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Exploring the potential of Brassica crop wild relatives: Insights for sustainable agriculture and biodiversity conservation

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Background:

Gaining a comprehensive understanding of the evolutionary history of crops, including the identification of their wild relatives, plays a crucial role in informing conservation and crop breeding endeavours. Cultivated *Brassica oleracea* has long captivated researchers due to its remarkable diversity, giving rise to various forms such as cabbage, broccoli, cauliflower, kale, kohlrabi, and Brussels sprouts. Despite its significance, the evolutionary history of this species still remains unclear. A better understanding of the evolutionary history of B. oleracea holds relevance not only for *B. oleracea* cultivars but also for rapeseed breeding, particularly for the allopolyploid agricultural species derived from the C genome in B. oleracea, which are *B. napus* (oilseed rape) and *B. carinata* (Ethiopian mustard).

Objective:

Through this investigation, we seek to unravel the origins of *B. oleracea*, which holds considerable importance in the field of agriculture. By shedding light on these intricate relationships, we aim to contribute to the broader knowledge and understanding of the evolutionary history and domestication process of this species, thereby offering valuable insights for future breeding and cultivation efforts.

Methods:

Leveraging newly generated RNA-seq data from a diverse panel of 224 accessions, encompassing 14 distinct *B. oleracea* crop types and nine possible wild progenitor species, we employed a comprehensive analytical approach integrating phylogenetic and population genetic methods with ecological niche modelling, archaeological findings, and literary evidence.

Results:

Our analyses indicate that the Aegean endemic *B. cretica* is the closest extant relative of cultivated B. oleracea, supporting the hypothesis that cultivation originated in the Eastern Mediterranean region. Furthermore, we have identified multiple feral lineages, suggesting that cultivated plants of this species have the capacity to revert to a state resembling their wild counterparts quite easily.

Conclusions:

By enhancing our comprehension of the evolutionary history of B. oleracea, these findings contribute to an expanding pool of knowledge on crop domestication. This knowledge will aid in advancing ongoing breeding endeavours, particularly in adapting to changing environmental conditions and novel disease pressure for *B. oleracea*, as well as for *B. napus* and *B. carinata*, which share its C genome.