

An Overview of Brassica Species for Crop Improvement

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Abstract: Brassica species has great important for edible oil production in worldwide. The production has been observed a steady upward movement during the past 25 years. *Brassica* is belonging to a Brassicaceae family also known as the family Cruciferous is their older name mean cross. The family Brassicaceae, encompasses about 3,500 species and 350 genera, is one of the most economical plant families. Brassica has great nutritional value for human consumption for its edible oil and meal. Traditional breeding, as well as, modern biotechnological tools has led to the improvement of various quantitative and qualitative traits in Brassica. In Brassica genetic diversity study is major requirement for success in plant breeding and crop improvement. Brassica species has also great importance in agriculture sector like oil, silage, feed, green manure and in condiments. From this review, reader will be able to understand the general aspect of crop genetics, origin establishment and its importance for industry and food consumption.

Key words: Oil Seed • Domestication • Breeding and Genetics

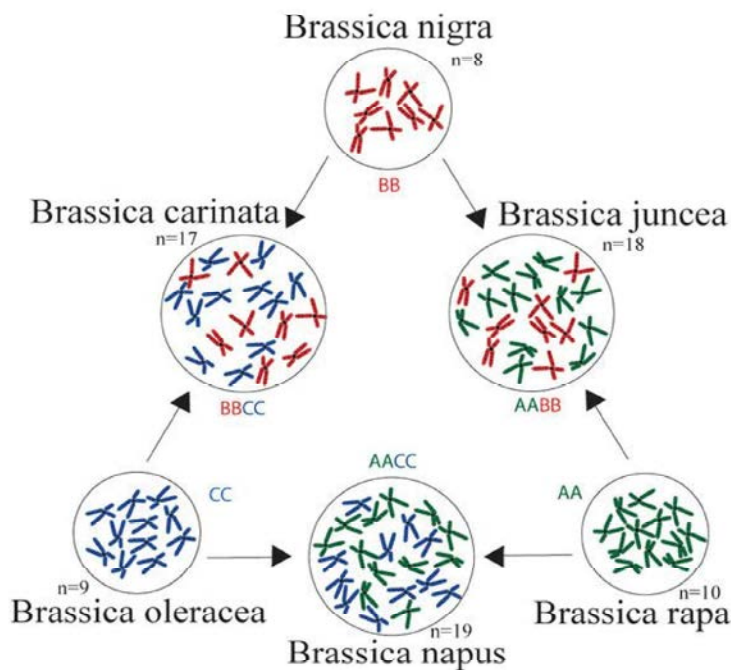
INTRODUCTION

Brassica napus (canola or oilseed rape) has emerged as an important cultivated oilseed crop species grown in temperate climates of both the northern and southern hemispheres *Brassica napus* L. is generally grown in Canada Europe. Oils extracted from plants have been used since ancient times and have been exploited in many ways. Predominantly, it is used as edible oil. It is also used in medicines and pharmaceuticals, biodiesel, industries pet foods and constituent of many other products. A concentrated source of energy, dietary fat, supplies about half of the calories and carries fat soluble vitamins. Its by-products are being used as feed, manures and find uses in many other industrial and domestic uses. There is large number of oil crops grown worldwide.

Total area under oil crop is 0.00317692 million hectare out of which area under cultivation for *Brassica* is 0.00022996 million hectare, seed production is 0.000218 million tonnes and oil production is 0.000068 million tones [1]. There is sub division of oilseed rape into winter and spring types [2]. Canola-type cultivars having low level of

erucic acid (<2%) and glucosinolate (<30iM) of *B. napus* and *B. rapa*. There is an imperfect variety of forms within *B. napus* as this species has a European origin drawing back only 500- 2000 years depending on the form. Many modern *B. napus* cultivars have been produced by crossing these two parent species and doubling the chromosome number [3]. *B. napus* L. is an Amphidiploid (AACC genome, $2n = 38$) and is believed to have arisen by interspecific hybridization between the diploid species *B. rapa* L. (AA genome, $2n = 20$) and *B. oleracea* L. (CC genome, $2n = 18$) [3]

The *Brassica rapa* genome sequencing project (BrGSP), a multinational project has produced an important genomic resources bacterial artificial chromosomes (BAC) libraries and BAC-end sequences by SSR markers, physical and genetics maps and seed bacterial artificial chromosome sequence for *B. rapa*. This linkage map between the *B. rapa* and *B. napus* will permit the rapid transfer of these important genetic resources from *B. rapa* to *B. napus* by gene tagging and map-based cloning in *B. napus* and for comparative study of genome in *Brassica* species [4, 5].



In the crushing industry, about 80% of the value of rapeseed is related to oil production. In rapeseed 1% point increasing of oil content is equivalent to 2.3-2.5 % points increasing in seed yield. Therefore, breeding for high seed oil content is most important objective in oilseed breeding in world. The reasons for the low production are; rapid rise in population thus decreasing cultivated area and living standards of its people, lack of high yielding varieties, lower production per unit area and lack of proper production technology [7, 8]. Due to high photosynthetic rate per unit leaf area it has high yield potential and it is positively correlated with number and volume of chloroplast per unit leaf area.

Genetic diversity study is major requirement for success in plant breeding and crop improvement. It is a step wise processes by which existing variation in present germplasm are identified by use of different statistical methods and their combinations. *Brassica napus* have great importance for breeding program because in Plant breeding genetic diversity provides information about quantum of genetic divergence and specific breeding objectives can be achieved through its help. So genetic diversity is most important objective for *Brassica* in breeding [8].

Origin and Establishment: *Brassica napus* L. (n = 19) is an amphidiploid species derived from interspecific crosses between *B. oleracea* (n = 9) and *B. rapa* (n = 10).

Wild forms of *B. napus* have been reported to occur on the beaches of Goth land, Sweden, the Netherlands and Britain. Therefore, it was also reported that naturalized forms of *B. napus*, which are very distinct from any cultivated *B. napus*, were found on coastal cliffs of New Zealand, where *B. rapa* and *B. oleracea* grow wild. It is believed that *B. napus* L. was formed on the coast of northern Europe where both *B. oleracea* and *B. rapa* grow wild; other researchers believe that *B. napus* originated in the Mediterranean region or in western or in northern Europe [8,9]. Its high yield potential might be related to the high photosynthetic rate per unit leaf area which is positively related to chloroplast number per unit leaf area and to chloroplast volume. Similar associations have been reported for high-yielding rice and wheat. There are also root-forming *B. napus* L. types known as rutabaga, grown as vegetables and fodder for animals.

B. napus L. is an amphidiploid and is comparatively of recent origin [11]. It is uncertain to maintain if *B. napus* is found wild or not, since wild forms of this crop are difficult to find [10]. However, if wild napus exists, it must be a European-Mediterranean species that originated in the area of overlap between *B. oleracea* and *B. campestris* [9]. Though the origins of *B. napus* are ambiguous, these are proposed to involve natural interspecific hybridization between the two diploid species, *B. oleracea* (n ¼ 9) and *B. rapa* (n ¼ 10) [12]. Song and Osborn [13]

on the basis of their analysis of chloroplast and mitochondrial DNA suggested that *B. montana* (n ¼ 9) might be closely related to the prototype that gave rise to both the cytoplasms, that is, of *B. rapa* and *B. oleracea*. They also suggested that *B. napus* has multiple origins and the most cultivated forms of *B. napus* were derived from a cross in which a closely related ancestral species of *B. rapa* and *B. montana* was the maternal donor. The parental origins of *B. napus* were also investigated using six microsatellite markers located in the chloroplast genome by Allender et al. [14]. They also suggested that either of *B. rapa* or *B. montana* or a common ancestor could have been the maternal parent of *B. napus*. They suggested that *B. oleracea* was not the parental parent of most of *B. napus* accessions, a small number of accessions shared *B. oleracea* haplotype. Similarly, the phylogenetic analysis based on nuclear RFLP data also suggests that *B. napus* has multiple origins [15]. The various cytoplasm types found in *B. napus* accessions correspond to the progenitor diploid species which provide a strong evidence for the multiple origins of this crop [16-18].

In *B. napus*, as well as, *B. campestris*, a range of morphological forms are found, both having annual and biennial types. Keeping this in view, Olsson [11] suggested that *B. napus* could have arisen several times by spontaneous hybridization of different forms of *B. campestris* and *B. oleracea*. The majority of the cultivated *B. napus* accessions appear to have arisen by an interspecific cross in which a wild 9 or 10 chromosome species having the *B. montana* cytoplasm type or the M/N type was the female donor [16]. Thus, the Swede rapes could have originated in the medieval gardens where turnips and kales grew side by side. The spontaneous formation of *B. napus* is likely to have been an extremely rare event, not only due to post fertilization barriers but also due to Variation in floral morphology leading to discrimination by insect pollinators thereby reducing the chances of the inter specific hybridization. Mizushima and Tsunoda [19] inferred that *B. napus* was found in the coast of northern Europe because *B. oleracea* extended its territory up to northern Europe from the Irano Turanean regions with its high adaptability to low temperatures. Sinskaia [20] and Schiemann [22] were also of the view that it might have originated in the Mediterranean region or in the western or northern Europe. In Europe, production of oleiferous *B. napus* might have started during the middle Ages. In Asia, it was

introduced during the nineteenth century. The Chinese and Japanese germplasm was developed by crossing European *B. napus* cultivars with indigenous *B. rapa* cultivars [22].

Genetics of Crop: The extensive duplication of loci may be expected in a species that has evolved through polyploidy ancestor. The diploid progenitors of *B. napus* (C and A genomes) are widely duplicated clones (about 73%) of two or more duplicate sequence within each genome. Most of these duplicated loci have been found as distinct linkage groups as collinear blocks and rearrangements including translocations and inversions. A large number of rearrangements have been found in two diploid genomes indicating that they have formed prior to the divergence of the two species. The linkage may also consist of central fusion or fission which shows that this mechanism has played an important role in the evolution of *B. napus*. The *B. napus* genome and its duplication resulted in functional and epigenetic cross talk with various homologous exchanges and subtle structures. Especially *B. napus* L. can increase the genetic variation for starting a reserved gene pool for production of hybrids and variation of breeding material. Expression divergence and initial gene loss has begun in *B. napus*. Previous studies suggested that the genomes from two ancestral diploids in natural Brassica allotetraploids have different stabilities and that cytoplasm has exerted considerable influence on the evolution of nuclear genomes of allopolyploids [23]. It has been established that *B. rapa* and *B. nigra* have contributed the cytoplasm to *B. juncea* and *B. carinata*, respectively.

Brassica Species Interrelationships: Based on hybridization between species. Moringa [24] hypothesized that *B. juncea*, *B. napus* and *B. carinata* species with high number of chromosomes are amphidiploids which were derived from *B. oleracea*, *B. campestris* and *B. nigra* species with less number of chromosomes. The accuracy of this hypothesis was confirmed by U [12]. Who fruitfully found resynthesized *B. napus* from crosses between *B. oleracea* and *B. campestris* expressed the Brassica relationships between species are often cited U-triangle. Ramanjam and Srinivgach [25] resynthesized *B. juncea* and Frandse [26] resynthesized all three polyploid species from the appropriate diploids.

Crop Breeding: The first intergeneric fertile hybrid Raphanobrassica [27] and it was also forced that the diploid *Brassica* species are descended from a hexaploid ancestor [28]. In *B. napus* breeding for low seed glucosinolates have long been a primary target. For this associative transcriptomics (a novel association) have been applied to *B. napus* to identify the genes controlling total seed glucosinolates contents. Then deletion of these polymorphisms successfully converted into polymerase chain reaction. Due to high linkage disequilibrium by diagnostic markers in the genomes can be used for marker assisted breeding for low glucosinolates in seed [29-31]. In addition to this *B. carinata* (an allotetraploid) with C and B genomes, has a number of important traits that would be valuable to incorporate into *B. napus* by backcrossing. Later the traits can be confirmed by using SSR markers, genomic in situ hybridization (GISH) assay and counting of chromosomes to check the introgression into *B. napus* indicating that *B. carinata* (C genome) chromosomes pair and recombine normally with those of *B. napus* without major chromosomal rearrangements [32-34].

Uses: Brassica plays a key role in agriculture sector like oil, silage, feed, green manure and in condiments. *B. napus* L. Oil is used for edible purpose and oil is used in different ways like salad dressing, table oils, in cosmetics, making pickles and in industries for making soaps, lubricants, paints etc. Crucial as a source of protein for animals. The meal with low glucosinolates is best food for young ruminants and feeding cows, piggery and poultry purposes [35].

In meal it contains 40-45 % oil content and 36-40 % protein (Amin and Khalil, 2005). *B. napus* L. has been known as a rich source of oil with a low content of saturated fatty acids 5-7% and high content of polyunsaturated fatty acids with about 7-10% α -linolenic and 17-21% linoleic acids. It is considered as very healthy edible oil [23]. In breeding the improvement of seed quality is one of the most important objectives in Brassica for satisfying upcoming edible oil requirements. The functional and nutritional values of different vegetable oils are dependent on the nature of the different fatty acids, which are incorporated into the oil (triacylglycerols). On the other hand, erucic acid in the oil is one of the important characteristic components associated with *Brassica species*. High erucic acid oilseed rape cultivars may increase health risks [36].

Economic Importance of Brassica Species

Brassica Vegetables: Brassica vegetables have more economic value throughout the world and different species are used. The major Brassica vegetable species is *B. oleracea*, which runs a large range of unique cole and cabbage types. Much of the production is locally disbursed; however, there are production centers in certain countries, such as California, from where produce is transported to other states and into Canada year-round.

The breeding of *B. oleracea* vegetables is conducted in government institutions and universities and by private breeding firms. There are very specific breeding objectives for the different types with crop homogeneity being of greatest importance for marketing. The growth of disease and pest resistant germplasm and varieties is next in importance. More freshly, breeding programs have been started to develop F1 hybrid varieties to improve crop homogeneity and efficiency. Brassica rapa var. Chinese cabbage and var. Chinese are widely grown as vegetables in China.

Brassica Oilseeds World Production and Trade:

Brassica species using oilseeds increased are during last 42 years and important as a vegetable oil in the world after cotton. In India due to low seed yields, total oil production is lower as compared to China. In Europe valuable seed yields are obtained in France, Germany and with average development of about 4.0 tons/ha, which is more than twice the seed yields obtained in Canada and Australia. Because of the fact that, the winter types of *B. napus* are grown under favorable growing conditions in Europe, which are much more productive than summer annual *B. napus* forms grown in Canada. Major rapeseed exporting countries are Canada and Australia, while major importers are Japan and China [37].

Improving Crop Purity Standards: While, segregation space is a key factor in responsible crop purity it is clear that there are a number of other factors to consider in determining crop contamination. [38-40]. Brassica seeds may survive 11 -18 years in the soil so a cropping ancient times free of Brassica will be essential for a clean crop Isolation distance. This appearances to be well silent by growers but increasing the distance may offer less potential to improve purity than many of the other factors, mainly the size of the edge area [38]. The overlap of flowering time with nearby crops, off-types and tidies.

As flowering time of Brassica crops is quite prolonged there is a large window of chance for overlap of flowering. However, spring and autumn sown crops do not always overlap in flowering.

CONCLUSIONS

It was concluded that the oilseed crop is very important for nutrition, edible oil, market and industry. Brassica species using oilseeds increased are during last 42 years and important as a vegetable oil in the world after cotton. Based on hybridization between species and make a U-triangle for the evaluation of *B.napus* easily understands the interrelationship between and within species. A large number of rearrangements (a novel association) have been found in two diploid genomes indicating that they have formed prior to the divergence of the two species. The linkages also consist of central fusion or fission which shows that this mechanism has played an important role in the evolution of *B. napus*. Due to high linkage disequilibrium by diagnostic markers in the genomes can be used for marker assisted breeding for producing low glucosinolates and erucic acid in the seed. Overall cytogenetic and crossing, studies assisted by the use of molecular techniques have aided the plant breeders in studying their evolution. However, exact strategies are essential in future to evolve more auspicious and canola type cultivars, guided by the demands of industry and market.

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