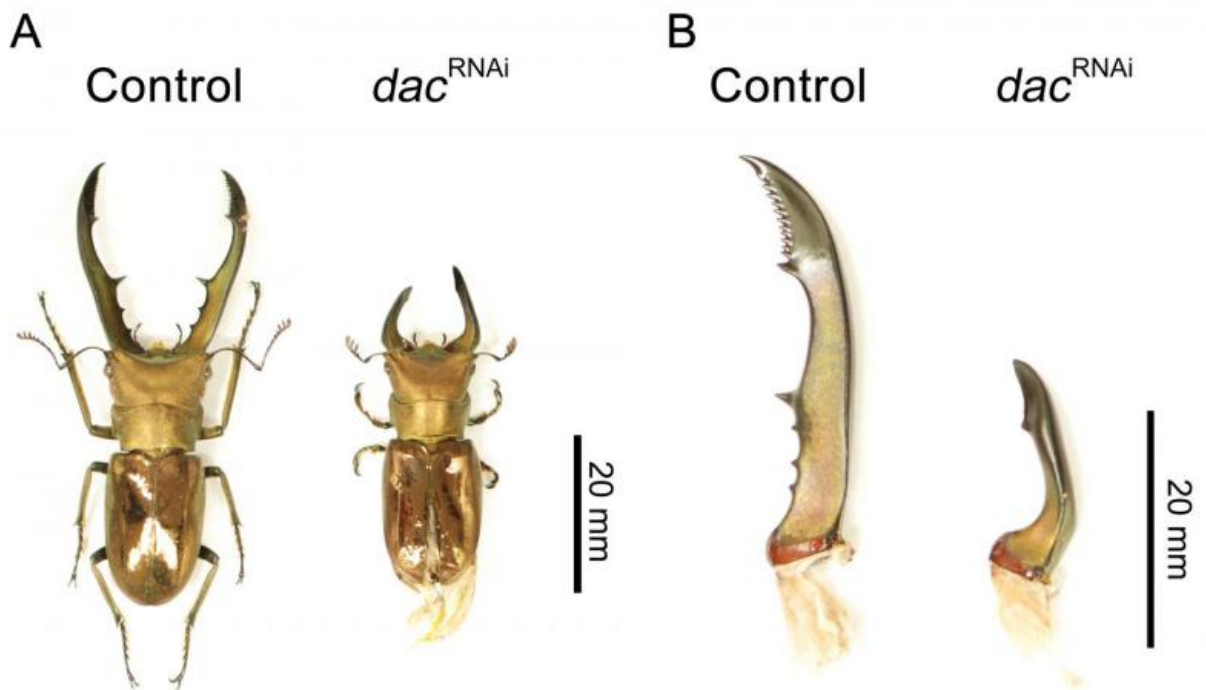


Identification of genes controlling mouthpart development key to insect diversity

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(A) Comparison of the large adult male whole body phenotypes of GFP RNAi control animal (left) and dachshund RNAi animal (right). Control animal did not show any defect compare to wildtype animals, while dachshund RNAi showed defect phenotype in appendages including legs, antennae and mandibles. (B) Magnified image of mandibles of GFP RNAi control animal (left) and dachshund RNAi animal (right). RNAi of dachshund gene affected both of mandible size and shape. Credit: Nagoya University

Nagoya University-led international research reveals functions of mouthpart-controlling genes in development of enlarged mandibles in the stag beetle.

Insects are a biological success story with their high abundance, dominating biodiversity, and almost worldwide distribution. Their evolutionary prowess in part reflects their ability to diversify and fill a variety of ecological niches. One means of doing this is developing a range of mouthparts that enables different foodstuffs to be consumed. Mouthparts can be highly modified, as in the straw-like maxillae of butterflies, or exceptionally enlarged, as in the mandibles of stag beetles that are used for fighting rather than feeding. However, the molecular mechanisms underlying mandible enlargement have been poorly understood. Collaborative Japan–US research coordinated by Nagoya University has now shed light on the genetic control of stag beetle mandible development. The study was published in *Developmental Biology*.

The development of appendages, such as limbs and mouthparts, at different distances from the body wall (proximal through medial to distal) is controlled by a series of genes highly conserved among all insects. The researchers used a molecular silencing technique to sequentially knockdown the expression of seven of these genes to investigate their function in the development and enlargement of stag beetle mandibles.

The dachshund (*dac*) gene, which controls regulation of the middle region of appendages in *Drosophila* and many other insects, had the greatest effect on mandible development of all seven genes analyzed.

"Knockdown of *dac* greatly reduced mandible size in male but not female stag beetles, and affected mandible morphology in both sexes," corresponding author Hiroki Gotoh says. "Knocked-down animals did

not develop the serrated teeth normally seen in all males, and also lacked the inner teeth characteristic of large males."

Genes *aristaless* (*al*) and *homothorax* (*hth*) were also shown to have important roles in the development of inner teeth. However, knockdown of the *Distal-less* (*Dll*) gene, which is functional in distal regions, had no effect on mandible development. This supports previous knowledge that insects lost their most distal mandible regions early in evolution.

Male-specific mandible enlargement in stag beetles is known to be regulated by juvenile hormone, such that larger males have disproportionately larger mandibles.

"We observed a size-specific link with the functions of *dac*, *al*, and *hth* in the knockdown studies," Gotoh adds. "This suggests that these genes control their function using a size-dependent factor – most likely juvenile hormone."

Genetic silencing also revealed that the seven genes largely controlled [stag beetle](#) leg development in a manner highly conserved with that of other insects, but that their roles in antennal formation were more diverse. These conserved developmental functions of some [genes](#) but varied roles of others are likely to have contributed to the evolution of mouthparts in different insect species.

More information: Hiroki Gotoh et al. The function of appendage patterning genes in mandible development of the sexually dimorphic stag beetle, *Developmental Biology* (2017). [DOI: 10.1016/j.ydbio.2016.12.011](https://doi.org/10.1016/j.ydbio.2016.12.011)

Provided by Nagoya University

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