

# Researchers study the genetics and biology of Brassica crop species

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Scientists at the University of York have contributed to a new study which represents a significant step forward in understanding the molecular processes which underpin the evolution of genomes in Brassica species.

Researchers from the Centre for Novel Agricultural Products (CNAP) in the Department of Biology at York were part of an international team which included scientists from China, Australia, USA, Canada, South Korea and France.

The research which is published in *Nature Communications* provides new insights into the establishment of the [genome sequence](#) of the main horticultural brassica species. The findings will underpin further research into the genetics and biology of this important crop species which includes cabbage, cauliflower, broccoli and Brussels sprouts, and is a close relative of oilseed rape.

In addition to contributing to the analysis of the data, the York team, led by Professor Ian Bancroft, improved the quality and utility of the genome sequence by relating it to [genetic linkage maps](#).

Professor Bancroft said: "This resource will be of tremendous benefit for research programs around the world, both those focussing on the fundamental biology of Brassica species and those aiming to bring about predictive genetic improvement of familiar brassica vegetables, such as broccoli, cauliflower and cabbage."

**More information:** "The Brassica oleracea genome reveals the asymmetrical evolution of polyploid genomes." Shengyi Liu, et al. *Nature Communications* 5, Article number: 3930 [DOI: 10.1038/ncomms4930](https://doi.org/10.1038/ncomms4930). Received 23 October 2013 Accepted 22 April 2014 Published 23 May 2014

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