Opinion

Role of Arylalkylamine N-Acetyltransferase (AANAT) In Evolutionary Genomics

Christina Behzadmehr*

Department of Biomedical Engineering, University College of London, UK

*Address Correspondence to Christina behzadmehr, E-mail: clairej@ed.ac.uk

Received: 03-October-2022; Manuscript No: JEM-22-81075; **Editor assigned:** 05-October-2022; PreQC No: JEM-22-81075 (PQ); **Reviewed:** 19-October-2022; QC No: JEM-22-81075; **Revised:** 24-October-2022; Manuscript No: JEM-22-81075 (R); **Published:** 31-October-2022; **DOI:** 10.4303/JEM/236088

Copyright: © 2022 Behzadmehr C. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Introduction

Around the world, several pathogenic species of "*Candidatus Liberibacter*" have been discovered from plant hosts. These species include "*Ca. Liberibacter asiaticus*" (CLas) and "*Ca. Liberibacter solanacearum*" (CLso), which are thought to be the causes of the devastating citrus *Huanglongbing* (HLB) and potato Zebra chip disease (ZC), respectively. Research on the biology and management of "*Ca. Liberibacter*" species is difficult because of their phloem colonisation, lack of pure culture, and intracellular existence in plant hosts. Despite the fast accumulation of genetic data on the "*Ca. Liberibacter*" species and the analysis of several virulence factors, it is still unclear how the three-way interactions between the pathogen, insects, and plants operate.

cDNA libraries taken from the gut of adult psyllids were sequenced on an Illumina platform in order to comprehend the molecular interactions of CLas-Diaphorina citri throughout the vector acquisition procedure. Through read mapping of CLas genes, a high copy number of genes (up to 95%) were expressed in the first stage of D. citri gut colonisation, indicating that such genes may play important roles in CLas invading insect organs. According to Tang et al., when CLso translocated into the gut cells, the expression of the IAPP5.2 gene an inhibitor of apoptosis was considerably increased. As evidenced by the detection of apoptosis, the acquisition of CLso, and the effectiveness of transmission when IAPP5.2 was silenced, it was hypothesised that CLso may inhibit the apoptotic response in the psyllid guts by upregulating IAPP5.2 in the early stages of infection. Finding new genetic sources of CLas/CLso tolerance and resistance might be important for the integrated management of HLB/ZC. One of the 52 screened accessions from a taxonomically varied group of tuber-bearing Solanum species was found to be ZC-resistant.

The variations in leaf trichome density and shape between the wild accessions may be significant contributors to the effects of antibiosis. A thornless pummelo bud-sport that developed more vigorously and was more resistant to HLB than the thorny wild type was found and studied. This germplasm provides a useful resource for potato breeding to create ZC resistance cultivars. Further investigation revealed that the phenotypic changes caused by the bud-sport were linked to large transcriptome changes, offering valuable information and opportunities for genetic breeding and gene editing to enhance citrus.

Description

Melatonin, a significant hormone, has a role in the endocrine control of several activities in vertebrates. Four cascaded enzymes, the most important of which is ARYLALKYL-AMINE N-ACETYLTRANSFERASE (AANAT), catalyse its production. The majority of vertebrate taxa have only one aanat gene, but researchers, including us, have shown that fish have the most extensive aanat gene repertoire, with several putative functions including seasonal migratory, amphibious aerial vision, and cave or deep-sea adaption. More putative sequences of fish aanat genes will likely be accessible as genome and transcriptome sequencing technologies advance quickly. Our knowledge of how AANAT operates in many fish species will be improved by related phylogenetic and functional studies. The GCN5-RELATED N-ACETYL-TRANSFERASE (GNAT) superfamily includes ARYLAL-KYLAMINE N-ACETYLTRANSFERASE (AANAT), often referred to as SEROTONIN N-ACETYLTRANSFERASE (SNAT or NAT), and other enzymes. It catalyses the transfer of the acetyl group from acetyl-CoA to an arylalkylamine and is an acetyl-CoA-dependent enzyme. Serotonin and dopamine are the typical arylalkylamine substrates for AANAT.



AANATs perform varied roles in several organismal groupings. Numerous AANATs have developed in insects, mainly in mosquitoes. The key functions of insect AANATs include cuticle development, pigmentation, and the metabolism of certain bioamine neurotransmitters, fatty acid amides, and circadian rhythms. In vertebrates, AANATs mostly work differently thanks to the tiny chemical melatonin (N-acetyl-5-methoxytryptamine).

Conclusion

Considered a possible novel pesticide target, ARYLALKYL-AMINE N-ACETYLTRANSFERASE (aaNAT) catalyses the acetylation of arylalkylamine substrates including serotonin and dopamine and hence facilitates a variety of activities in insects. The evolution that results in many aaNATs in mosquitoes and the genesis of insect aaNATs are mainly unclear. Here, in order to investigate and deepen our understanding of the molecular evolution of this gene family, we studied the genomes of 33 different species. We demonstrate that aaNAT orthologs are lacking in some species of Annelida, Echinozoa, Mollusca, and Arachnida but present in bacteria, Cephalochordata, Chondrichthyes, Cnidaria, Crustacea, Mammalia, Placozoa, and Teleoste. In particular, more than 10 aaNATs were found in mosquitoes belonging to the Culicinae subfamily. The Culicinae subfamily of mosquitoes saw gene expansion more than 190 million years ago, according to a study on the molecular evolution of the aaNAT/aaNATlike genes in mosquitoes.