Neofunctionalization of embryonic head patterning genes facilitates the positioning of novel traits on the dorsal head of adult beetles

Eduardo E. Zattara1, Hannah A. Busey1, David M. Linz2, Yoshinori Tomoyasu2 and Armin P. Moczek1

1Department of Biology, Indiana University, 915 East Third Street, Myers Hall 150, Bloomington, IN 47405, USA
2Department of Biology, Miami University, 700 East High Street, Oxford, OH 45056, USA

Received: 12 April 2016
Accepted: 20 June 2016

1. Introduction

Any complex organism can be seen as a mosaic of discrete traits. Each trait originated at some point along a lineage’s evolutionary history, and had to become integrated within a pre-existing context without compromising critical, ancestral functions. The developmental mechanisms that enable the integration of new traits into pre-existing contexts are poorly understood, as is their role in biasing, facilitating, or hindering evolutionary innovation. A growing body of work proposes that at least one major route for the origin and integration of novel traits lies in the co-option and recombination of pre-existing gene network components into new developmental contexts. Redeployment of gene networks on tissues or stages different from the ones in which these networks play their ancestral role may relax pleiotropic constraints and facilitate phenotypic innovation. This decoupling of gene networks and ancestral functional contexts may thus allow the origin of novel gene functions without the evolution of novel genes or pathways, e.g. as in the co-option of Hox genes to pattern vertebrate limbs [1], or the use of arthropod appendage patterning genes during butterfly eye spot formation [2]. If such spatial/temporal decoupling of gene networks and ancestral functions captures a general feature of innovation and integration of novel traits in developmental evolution, then even genes with deeply conserved, core functions would be available for co-option to facilitate the developmental evolution of novel structures. Furthermore, developmental contexts that are especially conducive to decoupling would then be expected to become hotspots for the evolution of novelties.
One spectacular example of a hotspot for evolutionary innovation is the dorsal head of insects. Despite having originated as part of the basic and highly conserved hexapod body plan more than 420 million years ago, the insect head has nevertheless managed to accommodate an enormous diversity of novel structures [3], such as the eye stalks of stalk-eyed flies, the weevil rostrum, or the dramatically exaggerated head horns of scarab beetles. Beetle head horns lack obvious homologues in other insects [4] and as such qualify as evolutionarily novel even by the strictest definition [5]. Head horns carry out critical functions as weapons used during male head-to-head combat [4], and previous work showed that their developmental evolution was enabled through the redeployment of several components of the arthropod appendage patterning gene network into the novel, appendage-free developmental context of the dorsal adult head [6,7]. Horned beetles in the genus Onthophagus, a model system for studying the origin and diversification of horn development, stand out with over 2,000 extant species and an enormous diversity of head horns [8]. However, how Onthophagus horns, a recent innovation, became integrated into the formation of the adult dorsal head, a conserved region in existence since the origin of insects, is entirely unclear, as are the developmental means by which head horns are positioned at species- and sex-specific locations. Here, we address these and related questions by investigating the differential redeployment and neofunctionalization of embryonic head patterning genes in adult beetle head formation.

Most arthropod body regions are composed of serially homologous segments whose identities are determined by Hox genes. However, anterodorsal head tissues pose an exception to this rule and are believed to derive from an anterior pre-segmental domain ancestral to all bilaterians (figure 1a) [9]. This anterior domain is patterned by a gene network distinctly different from the one that directs regular segment development. In the red flour beetle Tribolium castaneum, experimental embryonic knockdown of members of this network, which includes orthologues of orthodenticle, six3/optix, cap’n’ collar, and tailless, results in heads with severe developmental defects [9–12]. Interestingly, it is within this cephalic domain where the diversity of Onthophagus head horns has emerged.

In this study, we investigated the general hypothesis that genes instructing the embryonic patterning of this pre-segmental cephalic domain have been co-opted in post-embryonic Onthophagus development to pattern and position head horns. To do so, we took advantage of the fact that in beetles the adult head develops directly from the larval tissue (in contrast to dipterans like Drosophila, where all larval tissue dies and is replaced from imaginal discs and histoblasts), and developed a basic fate map to elucidate which embryonic/larval head regions are responsible for the formation and positioning of adult head horns in two closely related yet phenotypically highly divergent species of Onthophagus: O. taurus and O. sagittarius (figure 1d–f). We then measured and manipulated the gene expression of orthologues of otd and six3/optix, known core members of the embryonic anterior head gene network, in the same two species of horned beetles as well as in the red flour beetle Tribolium castaneum, which lacks horns and better reflects basal beetle head morphology. We find that, despite being expressed post-embryonically in the head epidermis of both genera, otd but not six3 dramatically affects dorsal head formation including horn development and positioning in Onthophagus, but has no effect in Tribolium.

![Figure 1](http://rspb.royalsocietypublishing.org/)

**Figure 1.** Fate maps of head horns in Onthophagus beetles. (a) Schematic of a generic late embryonic beetle head, showing the expression domains of six3 (red) and otd (blue) (after [9]). (b,c) Diagram of larval heads from Tribolium (b) and Onthophagus (c) beetles; colour dots in (c) represent regions ablated in fate-mapping experiments; OC: ocular region; CL: clypeolabral region. (d–f) Schematic and representative images of adult heads of Onthophagus taurus male (d,d'), O. sagittarius male (e,e'), and O. sagittarius female (f,f'); head horn colours represent mapping locations on the larval head shown in (c). (g–i) Examples of typical ablation phenotypes, including reduction of a posterior horn in an O. taurus male (g, arrowhead; n = 9), removal of an anterior horn in an O. sagittarius male (h, arrowhead; n = 19), and splitting of the medial posterior horn in an O. sagittarius female (i, arrowhead; n = 16). Sample size n represents the number of treated larvae surviving to adulthood; more than 90% of these showed an ablation phenotype.

### 2. Material and methods

**Animal husbandry and head fate mapping**

Onthophagus horned beetles and Tribolium red flour beetles used in this study were obtained and reared as previously described [13,14]. The head fate map was achieved by ablating select epi-dermal cell groups underlying the larval head cuticle with a Hyfrecator 2000 electrosurgical unit (ConMed, Utica, NY, USA) equipped with an epilation needle electrode (714-S, ConMed). Details can be found in the electronic supplementary material.

**Candidate gene scan and gene expression analyses**

Candidate gene sequence data for six3 and otd orthologues were retrieved from existing genomic and transcriptomic databases. Stage and tissue-specific expression levels of these genes were characterized using quantitative real-time polymerase chain reaction (qPCR) in Tribolium, and by in silico analyses of high-throughput RNAseq datasets. Details can be found in the electronic supplementary material.

**Cloning of six3 and otd fragments, dsRNA synthesis and injection**

Using primers designed against Onthophagus six3 and otd orthologues, we amplified and cloned fragments of each gene from complementary DNA (cDNA) libraries. Cloned fragments were used as templates to synthesize dsRNA and inject it into beetle
larvae as described previously [6]. We injected up to 3.0 μg of dsRNA into 417 O. taurus last instar larvae (Ot-six3: 70, Ot-otd1: 250, Ot-otd2: 53, Ot-otd1 + 2: 44) and 383 O. sagittarius larvae (Os-six3: 81, Os-otd1: 302). Sham control injections (47 O. taurus and 37 O. sagittarius) were made exactly as described above, except that larvae were injected with 1 μg of dsRNA from a 167 bp PCR product derived from a pBluescript SK vector. For Tribolium RNA interference (RNAi) we used previously described clones of Tc-otd1 and Tc-otd2 [15], and de novo synthesized 500 bp fragments (Integrated DNA Technologies (IDT) gBlock service, www.idtdna.com) based on the published Tc-six3 sequence [10]. We injected up to 0.7 μg of dsRNA; for each Tribolium gene, we made two sets of RNAi experiments targeting different transcript regions. Tribolium RNAi knockdown efficiency was validated by qPCR. We phenotypically scored 144 beetles that survived to adulthood (tc-six3: 29, tc-otd1: 41, tc-otd2: 40, tc-otd1 + 2: 34). Details can be found in the electronic supplementary material.

3. Results and discussion

(a) Onthophagus head horns map to the anterior pre-segmental region of the embryo

We sought to test the general hypothesis that genes used to pattern embryonic head development may have become redeployed during post-embryonic head differentiation. Embryonic head fate-mapping research in Tribolium has shown that the anterodorsal larval head, including the clypeolabral and ocular regions, derives from the terminal anterior region of the embryo, which undergoes a dorsal bending and subsequent dorsal closure, or zipping, of the subterminal region (a morphogenetic model known as bend and zipper [9,18], figure 1a). This region is considered pre-segmental and is characterized by a unique anterior gene network [9]. Because Tribolium and Onthophagus larvae exhibit very similar larval dorsal head morphologies (figure 1b,c), we reasoned that by relating larval to adult head regions in Onthophagus we would be able to use existing models on embryonic-to-larval transitions in Tribolium to inform our understanding of putative candidate pathways relevant to head horn development in Onthophagus. Thus, we first determined which regions of the larval head map to the adult head regions responsible for horn positioning in two closely related but morphologically highly divergent Onthophagus beetle species: O. taurus and O. sagittarius. Using selective ablation of small regions of the heads of last instar larvae, we established that posterior head horns as seen in male O. taurus are positioned in a head region homologous to the boundary between the ocular and clypeolabral head segments (figure 1d,f,g). By contrast, the anterior paired horns of male O. sagittarius (figure 1e,h,i) and posterior medial horn of the corresponding female (figure 1f,i) are positioned in head regions more firmly contained within the clypeal segmental. Even though our method only yields a very rough fate map and cannot discriminate whether loss of a feature is caused directly (by ablation of precursor tissue) or indirectly (by removal of inducers), our results strongly suggest that all three horn types appear to derive from the anterodorsal region of the larval head, itself derived from the embryonic anterior pre-segmental region.

(b) The embryonic anterior patterning genes sine oculis 3 and orthodenticle are expressed throughout metamorphosis in horned beetles

Since the anterior pre-segmental region is patterned by a unique gene network during embryogenesis [9], we tested whether components of this network have been co-opted to pattern horns during post-embryonic development. We focused our analysis on sine oculis 3 (six3) and orthodenticle (otd/otx), two genes coding for DNA-binding transcription factors, which in Tribolium exhibit complementary expression domains at the clypeolabral-ocular boundary of the presumptive embryonic head (figure 1a) [10,18,19] and, thus, the region which in Onthophagus is responsible for horn growth and integration, and which more generally play fundamental roles in patterning the anterior end across several metazoan phyla [20]. We used previously published sequences of Tribolium Tc-six3 [10], Tc-otd1, and Tc-otd2 [19] to search for orthologous genes in the O. taurus genome and an O. sagittarius transcriptome. We found a single sine oculis 3 orthologue, Ot-six3 (figure 2a) and two orthodenticle orthologues, Ot-otd1 and Ot-otd2 (figure 3a) in O. taurus. In our O. sagittarius transcriptome, we found one sine oculis 3 orthologue, Os-six3 (figure 2a), and only a single orthodenticle orthologue, Os-otd1 (figure 3a). However, we were able to use PCR to amplify a 660 bp fragment from O. sagittarius genomic DNA closely matching Ot-otd2, most likely part of Os-otd2. Alignment with Ot-otd2 shows a substitution rate of 0.05 (all synonymous) and 38.2% CG within exonic coding regions (477/660 bp), and a rate of 0.25 and 20.1% CG within intronic regions (183/660 bp). This suggests that, despite being absent from our transcript data, Os-otd2 is a functional gene, likely expressed earlier in development.

Sequence analysis and gene family phylogenetic reconstruction show that Ot-six3 and Os-six3 are indeed orthologous to Tribolium and other known insect sine oculis 3 (six3) and orthodenticle (otd/otx) genes (electronic supplementary material, figure S1). Similar analyses show that Ot-otd1 and Os-otd1 cluster with Tribolium Tc-otd1 and Drosophila otd, while Os-otd2 groups with Tc-otd2 in a sister cluster missing in dipterans and lepidopterans (electronic supplementary material, figure S2).

Expression patterns and functions of six3, otd1, and otd2 during embryogenesis are well characterized in Tribolium [10,19], as is the function of otd genes during adult eye formation [21]. However, neither expression nor function of these genes is known in other post-embryonic contexts in Tribolium, nor during any stages of Onthophagus ontogeny. Because horns do not form until the final days of the last larval instar [13], we first sought to assess expression of six3 and otd just prior, during, and right after metamorphosis
in both taxa. In Tribolium, we used quantitative PCR to confirm the expression of \textit{Tc-six3}, \textit{Tc-otd1}, and \textit{Tc-otd2} transcripts in late-larval instars, pre-pupae, early pupae, as well as adults (electronic supplementary material, figure S3). In Onthophagus, we used high-throughput sequencing of total mRNA (RNAseq) across four stages of \textit{O. taurus} (late-last instar larva to adult) and eight stages of \textit{O. sagittarius} (mid-last instar larva to adult). We found that \textit{Onthophagus six3} is expressed during most stages we assayed, with the highest median expression found in late-last larval instars, pre-pupae, early pupae, and adults (electronic supplementary material, figure S4). However, we failed to detect any other obvious phenotypic differences between \textit{six3} RNAi and control beetles in the head (figure 2d; electronic supplementary material, figure S5) or the remainder of the body in any of the three species. In particular, we found no obvious differences in horn size or position between knockdown and control animals in either \textit{Onthophagus} species. Taken together, these results suggest that \textit{six3} is involved in the regulation of post-embryonic eye development in both \textit{Onthophagus} and \textit{Tribolium}, but does not play a role in patterning major components of horn development in horned beetles.

(c) Beetle \textit{six3} is involved in post-embryonic eye development but not in horn formation

We next used larval RNAi to experimentally knockdown \textit{six3} expression and assess its potential role in adult head patterning and horn formation. We injected dsRNA fragments targeting \textit{Tc-six3}, \textit{Ot-six3}, and \textit{Os-six3} (figure 2a, black bars) into early-to-mid last instar larvae, followed the injected individuals through metamorphosis, and compared their phenotypes to those of control individuals injected with a non-sense dsRNA construct. In all three beetle species, \textit{six3} RNAi consistently reduced eye size compared with controls (\textit{Ot-six3}: 48/50; \textit{Os-six3}: 10/22; \textit{Tc-six3}: 29/40; + figure 2h,c; electronic supplementary material, figure S4). However, we failed to detect any other obvious phenotypic differences between \textit{six3} RNAi and control beetles in the head (figure 2d; electronic supplementary material, figure S5) or the remainder of the body in any of the three species. In particular, we found no obvious differences in horn size or position between knockdown and control animals in either \textit{Onthophagus} species. Taken together, these results suggest that \textit{six3} is involved in the regulation of post-embryonic eye development in both \textit{Onthophagus} and \textit{Tribolium}, but does not play a role in patterning major components of horn development in horned beetles.

(d) \textit{Otd} regulates development of non-cephalic midline structures, including the thoracic horn

We used the same approach as above to investigate the potential function of \textit{Tc-otd1}, \textit{Tc-otd2}, \textit{Ot-otd1}, \textit{Ot-otd2}, and \textit{Os-otd1} (figure 3a, black bars). In all three beetle species, \textit{otd1RNAi} resulted in the incomplete development of sternal structures located along the ventral midline (figure 3b,c). This phenotype was mild but evident in \textit{Tribolium} (figure 3b): \textit{Tc-otd1RNAi}
Figure 3. *Orthodenticle* (*otd*) regulates adult body midline development in beetles, and adult dorsal head shape in *Onthophagus*, but not *Tribolium*. (a) Gene structure of *otd* orthologues from *Tribolium castaneum* (*Tc-otd1* and *Tc-otd2*), *Onthophagus taurus* (*Ot-otd1* and *Ot-otd2*), and *O. sagittarius* (*Os-otd1*). Thick colour bars represent exons (dark red for coding region, light red for UTR), thin green bars highlight the homeodomain region, and thin black bars show the fragments used for dsRNA interference. (b,c) Sham control (left) and *otd1* RNAi (right) ventral midline phenotypes in *Tribolium castaneum* (b) and *O. sagittarius* (c); the dotted outline demarcates the mesosternum. (d) Sham control (left) and *otd1* RNAi (right) pupal horn phenotypes in *O. taurus*; dotted line shows pronotum profile. (e) Sham control (left) and *otd1* RNAi (right) adult horn phenotypes (filled and empty arrowheads show, respectively, the presence and absence of a thoracic horn) in *O. sagittarius* females. (f) Sham control (left) and *otd1* RNAi (right) dorsal head phenotypes in *Tribolium castaneum* (top), *O. taurus* (second and third row from top), and *O. sagittarius* (bottom two rows); arrowheads highlight ectopic structures. (g,h) Ectopic anterior horns (arrowhead) in adult male (g) and female (h) of *O. taurus* after *otd1* RNAi. (i) Ectopic dorsal eyes (arrowhead) in pupal (i) and adult (j) of *O. sagittarius* after *otd1* RNAi; arrowheads point at the intersection of the posterior edge of the ectopic eyes and the head midline; the boxed area in (j) corresponds approximately to the area shown in (i).

resulted in a reduction of the T1 postcoxal bridge, T2 mesosternellum, T3 intercoxon process, and median groove, and A3 intercoxon process (*Tc-otd1* F1R1: 31/36; *Tc-otd1* F2R2: 10/25; see note on the electronic supplementary material, table S2). *Tc-otd2* RNAi individuals had either a more subtle version of the above defects (*Tc-otd2* F2R2: 10/25; see note on the electronic supplementary material, table S2) or were indistinguishable from control animals (*Tc-otd2* F1R1: 30/35). Similarly, in both *Onthophagus* species, *otd1* RNAi resulted in a strong reduction of the metasternal plate (*Ot-otd1*: 98/102; *Os-otd1*: 61/105), while *otd2* RNAi resulted in no visible phenotype (*Ot-otd2*: 0/33) (figure 3c; electronic supplementary material, figure S5a,b).

In *Onthophagus* beetles, *otd1* RNAi also affected thoracic horns, a dorsal midline structure. All *Onthophagus* pupae develop such thoracic horns on their pronotum (dorsal T1 segment) to aid in ecdysis of the larval head capsule during the larval-to-pupal moult [17,22], though only a subset of species then convert them to adult structures, while the remainder resorb them during the pupal stage via programmed cell death [23]. Among the two species studied here, only *O. sagittarius* females convert their pupal thoracic horn into an adult counterpart. *otd1* RNAi drastically reduced the size of pupal thoracic horns in males and females of both *Onthophagus* species (figure 3d; electronic supplementary material, figure S5c-d), and removed thoracic horns in adult female *O. sagittarius* (figure 3e). In *Tribolium* flour beetles, which lack thoracic horns in pupae or adults, neither *Tc-otd1* RNAi nor *Tc-otd2* RNAi caused any obvious change in the pronotum relative to controls. These results suggest that *orthodenticle* class genes play a critical role in post-embryonic patterning of epidermal midline structures in beetles. This finding is congruent with earlier work documenting midline expression of *otd* genes in the ventral nerve cord of late *Tribolium* embryos [19] and parallels results on *otd* function in the development of medial structures of larval and adult *Drosophila* [24], suggesting that the role of *orthodenticle* in instructing the development of midline structures may be an ancestral feature of post-embryonic insect development.

(*otd1* RNAi dramatically alters adult head formation in *Onthophagus* but not *Tribolium*).

*otd1* RNAi resulted in strong cephalic phenotypes in both *O. taurus* and *O. sagittarius* but not in *Tribolium* (figure 3f). Specifically, *otd1* RNAi caused a reduction or deletion of the dorsal cephalic midline region, resulting in an apparent ‘lateralization’ of the head relative to sham controls. By contrast, no defects were
observed on the ventral head. \textit{otd1} RNAi also dramatically affected horn formation, resulting in complete loss or severe reduction of the paired posterior head horns in larger males of \textit{O. taurus} (figure 3f; electronic supplementary material, figure S5c. 9/9 males large enough to be horned; note that smaller males are normally hornless in this species), the paired anterior horns of male \textit{O. sagittarius} (25/30), and the single medial posterior horn of female \textit{O. sagittarius} (20/21) (figure 3f; electronic supplementary material, figure S5f).

Strikingly, \textit{otd1} RNAi not only reduced or deleted head horns, but also consistently induced the formation of an ectopic pair of anterior horns in \textit{O. taurus} (69/86, figure 3g,h). Ectopic horns were present in both males and females, and located at a position homologous to the lateral ends of an anterior cephalic ridge usually found in wild-type \textit{O. taurus} females, thus resembling the paired anterior horns of wild-type male \textit{O. sagittarius} in placement (figure 3f).

While ectopic anterior horns were consistently found in \textit{O. taurus} Ot-\textit{otd1} RNAi individuals, they were never observed in \textit{O. sagittarius}. Instead, in \textit{O. sagittarius}, Os-\textit{otd1} RNAi resulted in a fairly penetrant and completely unexpected phenotype: development of single or paired compound eyes at or near the midline of the postero-dorsal head (43/61, figure 3f,ij; electronic supplementary material, figure S6e–c). Ectopic dorsal eyes became evident during early pupal development and varied in size, but consistently presented all external features typical of regular compound eyes, including hexagonal ommatidia and lenses. By contrast, we never observed ectopic eyes in \textit{O. taurus} Ot-\textit{otd1} RNAi individuals or in sham controls in either species (but see below).

In \textit{Tribolium}, in contrast, larval \textit{Tc-otd1} RNAi using constructs targeting two different regions of the gene had no discernible effect on pupal or adult head morphology (figure 3f), despite all individuals showing midline defects at other regions of the body (figure 3c). qPCR measurements detected significantly lower levels of \textit{Tc-otd1} transcripts in \textit{Tc-otd1} RNAi pupae relative to controls, both for whole-body and tissue-specific samples (electronic supplementary material, figure S9), indicating that the lack of a head phenotype is not due to systemically or locally ineffective gene knockdown after dsRNA injections. These results stand in stark juxtaposition to the striking \textit{otd1} RNAi phenotypes found in \textit{Onthophagus} beetles, suggesting that the lineage including \textit{Tribolium} either secondarily lost the ancestral role of \textit{otd1} in post-embryonic head development, or alternatively, that such a role may be a novel developmental feature unique to the lineage leading to \textit{Onthophagus}.

\textbf{(f) Nonlinear effects of Ot-\textit{otd1} and Ot-\textit{otd2} RNAi suggest partial redundancy of orthodenticle class transcription factors}

In contrast to the striking phenotypes resulting from \textit{otd1} RNAi, \textit{otd2} RNAi individuals exhibited no detectable morphological differences compared to controls in any obvious aspect of head or horn morphology (electronic supplementary material, figure S8). This may be due to \textit{otd2} simply being non-functional during post-embryonic development, or alternatively, to \textit{otd2} being partially redundant to \textit{otd1}, so that it can be functionally replaced by \textit{otd1}, but itself can only partially replace \textit{otd1} functions.

To discriminate between these alternate hypotheses, we performed simultaneous larval RNAi against \textit{otd1} and \textit{otd2} (\textit{otd1} + 2) in \textit{O. taurus} and \textit{Tribolium}. In \textit{O. taurus}, Ot-\textit{otd1} + 2 RNAi resulted in strong reduction of metasternal plates and thoracic pupal horns (electronic supplementary material, figure S5a, c), and complete deletion of paired posterior horns in males (13/14) and a reduced proportion of ectopic anterior horns compared with Ot-\textit{otd1} RNAi individuals (Ot-\textit{otd1} + 2: 10/25; Ot-\textit{otd1}: 69/86). Surprisingly, four out of 25 \textit{otd1} + 2 RNAi animals surviving to adulthood also developed ectopic compound eyes at a medial postero-dorsal region of the head, similar to Os-\textit{otd1} RNAi individuals in \textit{O. sagittarius} (electronic supplementary material, figure S6d-f). Similarly, double knockdown of \textit{Tc-otd1} and \textit{Tc-otd2} in \textit{Tribolium} resulted in defects along the ventral midline more pronounced than those described for \textit{Tc-otd1} RNAi alone (electronic supplementary material, figure S7), but had no detectable effects on the dorsal head shape. Together, these results support the hypothesis that \textit{orthodenticle} class transcription factors show asymmetric functional redundancy [21]. If correct, this could also explain the difference in \textit{otd1} phenotypes observed between \textit{O. taurus} and \textit{O. sagittarius}: since we were not able to detect Os-\textit{otd2} transcripts in \textit{O. sagittarius}, it is conceivable that this gene is not actively transcribed during post-embryonic development in this species and thus unable to partially rescue Os-\textit{otd1} RNAi individuals.

\textbf{(g) Beetle \textit{otd1} and \textit{otd2} are expressed in epidermal tissues at early pupal stages}

Our \textit{otd} RNAi experiments dramatically affected the formation of head and thoracic horns, i.e. evolutionary novel structures of strictly epidermal origin. However, current knowledge of \textit{otd} embryonic expression in \textit{Tribolium} emphasizes that in older embryos the expression domain of \textit{otd} genes becomes restricted to the brain, ventral nerve cord, and eyes [19]. This raises the possibility that \textit{otd} expression in \textit{Onthophagus} either remains restricted to nervous tissues during post-embryonic development, and epidermal development is indirectly controlled by \textit{otd} through signalling between tissues or, alternatively, that \textit{otd} is post-embryonically reemployed in epidermal tissues and directly patterns local epidermal development. To distinguish between these scenarios, we used RNAseq of early \textit{O. taurus} pupae to estimate tissue-specific gene expression for three epidermally derived tissues that vary in the degree to which they are affected by \textit{otd} knockdown—dorsal head epidermis, T1 dorsal epidermis, and posterior ventral abdominal epidermis—as well as brain tissue. Our results indicate that \textit{Ot-otd1} expression levels relative to abdominal epidermis are approximately four times higher in the brain, approximately 24 times higher in the T1 dorsal epidermis, and approximately 42 times higher in the dorsal head epidermis (electronic supplementary material, figure S8, bottom row). By contrast, \textit{Ot-otd2} levels are only approximately two times higher in the brain, one half in the T1 dorsal epidermis, and approximately five times higher in the dorsal head epidermis (electronic supplementary material, figure S8). Thus, our results support a scenario whereby \textit{otd} genes are reemployed in epidermal tissues during post-embryonic development.

Next, we sought to determine whether \textit{otd} expression in the dorsal head epidermis is restricted to horned beetles. Using tissue-specific qPCR in early pupae of \textit{Tribolium}, a taxon belonging to a family lacking any type of head and thoracic horns, we found that both \textit{Tc-otd1} and \textit{Tc-otd2} exhibit relatively high expression levels in the dorsal head epidermis (electronic supplementary material, figure S8, top row),
suggesting that post-embryonic expression of \textit{otd} class genes during head development may be a shared ancestral feature, at least among beetle families.

Importantly, independent work on \textit{Drosophila} also documented late post-embryonic \textit{otd} expression and function in the medial region of the eye-antennal, leg, and genital discs, as well as ventral epidermis [24]. Moreover, adult midline defects resulting from \textit{otd} knockdown in \textit{Drosophila} [24,25] are at least partly reminiscent of those described here for beetles, including defects to the dorsal head. However, it is worth emphasizing that head formation in cyclorrhaphan flies such as \textit{Drosophila} is highly derived and non-representative compared with that of most other holometabolous insects, including beetles. Specifically, in complete contrast to head formation in \textit{Onthophagus} and \textit{Tribolium}, no larval head epidermis is used during metamorphosis to build the adult head of \textit{Drosophila}, which instead derives anew from anterior imaginal discs and histoblasts [26]. It is therefore difficult to ascertain whether superficial similarities in \textit{otd} function during dorsal adult head formation reflect a synapomorphy shared across holometabolous insects but lost in \textit{Tribolium}, or independent functional co-options of this gene class in \textit{Onthophagus} horned beetles and fruit flies. Furthermore, we cannot completely exclude the possibility that \textit{otd} does have a function in \textit{Tribolium} adult head formation, but defects caused by RNAi are too subtle to be detected by our methods. Even though a wider taxonomic sampling is clearly necessary to address this question, our results nevertheless highlight the conservation of post-embryonic \textit{otd} expression in insects, and its independent co-option in the formation and integration of novel head structures in \textit{Onthophagus}.

**(h) Orthodenticle genes regulate post-embryonic patterning of evolutionary novel structures**

Insects in general, and beetles in particular, present an enormous diversity of head morphologies. Moreover, from the stalks of stalk-eyed flies and the rostrum of weevils to the horns of scarab beetles, insects have managed to integrate numerous novel cephalic features into head formation, yet how such innovation and integration was enabled during developmental evolution remains largely unclear [9]. A growing body of evidence emphasizes the recruitment of modular developmental genetic components into new ontogenetic contexts as a central mechanism facilitating the integration of novel traits into ancestral contexts without necessitating the origin of novel genes or pathways [27,28]. Here, we examined \textit{six3} and \textit{otd}, two members of an ancient gene network controlling embryonic head formation across diverse phyla [20]. In insects, these transcription factors tightly interact and cooperate to pattern the larval head from the anterior pre-segmental region of the embryo [9–12]. However, despite this deep phylogenetic and functional entrenchedness, these genes appear to have become disconnected during post-embryonic development of the adult beetle head: \textit{six3} regulates adult compound eye size, but is not involved in shaping other adult structures. By contrast, \textit{otd} regulates post-embryonic development of epidermal midline structures along the body in both horned and flour beetles and, most significantly, regulates the formation of cephalic and thoracic horns, true and rather recent evolutionary novelties in the genus \textit{Onthophagus}. As such, the adult \textit{six3} and \textit{otd} RNAi phenotypes we describe here are markedly different from those seen after embryonic knockdown [10–12]. Furthermore, we found no evidence that the tight embryonic interaction between these genes is present during post-embryonic development, showing that gene coupling is strongly context dependent. If this is true for other genes that pattern the anterior pre-segmental region, this suggests that the insect dorsal head may be decoupled from, and less constrained than, its appendage-bearing ventral counterpart, thus explaining why this region is such a hotspot of morphological diversity.

**(i) Neofunctionalization of orthodenticle may have been facilitated by latent yet non-adaptive tissue-specific expression in beetle heads**

Recruitment of ancestral transcription factors into new developmental contexts requires the evolution of novel spatio-temporal expression domains, developmental genetic interactions or both. Here, we document a novel function for \textit{orthodenticle} class genes in patterning apomorphic structures in the dorsal heads of adult \textit{Onthophagus} beetles. Notice that our approach was not predicated on the implicit expectation of gene sequence or structure change upon acquisition of a novel function. Function emerges through context and interactions, and changes in functionality during development may therefore result from changes in the associated genes themselves, their interactions, or the context within which they occur. Thus, just as a hammer (whose original function is hammering nails) can be used for a novel function as a nutcracker without any fundamental changes in the hammer itself, a gene can acquire a novel function by virtue of being redeployed in a novel context or by changes in its regulatory interactions with other genes, without a single structural change within its coding region. A scenario of evolution by contextual novelty is also supported by our results showing that both \textit{otd} orthologues are expressed at relatively high levels in the dorsal head epidermis of early pupae, suggesting that post-embryonic development of dorsal head structures including horns is directly regulated by tissue-specific expression of \textit{orthodenticle} class genes, rather than inductive interactions with the nervous system. Strikingly, we also found evidence for the expression of \textit{otd} in the dorsal head epidermis of \textit{Tribolium} flour beetle pupae, even though \textit{otd\_RNAi} individuals showing knockdown phenotypes in the ventral midline did not show any defect on their dorsal heads. Although a wider taxonomic sampling is needed to ascertain dorsal head specific post-embryonic \textit{otd} expression and function, it is tempting to speculate that if latent yet non-functional expression of \textit{otd} is common to most beetles, then such pre-existing, function-less, yet already tissue- and body region-specific expression patterns could have provided a critical developmental genetic substrate for the evolution of novel head morphologies. More generally, the strong spatio-temporal phylogenetic conservation of \textit{otd} expression on one side, coupled with the frequent acquisition of diverse functions observed across Metazoan phyla on the other [11–13,25,29–32], suggests that \textit{orthodenticle} class transcription factors may be particularly suitable to provide positional information facilitating the patterning of evolutionarily novel structures.

**Data accessibility.** The datasets supporting the conclusions of this article are available from the Dryad repository (https://datadryad.org/resource/doi:10.5061/dryad.nd1j]s [33].

**Authors’ contributions.** E.E.Z. and A.P.M. designed the experiments; H.A.B. performed ablation experiments in \textit{Onthophagus} spp.; E.E.Z.
performed all other experiments in Onthophagus spp.; D.M.L. and Y.T. performed all experiments in Tribolium castaneum; E.E.Z. and A.P.M. analysed the data and wrote the manuscript. All authors read and approved the manuscript for publication.

Competing interests. All authors declare that they have no competing interests.

Funding. Funding for this study was provided by National Science Foundation grants IOS 1256689 and IOS 1120209 to A.P.M., and IOS 0950964 and IOS 1557936 to Y.T.

Acknowledgements. We would like to thank Erik Parker, Adam Moore, Alexander Neufeld, Justin Song, Keeley Newsom, Justine Christian, Hailey Riggs, Peyton Joachim, and Bonnie Young for expert help with beetle collecting and care. We also thank Melissa Pespeni for generating the developmental RNAseq dataset, cris Ledon-Rettig, James Ford, and the Indiana University Center for Genomics and Bioinformatics for help with tissue-specific RNAseq. Finally, we would like to thank our two anonymous reviewers who provided valuable, detailed, and insightful feedback that greatly helped improve this manuscript.

References


