

United States Department of Agriculture

Cooperative State Research, Education, and Extension Service

2001 No. 2

HIGH-RESOLUTION GENETIC AND PHYSICAL MAPS OF THE *VRN2* REGION IN BARLEY, WHEAT, AND RICE.

Plant gene cloning may lead to better timing of flowering

Jorge Dubcovsky, University of California at Davis

ernalization is the acquisition or acceleration of the ability to flower by a long exposure of plants to low temperatures. Cloning the genes that control this process can have a major impact on crop production.

Vernalization genes *Vrn1* and *Vrn2* are the main genes in wheat and barley that control genetic variation in sensitivity to low temperature for the initiation of flowering. These two genes play a major role in the adaptation of wheat and barley to autumn sowing, preventing flowering in the cold months of winter. Variants of these genes are also important in regulating flowering time. With support from USDA's National Research Initiative (NRI), researchers at the University of California at Davis are studying ways to clone these two genes, using a map-based approach.

HIGH-DENSITY MAPS

First, they constructed high-density genetic maps in diploid wheat, using thousands of plants to find molecular markers closely linked to the targeted gene. They used these molecular markers completely linked to the vernalization gene and others flanking it to find clones from wheat and barley bacterial artificial chromosome (BAC) libraries. These





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clones, which included large segments of genomic DNA, were used to construct physical maps.

Constructing these physical maps was no simple task in the large genomes of barley and wheat because of the frequent presence of large stretches of repetitive elements that can interrupt the chromosome "walking." To solve this problem, they constructed three physical maps in parallel in the corresponding regions in wheat, barley, and rice.

This strategy facilitated the selection of clones from one grass species to "jump" over blocks of repetitive DNA in the other grass species.

Physical maps for the *Vrn2* region have been completed in barley and rice and are being completed in wheat. Since flanking markers are included in the physical map of the *Vrn2* region, the researchers say it is reasonable to assume that the vernalization gene would also be included in these clones. Clones covering the *Vrn2* and *Vrn1* regions are being sequenced to identify candidate genes.

COMPARATIVE GENOME ANALYSIS

Analysis of the *Vrn2* region showed that many markers are colinear in wheat, barley, and rice – confirming the power of the comparative genomic approach. However, some differences were evident.

In the *Vrn2* region, the physical map of barley showed two large deletions when compared to the physical map of wheat.

June 2001

In the *Vrn1* region, one of four genes was duplicated in wheat and barley but not in rice, and one gene was inverted in barley compared to the other two species.

When the rice, barley, and wheat *Vrn2* regions are compared, the rice region seems to be smaller than the corresponding barley and wheat regions. A similar result was found for the *Vrn1* region.

Results from these studies confirm that wheat and barley genes are clustered in "gene islands" that have a gene density higher than the expected average for the complete genome. Recombination in these regions is also higher than the expected average, indicating that mapbased cloning projects are possible in the large genomes of wheat and barley.

Імраст

Vernalization genes *Vrn1* and *Vrn2* play a central role in determining growth habit in many temperate cereals. Therefore, results from these studies are expected to be applicable to other temperate grasses.

Cloning of these genes will provide the means to modify growth habit by transformation and to modulate the strength of the vernalization response to regulate flowering date. Understanding this regulatory pathway may also be useful in manipulating other traits at specific stages of the growing season.

Another interesting possibility is the ability to regulate flowering in forage grasses in which flowering is undesirable.

The research reported in this factsheet was sponsored by the Plant Genome Program of the Plants Division of the National Research Initiative Competitive Grants Program. To be placed on the mailing list for this publication or to receive additional information, please contact the NRI (202/401-5022 or NRICGP@reeusda.gov). The factsheet also is accessible via the NRI section of the Cooperative State Research, Education, and Extension Service website (http://www.reeusda.gov/nri).

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