Current Status of Research on Developing Rapeseed-Mustard Genotypes having low Glucosinolate Content in India

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Traditional varieties of rapeseed-mustard in India are non-canola type possessing high amounts of erucic acid and meal glucosinolates. Though, India requires to import large quantities of oil to augment domestic supplies, the country is a net exporter of oilseed cake. A significant proportion of this export commodity is made up of rapeseed-mustard cake. Lately, however, this lucrative export market is threatened by the reluctance of major meal importing countries as the Indian rapeseed-mustard meal does not fulfil the internationally accepted norms for meal glucosinolate content (<30 µ moles glucosinolates g^{-1} defatted meal). The glucosinolate content in current varieties of Indian mustard (*Brassica juncea*), the main oilseed *Brassica* type, ranges from 97.4 to 121.3 µ moles g^{-1} seed (Table 1). Most of the Indian strains contain 3-butenyl as the major aliphatic glucosinolate component, 2-propenyl is another important component. The higher level of 3-butenyl in Indian cultivars is in contrast to Europian *B. juncea* types which have 2-propenyl as the major glucosinolate.

Aside export compulsions, the necessity to provide good quality feed for domestic livestock has led to growing realization among the scientists and policy makers to lay emphasis on bringing down the current level of glucosinolates, primarily in, domestic mustard cultivars to the level at par with those prevailing in advanced countries (<30 µ moles g^{-1} defatted meal). This is expected to improve the feeding value (protein efficiency ratio) of rapeseed-mustard meal for livestock and poultry.

Basic investigations

In view of the low variation for the trait in indigenous mustard germplasm, the major emphasis had been on sourcing superior alleles for low glucosinolate content from recognized Canadian low glucosinolate donor BJ 1058 or canola quality mustard strain

Heera developed by pedigree breeding from a cross between low erucic acid variety Canadian line ZYR-4 and BJ 1058 (Khalatkar et al. 1991). Attempts were also made to introgress desirable alleles from *B. rapa* cv Tobin to Indian mustard genotype, WF-1 using Tobin as the female parent. Two cycles of backcrossing with Indian mustard followed by several cycles of repeated selfing and selection helped to develop mustard (2n=36) genotypes having low glucosinolate content (Banga 1996). A major problem encountered during the breeding process was the instability of glucosinolate content over generations and locations. Evaluation of putative low glucosinolate experimental strains helped to establish that sulphur application influenced glucosinolate expression in most of the test genotypes. This instability was attributed to certain modifiers with low penetration (Banga et al. 2001). Screening for stable donors and breeding progenies under high sulphur application was thus advocated. Genetic analysis of total glucosinolate in crosses involving high glucosinolate mustard variety and low glucosinolate genotype(s) have indicated the involvement of four (Banga Unpub.) or seven (Sodhi et al. 2002) dominant genes controlling total glucosinolate content. Complex inheritance is expected as this compound is the end result of a complex biochemical pathway having several steps, apparently under the control of different genes.

Breeding for low glucosinolate content

Systematic breeding efforts towards developing high yielding and '00' mustard varieties, supported by the Indian Council of Agricultural Research, are being carried out at Agricultural Universities in Ludhiana, Hisar, Pantnagar besides, Tata Energy Research Institute, New Delhi and National Research Centre (Rapeseed-Mustard) at Bharatpur. In addition, the National Dairy Development Board is supporting a massive breeding programme at the University of Delhi. Agronomically well-adopted mustard cultivars like Varuna, Pusa bold and RL 1359 have been mainly used for developing desired quality cultivars using Heera / BJ 1058 as donors for low meal glucosinolate content. Pedigree breeding and backcross methods have been used to achieve '00' characteristics in good agronomic base. Limitations in terms of analytical capabilities and consequently, inadequate population size in segregating populations have so for precluded adequate

selection pressure for '00' characteristics together with higher productivity. Many experimental strains having low glucosinolate content are now available in the superior agronomic backgrounds, but these are still inferior in yield than the conventional mustard cultivars. Efforts are on to improve their yield potential by selective intermating between '00' genotypes. The exotic nature of '00' genotype Heera and accompanying limitations like late flowering, small seededness and poor productivity has prevented its commercialization (Khalatkar et al. 1991). Attempts to develop improved '00' versions by hybridizing Heera with adapted cultivar, Pusa bold were also not very successful (Malode et al. 1995). Use of doubled haploidy and whole genome selection, based on AFLP markers, during backcrossing at University of Delhi have enabled transfer of low glucosinolate trait to a predominant mustard variety, Varuna (Sodhi et al. 2003).

In *Brassica napus* free availability of '00' donors allowed extensive hybridization programmes aimed at the development of productive canola cultivars having maturity duration matching those of popular high yielding mustard cultivars. Some of such canola quality genotypes having <30 µm/g oil free meal have been registered (Agnihotri and Kaushik 2003). Many of the truly productive and early maturing '00' rapeseed genotypes developed at Punjab Agricultural University, PAU have excelled even the mustard checks in All India Coordinated trials. Notable among these are BCN 14, OCN 3, ACN 130 etc. First Indian bred canola quality rapeseed variety GSC 5, developed at PAU, was released for commercial cultivation in Punjab during this year. Canola quality rapeseed hybrids based on *can* CMS are also in the process of development.

Outlook

Inspite of intensive efforts, only limited progress has been achieved in mustard due mainly to restricted initial availability of superior low glucosinolate donors. In addition, the quest for large population size in initial segregating generations is almost always limited by severe restriction imposed on sample size owing to difficult and time consuming analytical procedures for glucosinolate content. Although several experimental stocks have been developed which are much superior in terms of agronomic attributes than the initial donors, there are still inferior in yield than the standard mustard cultivars. Use of doubled haploidy and marker assisted selection is expected to hasten the

pace and efficiency of the breeding programmes. Pending the development of high yielding '00' mustard strains, efforts are being made to commercialize early maturing canola quality *B. napus* strains, especially for cultivation in cooler areas of north-west India. Two canola quality varieties (PAU bred pure line GSC-5 and Adventa hybrid Hyola 401) have been recommended recently by Punjab Agricultural University for general cultivation in Punjab. These are being actively promoted in Punjab. In addition many more productive genotypes are in various stages of evaluation. All these strains possess <25 µ moles glucosinolates g^{-1} defatted meal. Inspite of these achievements, a significant breakthrough in terms of really productive '00' mustard genotypes is still awaited and anticipated.

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Table 1 : Glucosinolate profile and content (μ mol / g^{-1} seed) of key Indian mustard cultivars.

Genotype	2-Propenyl	3-Butenyl	4-Pentenyl	Others	Total
Varuna	22.0±3.2	89.8±2.7	2.3±0.2	1.7±0.2	115.8±4.1
Pusa Bold	37.1±4.5	80.4±3.6	1.9±0.1	1.9±0.2	121.3±5.4
Kranti	21.3±3.5	86.7±4.1	1.5±0.0	3.2±0.1	115.9±5.2
Krishna	27.3±1.2	74.7±2.3	2.5±0.1	2.7±0.3	107.2±3.1
Bio 902	22.7±4.6	81.3±3.9	1.2±0.0	1.9±0.1	107.1±5.9
Sej 2	31.5±3.3	75.4±4.1	0.9±0.0	2.7±0.1	110.5±5.3
RH 30	25.3±3.8	87.1±3.6	1.4±0.2	2.1±0.1	115.9±5.2
RLM 198	30.2±2.1	65.5±3.2	0.4±0.0	1.6±0.1	97.7±3.7
RLM 514	23.1±2.8	71.8±2.3	0.5±0.0	2.0±0.1	97.4±4.1
RLM 619	19.8±3.1	85.6±2.3	1.6±0.0	2.4±0.1	109.4±4.9
RL 1359	21.3±1.5	72.9±1.8	1.8±0.1	2.6±0.2	98.6±3.2
PBR 91	33.3±2.0	83.2±3.1	1.9±0.1	1.7±0.2	120.1±2.1

Adopted mainly from Sodhi et al. (2002)