Matk and rbcl identification of Brassica Oleracea subspecies

Jaylynn Castro, Amanda Hiciano, Cassidy Marcus, Sharissa Marsh, Tristyn Pagan, Alessandra Sanchez, Amanda Torres
Dr. Marianne Williams
St.Raymond Academy for Girls

Funded by the Thompson Family Foundation

Abstract

In this research the rbcl and matK genes of Brassica oleracea subspecies (kale, broccoli, cauliflower, kohlrabi, and brussel sprout) were compared to determine if there are significant differences in the matK gene and the rbcl gene to differentiate the subspecies or did evolution conserve the genes so no obvious differences are present. It was determined that no significant differences exist in these two genes in all five plant subspecies.

Introduction

Greens and vegetables are a staple of any healthy balanced diet. You can get these nutrients through brussel sprouts (Brassica oleracea var. gemmifera), broccoli (Brassica oleracea var. italica), cauliflower (Brassica oleracea var. botrytis), kale (Brassica oleracea var. acephala), and kohlrabi (Brassica oleracea var. gongylodes). As different as these vegetables might be, they all are connected as one species. Brassica oleracea is the species that connects all these vegetables. Each one is a subspecies of Brassica oleracea. This raises the question, are these variants different on a genetic level? Can DNA barcoding identify each variety? In this research, we compared the matK genes and the rbcl genes of the variants side by side to determine if the evolution of Brassica oleracea changed the genes to differentiate the subspecies or if their genes are so conserved that they cannot be differentiated by barcoding.

Materials & Methods

Procedure:

1.) The DNA from the variants was isolated using the Chelex method. A small size piece of leaf, approximately a quarter of an inch in diameter,was used from each of the varieties.

2) The DNA products were then amplified using both rbcl and matK primers.

3) The amplification products were checked using gel electrophoresis to determine if the amplification was successful.

4) The amplification products were sequenced

5) Once the DNA sequences were obtained bioinformatics on the DNA subway platform was done to both identify the species but also to compare the DNA sequences for both the matk and rbcl genes for each variant.

6) All of the species were compared to the Kale
sequence since the literature states that Kale is likely the oldest of the varieties.

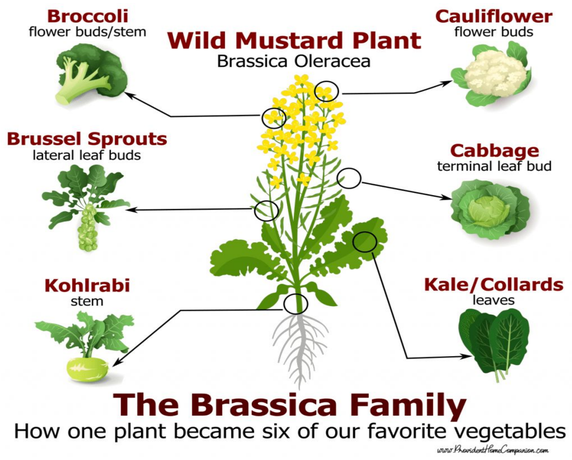
6) Any differences in the DNA sequences was noted as was the identification of each sample.

Results

Our results show that even though the Brassica oleracea species has evolved physically, the matK and rbcl genes remain nearly identical. Inputting our data into the BLAST search, the results answers our question on genetic differences or similarities. All five species are virtually identical at the genetic level for the matk and rbcl genes.

COMPARISON TO KALE

	matk	rbcl
cauliflower	100%	99.84%
brussel sprouts	100%	100%
broccoli	100%	100%
kohlrabi	100%	99.84%



Discussion

Conclusively, although Brassica oleracea has many variants, on a genetic level with rbcl and matK, they are all the same species nonetheless. However, if we did research on structural genes, we may have found differences. This discovery raises questions for future discussions about the preservation of genes despite evolution or external influences.

References

Dixon, Geoffrey Richard “The Origins of Edible Brassicas.” Plantsman 16 (3) .pp. 180-185. docslib.org/doc/12394956/the-origins-of-edible-brassicas. Accessed 3 Nov. 2023.

Mabry, Makenzie E, et al. “The evolutionary history of wild, domesticated, and feral brassica oleracea (brassicaceae).” Molecular Biology and Evolution, vol. 38, no. 10, 2021, pp. 4419–4434, https://doi.org/10.1093/molbev/msab183.

Maggioni, Lorenzo, et al. “Origin and Domestication of Cole Crops (Brassica Oleracea L.): Linguistic and Literary Considerations1 - Economic Botany.” SpringerLink, Springer-Verlag, 31 Mar. 2010, link.springer.com/article/10.1007/s12231-010-9115-2.

Acknowledgements

We would like to thank the Thompson family foundation for funding our research and Dr. Williams with helping us conduct our research.