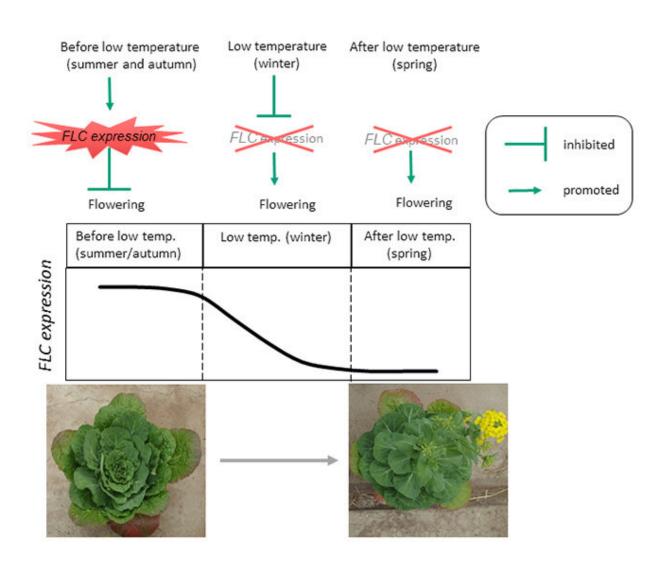


The mechanism that controls Chinese cabbage flowering

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.Floral induction (flowering) in Chinese cabbage. Credit: Kobe University



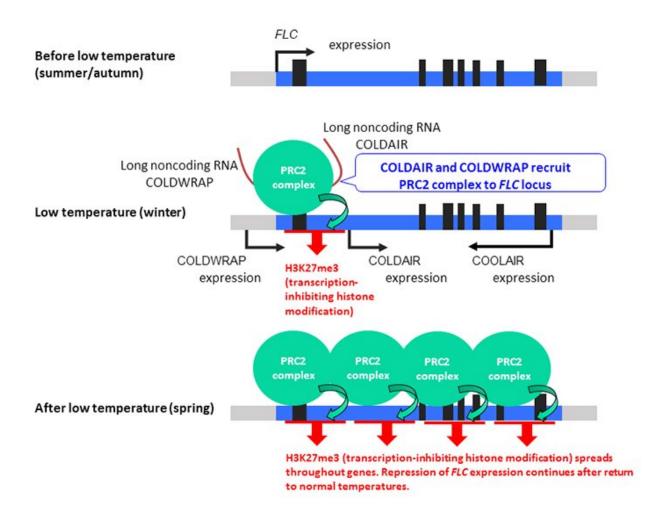
Chinese cabbage is part of a crop family that must be exposed to cold temperatures for a particular period of time in order to flower. Scientists have succeeded in comprehensively identifying the long noncoding ribonucleic acids (IncRNAs) that are expressed when Chinese cabbage is temporarily exposed to cold temperatures for four weeks. LncRNAs that are known to be involved in responding to cold in Arabidopsis thaliana do not exist in Chinese cabbage, which suggests that Chinese cabbage has its own independent mechanism for flowering.

The research team was led by Namiko Nishida (Kobe University Graduate School of Agricultural Science) and Daniel Shea (Niigata University Graduate School of Science and Technology). The team also included Associate Professor Ryo Fujimoto (Kobe University Graduate School of Agricultural Science), Professor Keiichi Okazaki (Niigata University Graduate School of Science and Technology), Team Leader Motoaki Seki (RIKEN Center for Sustainable Resource Science), members of Japan's National Agriculture and Food Research Organization (NARO) and Australia's Commonwealth Scientific and Industrial Research Organisation. The findings were published on June 26 in the online edition of *Scientific Reports*.

Non-coding RNAs lack the information needed to create proteins. These noncoding RNAs are classified into small RNAs (around 20 nucleotides long) and long noncoding RNAs (IncRNAs, over 200 nucleotides long). LncRNAs are expressed in most plants, with tens of thousands known to be expressed in the model plant A. thaliana.

LncRNAs have been linked to the phenomenon of vernalization: when plants need to be exposed to a period of cold treatment in order to flower. This phenomenon can be seen in many subspecies of Brassica rapa L. including the Chinese <u>cabbage</u>, which grows during winter to bloom in spring (Figure 1).





Vernalization mechanism of Arabidopsis thaliana. Credit: Kobe University

The research team extracted total RNAs from Chinese cabbage leaves cultivated for two weeks at 22°C and Chinese cabbage leaves cultivated at room temperature for two weeks, then at a low temperature (4°C) for a further four weeks. Using RNA-sequencing, they obtained enough information to identify the changes in the expression of IncRNAs after exposure to low temperatures.

When the team investigated the mRNAs (messenger RNAs) expression



patterns induced by low temperatures whose transcription domains overlapped with incRNAs (intronic RNAs, a type of IncRNA) and NATs (natural antisense transcripts, another type of IncRNA), they found similar expression patterns but a strong association to vernalization was not found. However, they found combinations of mRNA and NATs that showed the same altered expression under low temperatures (Figure 2), suggesting that NATs are connected to changes in mRNA expression under cold treatment.

The team searched for the existence of IncRNAs whose expression is induced by cold treatment, focusing on the BrFLC loci. One NAT called BrFLC2as showed similar structure and expression patterns to COOLAIR (a key IncRNA of A. thaliana), but these similarities were not found in BrFLC1, BrFLC3 or BrFLC5. In all four BrFLC types, the IncRNAs COLDAIR and COOLWRAP known to recruit the PRC2 complex in A. thaliana was not identified in Chinese cabbage. Their results suggest that for Chinese cabbage exposed to low temperatures, the PRC2 complex may be recruited to the FLC locus based on a different mechanism from A. thaliana.

From these findings we now know that IncRNA expression is not induced in Chinese cabbage from the FLC locus, suggesting that it follows a different flowering mechanism from the model in A. thaliana. The next step is to reveal how the PRC2 complex is recruited to the FLC locus under cold treatment. Revealing the full vernalization mechanism via FLC genes could contribute to selective breeding of Chinese cabbage.

More information: Daniel J. Shea et al, Long noncoding RNAs in Brassica rapa L. following vernalization, *Scientific Reports* (2019). <u>DOI:</u> <u>10.1038/s41598-019-45650-w</u>



Provided by Kobe University

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