

Mismatches between feeding ecology and taste receptor evolution: An inconvenient truth

Comparative and evolutionary biology can not only verify laboratory findings of gene functions but also provide insights into their physiological roles in nature that are sometimes difficult to discern in the laboratory. Specifically, if our understanding of the physiological function of a gene is complete and accurate, the gene should be inactivated or pseudogenized in and only in organisms in which the presumed function of the gene has become useless or harmful. On the basis of multiple independent pseudogenizations of the sweet taste receptor gene *Tas1r2* in obligated carnivores and piscivores (fish eaters) and similar independent pseudogenizations of the umami taste receptor gene *Tas1r1* in marine mammals, Jiang et al. (1) concluded that “loss of taste receptor function” is “directly related to feeding specializations.” We believe that this conclusion is unwarranted.

Jiang et al. (1) contended that obligated carnivores and piscivores need not sense sweet because meat contains little carbohydrate. Although pseudogenized *Tas1r2* was indeed found only in obligated carnivores and piscivores among 18 studied species of Carnivora, two obligated carnivores they examined (ferret and Canadian otter) still possess an intact *Tas1r2* (1). There is no indication that the current feeding ecology of these two species appeared so recently in evolution that neutral null mutations have not had time to fix in their *Tas1r2*. The three pinnipeds studied share a common ancestry of obligated meat-eating, yet no single null mutation of *Tas1r2* is shared between them, suggesting that the pseudogenizations are not closely related to their diet. Outside Carnivora, vampire bats lack an intact *Tas1r2* despite the presence of carbohydrates in blood, their sole diet (2). It is probable that the pseudogenization of *Tas1r2* in vampire bats is related to the narrowness of their diet rather than the specific diet they use. *Tas1r2* is also missing in the genome sequences of the herbivorous horse and omnivorous pig, but no

satisfactory explanation exists (2). Furthermore, *Tas1r2* is absent in all bird genomes sequenced thus far (2), irrespective of their diet.

Jiang et al. (1) further contended that sea lions and dolphins need not sense the umami taste because they swallow food whole. Although it is true that *Tas1r1* is pseudogenized in these two species, the authors ignore the previous finding that *Tas1r1* is also pseudogenized or missing in all bats examined, regardless of their diet (fruits, insects, or blood) (3). Although the pseudogenization of *Tas1r1* in the giant panda (4) occurred at approximately the same time as it switched from being a meat-eater to a plant-eater (5), and thus may be related to the feeding ecology, herbivorous mammals, such as the horse and cow, still carry an intact *Tas1r1* (5).

Clearly, the presence/absence of intact *Tas1r2* and *Tas1r1* in mammals and other vertebrates is sometimes inconsistent with the known functions of these genes and the involved tastes. These mismatches indicate that our understanding of the physiological functions of these tastes and/or their receptor genes is far from complete. Recognizing such inconvenient truths would stimulate further studies toward a complete and accurate understanding of tastes and taste receptor genes.

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