

BREEDING AND GENETIC IMPROVEMENT OF RAPESEED FOR BIO-FUEL

Yeh Bong Lee, Hyeon Guk Yang and **Yong Pyo Lim**

Department of Horticulture, College of Agriculture and Life Sciences, Chungnam National University, Daejeon, 305-764, Korea. E-mail yplim@cnu.ac.kr

Abstract

The genus *Brassica* constitutes many important species which are cultivated as oilseed and vegetable crops around the world. In Korea, rapeseed (*Brassica napus*) was grown as an important oilseed brassica crop in large areas of land since 1950 to until recently. However, its cultivation has presently reduced to only 1000 ha of land annually due to the availability of cheaper price major vegetables oils (soybean oil, corn oil etc) from abroad. Recently, rapeseed has been chosen as ideal model crop species for producing biofuel by many countries of the world including Korea. As a result, present objective of rapeseed breeding in Korea is to develop bio-diesel in addition to the development of varieties suitable for cold tolerance, high yield and oil contents and oil quality. In line to the above objectives, research activities in our lab on rapeseed could develop a double zero F₁ hybrid, “Gangyu”, using male sterility system. Gangyu is a winter type cultivar having seed oil content 45.1%, 71.4 % of oleic acid and 16.1% of linolenic acid. The yield of this variety shows test results of 6-22% higher yield than that of European cultivar “Talent”. In addition, Gangyu has the cold tolerance traits which can survive at Yangu area. Especially, Yangu area, whose average temperature during January was -7.6°C, is one of the coldest regions in South Korea.

Keyword

Brassica napus, rapeseed, breeding, genome project

Introduction

The genus *Brassica* constitutes major oil and vegetable yielding crop plants. They include many species having diverse morphophytes such as oilseeds (*B. napus* and *B. juncea*), and vegetables (cabbage, cauliflower, broccoli belong to *B. oleracea* and Chinese cabbage and pak choi belonging *B. rapa*). Among vegetable brassicas, Chinese cabbage (*B. rapa* ssp *pekinensis* Makino), radish (*Raphanus sativus* L.), and cabbage (*B. oleracea* ssp *capitata*) are cultivated as major vegetable crops in Korea, while turnip (*B. rapa* ssp *rapa*), pack choi (*B. rapa* ssp *chinensis*), broccoli (*B. oleracea* var. *italica*), cauliflower (*B. oleracea* var. *botrytis*) and leaf mustard (*B. juncea*) are cultivated in some areas in small scale. Rapeseed (*Brassica napus*), an

oilseed brassica crop, was grown in large scale in Korea since 1950 to until recently. However, due to the availability of major vegetable oil (soybean oil, corn oil, etc.) in cheaper price from abroad, presently the cultivation of this crop has been reduced drastically to an area of 1000 ha of land. The development of recent concept “biodiesel” has attracted many researchers and hence, recently, in many countries of the world, rapeseed has been chosen as the model crop species for producing bio-diesel (1). As a result, the present focused of rapeseed breeding in Korea is mainly on developing rapeseed cultivars for bio-energy production in addition to the development of varieties suitable for cold tolerance, higher yield, high oil content and quality. Research on rapeseed breeding in our lab could develop F₁ cultivar “Gangyu’ using male sterility system.

The recent advances in genomics technology promises to supplement brassica crop breeding as a whole. So, looking into the high economic value of *Brassica* species throughout the world and their potential to be models for the study of polyploidization and genome evolution that in turn reflects various morphophytes, genome sequencing projects for *Brassica* species, especially *Brassica rapa* Genome Sequencing Project (*Br*GSP) has been initiated(2-5). *Brassica rapa* contributes 10 A genome chromosomes to amphidiploid oilseed brassicas such as *Brassica napus* (n=19, AACC) and *Brassica juncea* (n=18, AABB). Korea is a part of international *B. rapa* genome sequencing consortium. Of the ten chromosomes (or linkage groups), eight have been allocated to the participating countries as follow: Korea (R3 and R9), Canada (R2 and R10), UK and China (R1 and R8), and Australia (R7). However, R4, R5 and R6 have remained unassigned. The sequencing of A genome would give us information about genome structure and evolution, develop molecular markers and identify candidate genes for important agronomic and quality traits and would help in great extent in brassica oilseed breeding.

So, as an initial effort towards meeting the above objectives, The Korea *Brassica* Genome Resource Bank (KBGRB), has been established in the lab.

The Korea *Brassica* Genome Resource Bank (KBGRB).

The development of genomic resources and/or germplasm bank is a prerequisite to undertake any crop improvement and is an invaluable resource for structural and functional genomics. The Korea *Brassica* Genome Resource Bank (KBGRB), a *Brassica*-related seed and DNA stock center was established to supply foundation plant materials for structural and functional genomics of *Brassica* species. The KBGRB has developed populations, including doubled haploid mapping populations and recombinant inbred lines, mutants of *Brassica rapa* and linkage map consisting a total of 556 markers, including 278 AFLPs, 235 SSRs, 25 RAPDs, and

18 ESTPs/STS/CAPS markers have been constructed and besides constructing genomic bacterial artificial chromosome (BAC) and cDNA libraries (6). Three Chiffu BAC libraries, i.e. KBrH, KBrB, and KBrS consisting 56592, 50688, and 55296 clones were constructed with an average insert size of 115 kb, 124 kb, and 100 kb, respectively (5). These BACs are being used by International *Brassica rapa* genome sequencing consortium for brassica A genome sequencing.

Seeds and genomic DNA libraries of other *Brassica* species have also been collected. The germplasm held by KBGRB has been propagated and maintained. Information and other requests for genomic resources of *Brassica* are accessible at <http://www.brassica-resource.org>.

Breeding of *B. napus* cultivar

As the oil crop among the *Brassicaceae*, rapeseed (*Brassica napus*) was the most important crop in Korea since 1950. However, since major oil (soybean oil, corn oil, etc.) has been imported with cheap cost from abroad, cultivation of rapeseeds were dramatically reduced up to 1,000 ha, and used only for floricultural purpose.

Breeding of rapeseed in Korea was conducted at the National Institute of Crop Science, and private company. The first released varieties from National Institute of Crop Science were 'Asahi'(1964) and 'Miuki'(1967) introduced from Japan. Since then, they developed several new varieties as "Yu Dal", "Yong Dang"(1978), "No Jeok"(1979), etc. However, these developed varieties were low yielder (below 2.5t/ha), and double high or single low. In 1980, first double low cultivar, "Young San", was developed. The first F1 hybrid cultivar, "Cheong Pung" was developed using male sterile system at 1983. Since 2001, about 10 cultivars were released from National Institute of Crop Science.

As private company, Hung Nong Seed Company, which was merged to Seminis in 1997, started rapeseed breeding since 1988. Their purpose was the development of high yield, disease resistance, and cold tolerance F1 hybrids using male sterile system which could be exported to Europe and America besides selling it to Korean market. The male sterility system developed by Hung Nong was temperature sensitive male sterile which was not stable and due to which it could not be used in commercial hybrid seed production.

Hung Nong stopped the breeding program of rapeseed in 2000, and Chung Nam National University and New Gene Company started rapeseed breeding. We improved and selected new male sterile lines, and could successfully develop stable male sterile and maintainer lines.

Recently, Korea initiated research on developing biofuel and rapeseed is chosen as favorite model crop for production of bio-diesel. So the present objective of rapeseed breeding is mainly on developing varieties which could produced more oil for bio-energy besides breeding for cold tolerance, yield, oil contents, oil quality, and others. In line to the above objective, research on rapeseed breeding in our lab could recently develop F₁ hybrid “Gangyu” using male sterility system. We could produce the fully restored F₁ hybrid using stable male sterile line and maintainer system. From this progress, we could register new cultivar “Gangyu” at 2006.

Gangyu is the winter type cultivar, and belongs to the double low quality. The yield of this variety shows test results of 6-22% higher yield than that of European cultivar “Talent”. In addition, Gangyu has the cold tolerance trait that can survive Yangu where average temperature during January is -7.6°C and one of the coldest regions of the South Korea. Gangyu is a winter type cultivar having seed oil content 45.1%, 71.4 % of oleic acid and 16.1% of linolenic acid.

Conclusion

Our objective in the coming years would be to breed high oil yielding rapeseed cultivars that can be used for production of bio-energy using germplasm collection and genomics resources. The genomics resources such as molecular markers, cDNA sequence and functional candidate genes information that are /or would be available from *Brassica* genome sequencing project or from comparartive genomic information from *Arabidopsis thaliana* would be used in accelarting to meet the above objective.

References

- [1] F. Karaosmanolu, E. Tetik and E. Göllü. Biofuel production using slow pyrolysis of the straw and stalk of the rapeseed plant. *Fuel Processing Technology* , Vol . 59 , pp 1-12, 1999
- [2] T. J. Yang, J. S. Kim, K. B. Lim, et al., “The Korea *Brassica* genome project: a glimpse of the *Brassica* genome based on comparative genome analysis with *Arabidopsis*,” *Comparative and Functional Genomics*, vol. 6, no. 3, pp. 138–146, 2005.
- [3] Y. P. Lim, P. Plaha, S. R. Choi, et al., “Towards unraveling the structure of *Brassica rapa* genome,” *Physiologia Plantarum*, vol. 126, no. 4, pp. 585–591, 2006.
- [4] C.P Hong, S.J Kwon, J.S Kim et al . “Progress in Understanding and Sequencing the Genome of Brassica rapa.” *Int J Plant Genomics*. 2008; doi: 10.1155/2008/582837
- [5] S. R. Choi, G. R. Teakle, P. Plaha, et al., “The reference genetic linkage map for the multinational *Brassica rapa* genome sequencing project,” *Theoretical and Applied Genetics*, vol. 115, no. 6, pp. 777–792, 2007.