

Scientists sequence genome of the woodland strawberry, a model system for rosaceae plants

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The genome of a model plant related to peach, cherry and cultivated strawberry has been sequenced by a consortium of international researchers that includes scientists with the Agricultural Research Service (ARS).

The scientists announced the sequencing of the genome of woodland [strawberry](#) over the weekend at the Plant and Animal Genome Conference in San Diego, Ca. The project was funded by Roche Diagnostics.

Fragaria vesca, commonly known as the woodland or alpine strawberry, is a member of the Rosaceae family, which consists of more than 100 genera and 3,000 species. This large family includes many economically important and popular [fruit](#), nut, ornamental and woody crops, such as almond, apple, peach, cherry, raspberry, strawberry and rose.

F. vesca has many traits that make it an attractive model system for functional genomics studies. Its small size and rapid life cycle enable researchers to conduct genetic analyses with great efficiency and low cost. To determine the importance of a gene of interest, *F. vesca* can be transformed in order to modulate the activity of that gene in the plant. Most importantly, *F. vesca* has a relatively small genome, yet shares most gene sequences with other members of the Rosaceae family, making it an important tool for addressing questions regarding gene function.

ARS molecular biologist Janet Slovin, with the Genetic Improvement of Fruits and [Vegetables](#) Laboratory in Beltsville, Md., created the nearly inbred line used in the *F. vesca* genome sequencing project. Named "Hawaii 4," this line allowed the researchers to more easily program a computer to piece the genome together from the relatively short lengths of sequence data generated by modern sequencing machines.

Although the *F. vesca* genome is a model genome for the Rosaceae group, critical regulatory gene functions will probably differ, hypothesizes Slovin. Scientists can use the [genome sequence](#) to identify these genes, to test their function in *F. vesca*, and to develop molecular genetic markers for more rapid breeding of crops belonging to the Rosaceae group. Slovin will use the genome to study and improve heat tolerance during fruit production in strawberry.

Provided by United States Department of Agriculture-Research, Education, and Economics

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