

DNA methylation affects superiority of hybrid plants

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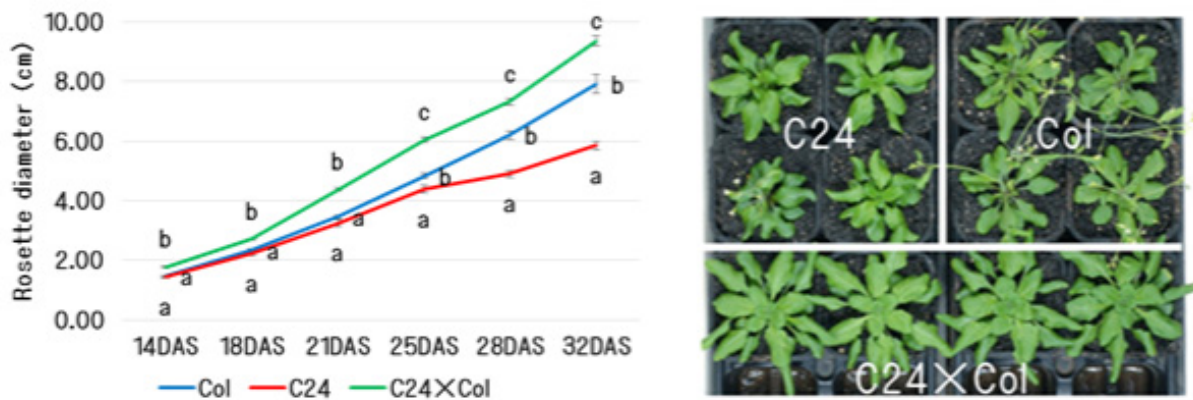


Figure 1: Hybrid vigor seen in the *Arabidopsis thaliana* C24 and Col hybrid. The graph shows rosette diameters at 14 days and 32 days after seeding, and we can see that the F1 hybrid (green line) is bigger than its parents (blue and red) from the early period of growth. Credit: Kobe University

Hybrid vigor refers to when a crossbreed plant or animal shows superior traits compared to its parents. A research group has discovered that a gene involved in maintaining DNA methylation is closely connected to hybrid vigor in *Arabidopsis thaliana*. This has potential applications for other cruciferous vegetables such as Chinese cabbage, and could lead to more efficient breeding of high-yield vegetables. The findings were published on October 8 in the online version of *Proceedings of the National Academy of Sciences*.

The research group included ISHIKURA Sonoko, MIYAJI Naomi, Associate Professor FUJIMOTO Ryo, Professor YASUDA Takeshi (all from the Graduate School of Agricultural Science, Kobe University) and Dr. Elizabeth S. Dennis and Dr. W. James Peacock (CSIRO Agriculture, Australia).

Hybrid plants have qualities useful in farming, such as increase of biomass and being stress resilient. First-generation hybrid plants (F1 plants) bred to exhibit these hybrid vigor attributes are widely cultivated. Globally speaking, currently maize, rice, and rapeseed are all F1 hybrid cultivars. This phenomenon was discovered over 100 years ago, and is recorded in Darwin's famous *On the Origin of Species*. Starting from developing F1 hybrid cultivars of maize at the beginning of the 1900s, a string of hybrid agricultural crops were applied, yields increased dramatically, and the results were comparable to the "green revolution". However, the molecular mechanisms behind this phenomenon remain unclear.

It is well known that plant traits are determined by DNA, specifically by the combination of four bases (a base sequence) of A (adenine), T (thymine), C (cytosine) and G (guanine). In recent years, scientists have discovered that even if the DNA base sequence is the same, different traits can be observed – as you can see from looking at identical twins. This altered expression that does not correlate with changes in the base sequence is known as [epigenetic regulation](#) (as opposed to genetic regulation). DNA methylation has been held up as one example of epigenetic regulation. Adding or subtracting methyl to cytosine in eukaryotic organisms modifies gene expression, while the base sequence remains unchanged. DNA also combines with histone to form a [chromatin structure](#). DNA methylation and the change in chromatin structures caused by histone modification are both linked to modification of gene expression. Recently there have been multiple reports that hybrid vigor is influenced by epigenetic regulation as well as

genetics.

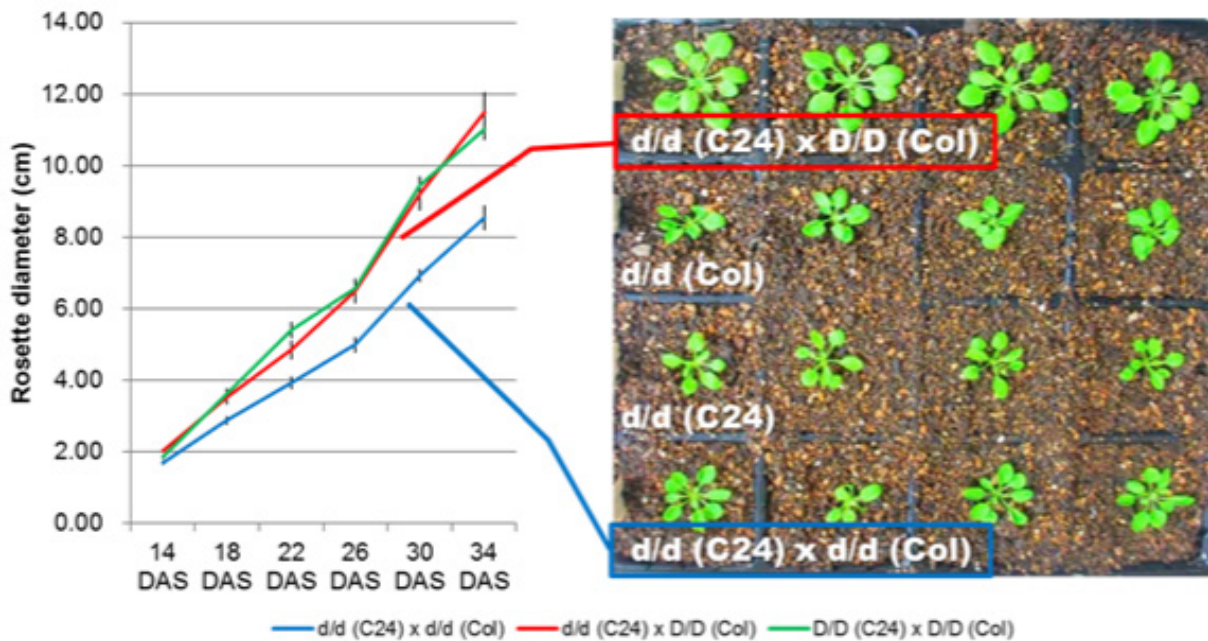


Figure 2: A plant size comparison between the *Arabidopsis thaliana* C24/Col hybrid and the hybrid with DDM1 mutations. We can see that the hybrid lacking DDM1 function (blue line) is significantly smaller than the hybrids with functioning DDM1 (green and red). Credit: Kobe University

Hybrid vigor can be seen in the model plant *Arabidopsis thaliana* (which belongs to the same Cruciferae family as Chinese cabbages). In a first generation hybrid crossed between C24 and Columbia-0 (Col), the plant has an increased biomass (Fujimoto et al. 2012, PNAS 109: 7109-7114) (see figure 1). However, it is still not fully understood why this F1 hybrid plant shows superior characteristics compared to its parents.

In this research, the team used *Arabidopsis thaliana* with mutations in a gene related to DNA methylation, and by confirming the instances of

hybrid vigor, they investigated which genes and epigenetic modifications regulating the genes were linked to hybrid vigor.

Various genes work together in regulating DNA methylation. Among them, when MET1 (Methyltransferase 1, involved in maintaining CG methylation) and Pol IV (related to RdDM, RNA directed DNA methylation, which causes de novo methylation) lost their genetic functions, abnormalities were observed in DNA methylation, but there was no observable effect on hybrid vigor. However, in an F1 hybrid created using a plant with a non-functional DDM1 chromatin remodeling factor (involved in maintaining DNA methylation by modifying chromatin structure), abnormalities were seen in DNA methylation, and the level of hybrid vigor was significantly lower (see figure 2). This demonstrated that DDM1 and hybrid vigor are closely linked, and the epigenetic modification regulated by DDM1 (DNA methylation) is important in hybrid vigor. There have been few concrete reports of the genes involved in hybrid vigor, but based on this research, one of the key genes for hybrid vigor has been clarified.



Figure 3: Hybrid vigor in Chinese cabbage (variation of figure published in Saeki et al. 2016 BMC Plant Biol. 16: 45) . Credit: Kobe University

Currently the research team is preparing to comprehensively analyze the changes in DNA methylation caused by loss of DDM1 function and the accompanying changes in DNA expression level. Based on these findings, they plan to conclusively identify the genes that regulate hybrid vigor.

Arabidopsis thaliana is a cruciferous plant, which means that the knowledge gained through this research can be applied to other plants in this family such as Chinese cabbage, cabbage, broccoli, and rapeseed. This could potentially be used to breed high-yield crop cultivars. The team is also investigating hybrid vigor using Chinese cabbage (see figure 3).

More information: Takahiro Kawanabe et al. Role of DNA methylation in hybrid vigor in, *Proceedings of the National Academy of Sciences* (2016). [DOI: 10.1073/pnas.1613372113](https://doi.org/10.1073/pnas.1613372113)

Provided by Kobe University

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