, actually began as an embryologist. His elegant description of germ cells in locusts (yellow color) and their specification from the mesoderm [18] helped Ewen-Campen and colleagues [12] identify germ cells in crickets over 100 years later. (B) Germ cells in the cricket *Gryllus bimaculatus* marked in red by expression of the gene *Piwi*. (C) *oskar* expression (red color) occurs at low levels in germ cells even though it plays no functional role. (Image in (A) reproduced with permission from *Journal of Morphology* [18]; images in (B) and (C) courtesy of Casandra Extavour, Harvard University.)

germ cells [13]. The *oskar* gene is the only gene known to be both necessary and sufficient to produce germ cells from this localized germ plasm [14] and is present in the genomes of all higher insects that use the germ plasm mode of germ cell specification [15]. In contrast, *oskar* is absent from the genomes of several basally branching insects that specify their germ cells through induction, including aphids, louse, and bugs [15]. This phylogenetic association between the presence of *oskar* and the presence of germ plasm across insects is striking and suggests that *oskar* was an innovation of higher insects enabling the evolutionary transition between the inductive and germ plasm mode of germ cell development [15].

Ewen-Campen and colleagues' [12] discovery of an *oskar* orthologue in a basally branching cricket, *Gryllus bimaculatus*, without germ plasm now forces us to change our current perspective on the phylogenetic origin and evolution of *oskar*. By knocking-down the function of *oskar* during embryogenesis they revealed that *oskar* is not required for germ cell development but instead plays a role in the nervous system. This suggests that *oskar* may have originally functioned in the nervous system and was subsequently co-opted during the evolution of higher insects to enable the transition from an inductive to a germ plasm mode of germ cell specification. Up to this point, this story appears to be a straightforward story of co-option of ancestral genes originally evolved for other functions. However, the expression domains of *oskar* during embryogenesis add an important twist to this story. Even though *oskar* does not function in germ cell specification, Ewen-Campen and colleagues show that it is expressed at low levels throughout the abdominal region including the germ cells (Figure 1). This low-level of non-functional expression may be a pleiotropic consequence of *oskar*'s association with genes involved in both nervous system and germ cell development. Indeed, *oskar* is embedded in a regulatory network of genes, like *nanos*, *pumilio*, and *staufen*, that have been shown in fruit flies to function in both nervous system development and germ cell specification [16,17]. The non-functional expression domain of *oskar* may therefore be the non-adaptive by-product of its network connections to other genes with multiple roles. This brings us full circle to Gould and Vrba's [11] insight on the role of non-adaptive by-products in co-optive evolution. The non-functional expression domain of *oskar* in the germ cell represents an adaptive potential or 'novelty in the waiting' that likely facilitated *oskar*'s co-option to germ cell specification in higher insects.

Co-option of non-functional variation in gene expression domains may be much more common than we might have initially expected, especially in cases when genes are embedded in networks composed of genes that have multiple functions. An important future goal in evolutionary developmental biology should be to document the prevalence of co-option of non-adaptive-by-products. We should therefore clearly specify the substrate of a co-option event as either an ancestral trait that originally evolved for other functions or as a non-adaptive, non-functional by-product of natural selection on other traits. Understanding the nature of substrates for co-option has important implications for evolutionary theory; co-option of ancestral traits that evolved for other uses may bias future paths of evolution, whereas co-option of non-adaptive by-products may open new adaptive possibilities.

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Evolution of Development: The Details Are in the Entrails

Historically, the position of the site of gastrulation has been used to understand the developmental basis for body plan diversity. A recent molecular study, however, challenges long-held views and shows that molecular patterning mechanisms can be used to understand body plan evolution despite variation in gastrulation movements.

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Organismal and evolutionary biologists have long tried to use changes in developmental features to help explain major transitions in animal body form. The study of gastrulation, in particular the site of gastrulation and the fate of