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Trends in Genetics - Genome of the month

Acyrtosiphon pisum

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Aphids are sap-sucking insects that comprise about 4700 species colonizing a wide variety of host plants. They are the dominant group (26%) among insect pests of the six main crops grown for human consumption, with the potential to cause worldwide economic impact. Aphids inflict damage directly by feeding and indirectly by phytovirus transmission. Since the initial sequencing of the genome of the pea aphid, *Acyrtosiphon pisum* and its symbiont *Buchnera aphidicola*, a further 12 aphid genome sequences have become available. Most of these genomes are accessible at the dedicated AphidBaseⁱ. Fourteen *Buchnera* genomes have also been sequenced. This provides a unique opportunity to study selection, adaptation, and evolution using aphids as a model family of species with broad distribution and adaptation to different environments and food sources. In addition, the availability of the genomes will facilitate future comparative studies focusing on the development, physiology and metabolism of aphids to identify novel pest control strategies.

TAXONOMY AND CLASSIFICATION:

KINGDOM: Animalia

PHYLUM: Arthropoda

CLASS: Insecta

ORDER: Hemiptera

SUPERFAMILY: Aphididoidea

FAMILY: Aphididae

GENUS: *Acyrtosiphon*

GENOME FACTS:

- The genome of *A. pisum* was the first sequenced genome of a hemimetabolous and hemipteran insect.
- The haploid genome comprises 4 chromosomes for a genome size of 542Mb and a total number of 18890 genes: 17317 protein coding genes, 163 miRNA and 945 lncRNAs (NCBI Annotation release 101).
- The genome is characterized by gene family duplications/expansions, and by loss/reduction of others (metabolic pathways and antibacterial defense pathways (e.g. IMD pathway, PGRPs, defensins, cecropins).
- There is significant expansion of genes encoding transporters (e.g. amino acid transporters, digestive enzymes, and RNAi machinery).

SPECIES FACTS:

- *A. pisum* is a soft-bodied insect that alternates between parthenogenetic, viviparous reproduction and sexual oviparous reproduction. Sexual reproduction is initiated upon lengthening of nights and reduction of temperature.
- It is a relatively large aphid (several millimeters in adults), readily reared on plants or on artificial medium in the laboratory.
- Aphids comprise different morphs (winged and non-winged), the occurrence of which is determined by population density and/or presence of danger.
- Aphids have a novel cell type, the bacteriocyte, that was initially assumed to simply house the endosymbiotic bacteria. However, recent data reveals a more prominent role in physiological plasticity by controlling nutritional needs when facing physiological or environmental constraints.
- *A. pisum* is readily tractable experimentally with genome editing methods becoming available.

FUN FACT ABOUT THE GENOME:

Novel genes are found with thus far unknown functions. These include BCRs (bacteriocyte cysteine-rich peptides) and SPs (Secreted Proteins), and a class of putative zinc finger containing transcription factors. It has been suggested that the BCRs may be related to the presence of endosymbionts while the Zn-finger TFs may play a role in phenotypic plasticity of aphids.

Resources

¹ <https://bipaa.genouest.org/is/aphidbase/>

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LITERATURE:

1. IAGC. Genome sequence of the pea aphid *Acyrtosiphon pisum*. PLoS Biol. 8(2):e1000313 (2010).
2. Shigenobu, S., Watanabe, H., Sakaki, Y. & Ishikawa, H. Genome sequence of the bacterial symbiont of aphids *Buchnera* sp. APS. Nature 407(6800):81-6 (2000).
3. Gerardo, N. M. et al. Immunity and other defenses in pea aphids, *Acyrtosiphon pisum*. Genome Biol. 11(2)R21 (2010).
4. Price, D. R. & Gatehouse, J. A. Genome-wide annotation and functional identification of aphid GLUT-like sugar transporters. BMC Genomics 15: 647 (2014).
5. Shigenobu, S. & Stern, D. L. Aphids evolved novel secreted proteins for symbiosis with bacterial endosymbiont. Proc. Biol. Sci. 280(1750):20121952 (2013).

6. Shigenobu, S. et al. Comprehensive survey of developmental genes in the pea aphid, *Acyrtosiphon pisum*: frequent lineage-specific duplications and losses of developmental genes. *Insect Mol. Biol.* 19(2):47-62 (2010).
7. Simonet, P. et al. Bacteriocyte cell death in the pea aphid/*Buchnera* symbiotic system. *PNAS* 115(8): E1819-E1828. (2018)
8. Colella, S., et al. Bacteriocyte reprogramming to cope with nutritional stress in a phloem sap feeding hemipterans, the pea aphid *Acyrtosiphon pisum*. *Front. Physiol.* 9:1498 (2018).
9. Le Trionnaire G., et al. An integrated protocol for targeted mutagenesis with CRISPR-Cas9 system in the pea aphid. *Insect Biochem. Mol. Biol.* 110:34-44 (2019).
10. Tagu, D., Calevro, F., Colella, S., Gabaldon, T. & Sugio, A. Functional and evolutionary genomics in aphids. In: *Biology and Ecology of Aphids*. Andreas Vilcinskis Editor, Taylor and Francis group (2016).



