

# Diversity of cabbage species explained

November 7 2011, Rob Ramaker

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The cabbage family is well-represented in the vegetable section of the supermarket. The cauliflower, red cabbage and broccoli found there were all bred from the cabbage species *Brassica oleracea*. Its sister species *Brassica rapa* produced vegetables such as the Chinese cabbage and the turnip. But it is not clear quite where this large natural variety came from. Plant scientists guess that there is an extremely large genetic variation in cabbage plants. The genome of the Chinese cabbage, published in this month's *Nature Genetics*, supports this explanation.

'The [genome](#) of the Chinese cabbage, a *B. rapa* crop, does indeed provide evidence of this', explains Guusje Bonnema, assistant professor of Plant Breeding at Wageningen University and member of the international research team. 'We see a strikingly large number of genes that regulate flowering time. This varies according to crop type from twenty days to as much as two years.' There is a clear link, then, between gene abundance and diversity. The hypothesis is further supported by the large number of genes involved in the hormonal system, which governs the formation of the plant.

The researchers also have an explanation for the source of these extra genes. It has been known for a while that the brassicas tripled their genetic material between five and nine million years ago. This is quite a common occurrence in plants, and afterwards, 'superfluous' genes mutate and disappear en masse. But a few groups of genes do seem to be kept and this made the eventual diversity of cabbage possible. The newly-mapped DNA sequence provides more than a fundamental insight into the characteristics of cabbage. 'The research is especially of use to the

breeding sector', says Bonnema. 'Breeders always need markers'. Such markers in the genome reveal the presence of a particular gene, such as one for virus resistance, for example. Breeders can then select for this gene, making it easier to cross-breed genes into other species.

Provided by Wageningen University

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