Trends in Genetics | **Genome of the Month**

Acyrthosiphon pisum

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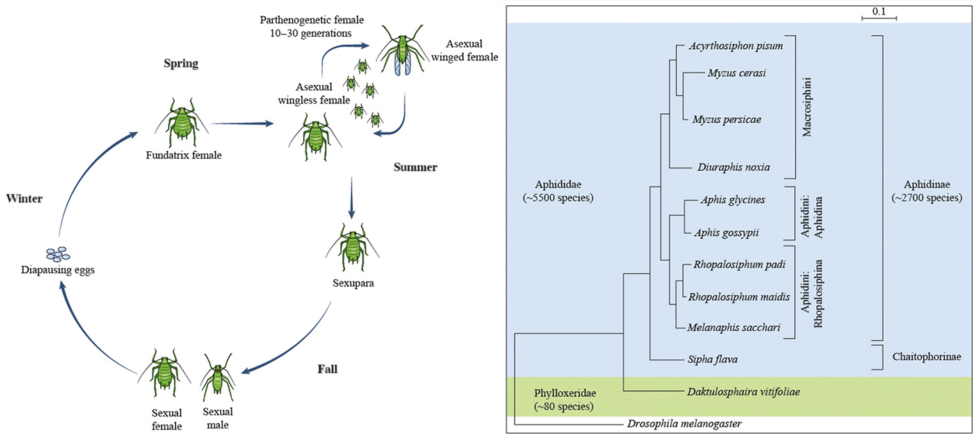

Trends in Genetics

Aphids are sap-sucking insects that comprise about 5500 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 a 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, *Acyrthosiphon pisum* and its symbiont *Buchnera aphidicola*, a further 12 aphid genome sequences have become available. Most of these genomes are accessible at the dedicated AphidBase[i]. 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.

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TAXONOMY AND CLASSIFICATION:
KINGDOM: Animalia
PHYLUM: Arthropoda
CLASS: Insecta
ORDER: Hemiptera
SUPERFAMILY: Aphididoidea
FAMILY: Aphididae
GENUS: *Acyrthosiphon*

GENOME FACTS:

The genome of *A. pisum* was the first sequenced genome of a hemimetabolous and hemipteran insect.

The haploid genome comprises four chromosomes for a genome size of 542 Mb and a total number of 18 890 genes: 17 317 protein coding genes, 163 miRNA, and 945 long non-coding RNAs (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., immune deficiency (IMD) signaling pathway, peptidoglycan recognition proteins (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 wingless), 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.

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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 (ZF-TFs). It has been suggested that the BCRs may be related to the presence of endosymbionts, while the ZF-TFs may play a role in phenotypic plasticity of aphids.

Acknowledgments

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Resources

[i] https://bipaa.genouest.org/is/aphidbase/

Literature

1. International Aphid Genomics Consortium (2010) Genome sequence of the pea aphid *Acyrthosiphon pisum*. *PLoS Biol.* 8, e1000313
2. Shigenobu, S. *et al.* (2000) Genome sequence of the bacterial symbiont of aphids *Buchnera* sp. APS. *Nature* 407, 81–86
3. Gerardo, N.M. *et al.* (2010) Immunity and other defenses in pea aphids, *Acyrthosiphon pisum*. *Genome Biol.* 11, R21
4. Price, D.R. and Gatehouse, J.A. (2014) Genome-wide annotation and functional identification of aphid GLUT-like sugar transporters. *BMC Genomics* 15, 647
5. Shigenobu, S. and Stern, D.L. (2013) Aphids evolved novel secreted proteins for symbiosis with bacterial endosymbiont. *Proc. Biol. Sci.* 280, 20121952
6. Shigenobu, S. *et al.* (2010) Comprehensive survey of developmental genes in the pea aphid, *Acyrthosiphon pisum*: frequent lineage-specific duplications and losses of developmental genes. *Insect Mol. Biol.* 19, 47–62
7. Simonet, P. *et al.* (2018) Bacteriocyte cell death in the pea aphid/*Buchnera* symbiotic system. *PNAS* 115, E1819–E1828
8. Colella, S. *et al.* (2018) Bacteriocyte reprogramming to cope with nutritional stress in a phloem sap feeding hemipterans, the pea aphid *Acyrthosiphon pisum*. *Front. Physiol.* 9, 1498
9. Le Trionnaire, G. *et al.* (2019) An integrated protocol for targeted mutagenesis with CRISPR-Cas9 system in the pea aphid. *Insect Biochem. Mol. Biol.* 110, 34–44
10. Tagu, D. *et al.* (2016) Functional and evolutionary genomics in aphids. In *Biology and Ecology of Aphids* (1st edn) (Vilcinskas, A., ed.), pp. 52–88, CRC Press

https://doi.org/10.1016/j.tig.2019.07.003