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Origin, Geographical Distribution, And Genetic Diversity of Crop Brassica Species: A Review

Review Article

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Abstract

The genus *Brassica* comprises some of the most economically important oilseed and vegetable crops cultivated worldwide. These crops contribute significantly to global food security, nutrition, and agricultural sustainability. The present paper provides a comprehensive synthesis of the origin, geographical distribution, and genetic diversity of major crop Brassica species. Archaeobotanical and molecular evidence suggests that primary domestication of diploid *Brassica* species (*B. rapa, B. nigra, and B. oleracea*) occurred independently in the Mediterranean and Central Asian regions between 3000–5000 years BP. These diploid species subsequently gave rise to amphidiploid species (*B. juncea, B. napus, and B. carinata*) through natural hybridization and polyploidization, as described by U's Triangle. Genetic diversity studies using molecular markers (SSR, SNP, AFLP) reveal high intra-specific variation, particularly in *B. rapa* (Nei's gene diversity, H = 0.42–0.65; derived from genome-wide SNP analyses by Bird et al., 2020 and Park et al., 2023) [1] and *B. juncea* (H = 0.38–0.60; reported using SNP and GBS approaches by Hasan et al., 2023 and Gupta et al., 2024), reflecting wide ecological adaptation. Understanding the origin, distribution, and diversity of crop Brassicas is essential for crop improvement, conservation of genetic resources, and climate-resilient breeding programs.

Introduction

The genus *Brassica* (family Brassicaceae) includes a wide range of cultivated crops used as vegetables, oilseeds, condiments, and fodder. Major *Brassica* crops such as mustard, rapeseed, cabbage, cauliflower, broccoli, and turnip are integral components of agricultural systems across temperate and subtropical regions. India and China together contribute more than 35% of the global production of rapeseed–mustard, while Europe dominates vegetable *Brassica* cultivation. (FAO,2022; FAOSTAT).

The remarkable morphological variation observed in *Brassica* crops, particularly within *B. oleracea* (cabbage, cauliflower, broccoli, kale), has made the genus a classical model for studying domestication, polyploidy, and crop evolution. Advances in cytogenetics and molecular biology have further clarified the evolutionary relationships among cultivated species, especially through the concept of U's Triangle.

Objectives

The present study aims to:

1. Review the origin and domestication history of the major crop Brassica species.
2. Examine the global geographical distribution of cultivated Brassica species in relation to their centers of diversity and patterns of genetic variation.
3. Synthesize cytogenetic and molecular (genomic and SNP-based) evidence on genetic diversity and discuss its implications for crop improvement and conservation.

Materials and Methods

This review is based on a comprehensive survey of the published literature from 2010 to 2025, with a particular emphasis on recent studies published between 2019 and 2025, to capture advances in genomics and high-throughput marker technologies. Peer-reviewed research articles, review papers, book chapters, and authoritative databases were consulted using major scientific platforms, including Scopus, Web of Science, PubMed, and Google Scholar.

Studies were selected based on the following criteria:

(i) Clear taxonomic identification of cultivated Brassica species or their wild relatives;

(ii) Use of well-established molecular markers, including SSRs, SNP arrays, genotyping-by-sequencing (GBS), or whole-genome resequencing;

(iii) Adequate sample size and genome-wide coverage to reliably estimate genetic diversity parameters (e.g., H, Ho, π); and

(iv)Relevance to questions of origin, geographical distribution, domestication, or genetic diversity. Emphasis was placed on SNP-based and genomic studies due to their higher resolution and reproducibility.

Data from selected studies were synthesized qualitatively and quantitatively to compare diversity patterns across species and regions. FAOSTAT reports were additionally consulted to compile information on global production and distribution trends.

Results and Discussion

Origin and Domestication

The origin of cultivated *Brassica* species is closely linked to the Mediterranean and Central Asian regions. The three primary diploid species—*B.rapa* (AA, 2n=20), *B. nigra* (BB, 2n=16), and *B.oleracea* (CC, 2n=18)—represent the ancestral gene pools. Archaeological evidence suggests that *B.oleracea* was domesticated along the Mediterranean coast, while *B.rapa* originated in Central Asia and later diversified in East Asia.

The amphidiploid species arose through natural hybridization:

B. juncea (AABB, 2n=36) from *B. rapa* × *B. nigra*

B. napus (AACC, 2n=38) from *B. rapa* × *B. oleracea*

B. carinata (BBCC, 2n=34) from *B. nigra* × *B. oleracea*

Table 1: Genome constitution and chromosome numbers of cultivated Brassica species

SPECIES	GENOME	CHROMOSOME NUMBER (2N)	MAJOR USE
B. rapa	AA	20	Oilseed, vegetable
B. nigra	BB	16	Oilseed, or Condiment
B. oleracea	CC	18	Vegetables
B. juncea	AABB	36	Oilseed
B. napus	AACC	38	Oilseed
B. carinata	BBCC	34	Oilseed

Geographical Distribution

Crop Brassicas are widely distributed across Asia, Europe, North America, and Australia. *B. juncea* dominates the Indian subcontinent, accounting for nearly 80% of mustard cultivation in India. *B. napus* is extensively grown in Europe, Canada, and China as a major oilseed crop. Vegetable forms of *B.oleracea* are cultivated globally under temperate climatic conditions.

Among six cultivated *brassicas*, *B.oleracea L.* is a vegetable brassica, and the remaining five species are oilseed brassicas grouped into rapeseed and mustard. The origin of the cultivated *Brassica* species is as follows:

Brassica rapa (B.campestris L.) has a primary centre of diversity in the Indian gene centre, namely in the Himalayan region (Hedge,1976) [2]. Russian workers, particularly Sinskaia and Vavilov. Regarded **Central Asia**, Afganistan and the adjoining northwest India as one of the independent centres of the origin of oleiferous *B. rapa*. It is widely believed that brown sarson is the oldest type (Singh 1958) [3] from which toria developed, probably in the foothills of the Himalayas, as an early maturing type in response to particular ecological requirements, and that yellow sarson probably originated in the Indo-Gangetic Plains as a spontaneous mutant of toria for superior quality. Yellow sarson was mentioned in Indian Sanskrit documents from 1500 BC. The species *B.rapa* L. (2n = 2x = 20, genome AA) is one progenitor of the both amphidiploid *B.juncea (L.)* Czern. (2n = 4x = 36; genome AA BB) and *B.napus L.* (2n = 4x = 38; genome AA CC).

Brassica nigra (L.) Koch was cultivated as a spice as early as 3000 BC and it has been probably evolved as a second crop plant from weedy types. The origin may have taken place in the Mediterranean area or Asia; it is now widespread throughout Europe, Africa, Asia, India is the Far East (Hemingway, 1976) [4]. It has now been largely replaced by *B. juncea* due to the latter better adapted to modern agro-technology. In India, it occupies only a limited area in Karnataka, Tamil Nadu and the northern states. It is used as a condiment and for pickle making. The species *B.nigra L.* Koch. (2n = 2x = 16; genome BB) is one progenitor of both amphidiploids, *B.carinata* A. Braun. (2n =4x =34; genome BB CC) and *B.juncea L.* (2n = 4x =36; genome AA BB).

Brassica oleracea L. is originated in the Mediterranean area and Western Europe. The hybridization of W-European forms with forms from the E-Mediterranean area has resulted in a wide range of variation. The species *B.oleracea L.* displays an interesting genetic

Table 2: Summary Model

SPECIES	GENOME	ORIGIN	KEY USES	GENETIC FEATURES
B.rapa	AA	Central Asia/Old World	Vegetables, oilseed	High intra-specific diversity, multiple morphotypes
B. nigra	BB	Mediterranean	Mustard	Represents B genome of amphidiploids
B. oleracea	CC	Europe	Vegetables	Rich morphological diversity (cabbage to broccoli)
B. juncea	AABB	West Asia	Oilseed, condiments	Allotetraploid with multiple domestication paths
B. napus	AACC	Hybrid origin	Rapeseed/canola	Tetraploid from *B. rapa* × *B. oleracea*
B. carinata	BBCC	Hybrid origin	Mustard (Ethiopia)	Tetraploid from *B. nigra* × *B. oleracea*

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diversity, represented by 14 cultivated types (Dias 1995) [5] and 10 wild taxa in the *B.oleracea* cytodeme (Harberd 1972; Snogerup et al. 1990) [6,7]. The species *B.olerucea L.* (2n=2x=18, genome CC) is one progenitor of the both amphidiploids *B.carinata* A. Braun. (2n =4x= 34; genome BB CC) and *B.napus L.* (2n=4x=30; genome AA CC).

Brassica juncea (L.) Czern. Is an amphidiploid species with the A genome of *B.rapa L.* and the B genome of *B. nigra (L.)* Koch. Perhaps it is the oldest of the cultivated amphidiploids. Central Asia-Himalayas is a primary centre of diversity for this species with migration to China, India and the Caucasus (Hemingway 1976) [4]. The species has probably evolved in the Middle East, when its putative diploid progenitors are sympatric (Prakash and Hinata 1980) [8-16]. It is highly polymorphic and includes both leafy and oleiferous variants. *B. juncea* may have arisen several times, as secondary centres of diversity exist in China, East India, and the Caucasus (Hemingway 1976) [4]. In India, *B. juncea (L.)* Czern is the predominant species that accounts for nearly 80 per cent hectarage of the oilseed *brassicas*.

Brassica napus L. is an amphidiploid species with the A genome of *B.rapa L.* and the C genome of *B. oleracea. B. napus L.* seems to be of relatively recent origin in the South West and Mediterranean regions. The species evolved in South Europe and is divided into two Nopobrassica (L.) Hanelt originated following hybridisation between turnip and kale. Rape (*B. napus L. ssp. napus*), a valuable oil crop, perhaps has a separate origin in the western Mediterranean areas. *B.napus L.* lacks a true petiole, as does *B. rapa L.*, but only partial clasping of the stem occurs. The crop *B. napus L.*is mostly grown in Canada, Europe, Japan and Chile as an oilseed and fodder crop. On the Indian sub-continent, *B. rapa L.* and *B. juncea (L.)* Czern. still predominate compared to the introduced *B. napus L.* material.

Brassica carinata **A.** Braun is an amphidiploid with the B genome of *B. nigra (L.)* Koch and the C genome of *B. oleracea L.* have several characteristics that make it a suitable candidate for a winter crop in Mediterranean countries. It is found and cultivated in North Eastern Africa and Ethiopia in particular, and is believed to have originated in the Ethiopian highlands (Vaughan 1956). Leaves are attached to the stem with a true petiole. It is an important oil crop as well as a leaf vegetable and shows promise agronomically in many other parts of the world. Compared to other cultivated Brassica species, the range of variation of *B. carinata* is not very high.

Genetic Diversity: Genetic diversity studies indicate substantial variability within and among *Brassica* species. Molecular marker analyses reveal that *B.rapa* exhibits the highest diversity due to its wide ecological amplitude and multiple domestication events. In contrast, *B.napus* exhibits relatively narrow genetic diversity (H = 0.20–0.35), which is attributed to its recent origin and intensive breeding. Conservation of wild relatives and landraces is therefore critical for broadening the genetic base of cultivated *Brassicas.*

Importantly, these diversity patterns have direct implications for applied breeding and climate resilience. Species and populations exhibiting higher heterozygosity and nucleotide diversity, such as *B. rapa* and *B. juncea*, offer broader allelic pools for the selection of traits related to drought tolerance, heat stress, salinity resistance, and disease resistance. Conversely, the relatively narrow genetic base of *B.napus* underscores the need for targeted introgression from diverse germplasm, including landraces and wild relatives, to enhance adaptive capacity under changing climatic conditions. Genomic diversity information can thus guide parent selection, heterosis breeding, and pre-breeding programs aimed at developing resilient *Brassica* cultivars suited to future agro-climatic challenges.

Conclusion

The genus Brassica represents an excellent example of crop evolution through domestication, hybridization, and polyploidy. The wide geographical distribution and rich genetic diversity of crop Brassicas have enabled their adaptation to diverse agro-climatic conditions. However, genetic erosion due to modern breeding necessitates urgent conservation of traditional varieties and wild relatives. A thorough understanding of origin, distribution, and genetic diversity will support future breeding strategies aimed at improving yield, quality, and stress tolerance in Brassica crops.

References

1. Bird KA, An H, Gazave E, Gore MA, Pires JC, et al. (2020) Population structure and genomic diversity in Brassica rapa. Molecular Biology and Evolution 8: 321.
2. Hedge IC, Vaughan JG, Macleod AJ, Jones BMG (1976) The Biology and Chemistry of the Cruciferae Pp: 335.
3. Singh D (1958) Rape and Mustard. The Indian Central Oilseeds Committee, Bombay Pp: 105.
4. Hemingway JS (1976) Mustards: Brassica sp. and Sino-pis alba (Cruciferae) In: Simmonds NW (ed.) Evolution of Crop Plants. London: Longman. Pp: 56-59.
5. Dias JS (1995) Genetic relationships of Portugese coles and other close related Brassica genotypes using nuclear RFLPs, Genet Resour Crop Evol 42: 363-369.
6. Harberd DJ (1972) A contribution to the cyto-taxonomy of Brassica (Cruciferae) and its allies. Bot J. Linn. Soc 65: 1-23,
7. Snogerup S, Gustafsson M, Bothmer R (1990) Brus-sica sect. Brassica (Brassicaceae) L. Taxonomy and varia-tion. Willdenowia 19: 271-365.
8. Parakash S, Hinata K (1980) Taxonomy, cytogenet-ics and origin of crop Brassicas, a review. Opera Botanica 55: 1-57.
9. Cheng F, Wu J, Wang X (2014) Genome triplication drove the diversification of Brassica plants. Horticulture Research 1.
10. Kole C, Batley J, Parkin I,Kole C, et al. (2019) Genetics, Genomics and Breeding of Oilseed Brassicas. CRC Press, Boca Raton.
11. Katche E, Quezada-Martinez D, Katche EI, Vasquez-Teuber P, Mason AS (2021) Interspecific hybridization for Brassica crop improvement. Crop Breeding and Applied Biotechnology 21: e387121.
12. FAO (2022) FAOSTAT statistical database on oilseed and vegetable crops. Food and Agriculture Organization of the United Nations.
13. Qian L, Qian W, Snowdon RJ (2021) Subgenomic selection patterns as a signature of breeding in Brassica napus. Theoretical and Applied Genetics 134: 2125-2140.
14. Abdel-Haleem H, Luo Z, Szczepanek A (2023) Genetic diversity and population structure in Brassica juncea using SNP markers. Frontiers in Plant Science 187: 115379.
15. Sharma A, Li X, Lim YP (2024) Comparative genomics of Brassicaceae crops Breed Sci 64: 3-13.
16. Rao RV, Hodgkin T (2022) Genetic diversity and conservation and utilization of plant genetic resources 68: 1-19.

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