POTENTIAL OF BRASSICA SPECIES AS PROTEIN SOURCES

By Frank Sosulski
Department of Crop Science, University of Saskatchewan
Saskatoon, Sask., Canada

Rapeseed meal is discounted as a protein supplement for animal feeds because of its low levels of digestible protein and energy, high crude fiber contents associated with problems in dehulling the seed, and the presence of glucosinolates, especially oxazolidinethione. Food uses of rapeseed protein are also limited by the brown colors which develop during aqueous processing of the flour. Brassica species exhibit wide variability in seed characteristics and interspecific crosses are a potential source of more useful biotypes for feed and food purposes. The objectives of the present investigation were to assess the chemical characteristics of the defatted meals, dehulled flours and protein isolates prepared from the principal Brassica species including an interspecific cross. Amino acid distributions were determined on meals and flours but, due to the similarity in the data, only values for the flours are reported in the present paper.

EXPERIMENTAL

Seed of six Brassica species and the bulk progeny (F_4 generation) from an interspecific cross was harvested from the experimental plots of the Canada Agriculture Research Station, Saskatoon, Sask. The species investigated were Target rapeseed (B. napus), Echo turnip rape (B. campestris), oriental mustard (B. juncea), Abyssinian mustard (B. carinata), black mustard (B. nigra), yellow mustard (B. hirta) and the cross Echo turnip rape x oriental mustard (B. campestris x B. juncea). Seed weight determinations were based on the mean weight of 300 seeds. Meals were prepared by defatting the ground seed with hexane followed by desolventization at 40°C for 16 hr. Hulls were separated from the meals by air classification but are reported as percent of the original seed weight. Protein isolates were prepared by alkaline extraction of the soluble proteins from the meals, centrifugation and protein precipitation at pH 4.7. Standard procedures were followed for the determination of proximate constituents and glucosinolate composition and are reported on a dry basis. After hydrolysis with 6 N HCl, the amino acid compositions of the proteins were determined in duplicate by the two-column procedure on a Beckman model 120C automatic analyzer.

RESULTS AND DISCUSSION

The rapeseed species contained substantially more oil than the mustard crops and the oil content of the interspecific cross was significantly less than either parental species (Table 1). However, food grade flours may have comparable market values to the oil component, and the total yield of oil and flour may be a better measure of the potential economic value of a species. B. juncea and B. hirta yielded 43 and 55% of dehulled flour, resp., which greatly exceeded the yields of rapeseed flour (32-33%). Similarly, the low oil and hull contents of the large-seeded B. campestris x B. juncea cross explained the high recovery of flour of nearly 49%. It was not feasible to quantitatively dehull the small seeds of B. nigra but a sample of hand-picked meats was defatted for chemical analysis.

The protein contents of mustard flours (53.7-56.0%) also exceeded those of the rapeseed flours but crude fiber and ash levels were high in all samples (Table 1). The B. hirta flour contained the lowest crude fiber (3.4%) and ash (5.9%) levels, as well as the highest protein content among all species. The colors of all dehulled flours were creamy, even in those species which exhibited greyish meals due to dark-colored hulls.

Because of low yields and protein contents, the recovery of meal protein in the protein isolates was only 60-65% for the rapeseed species (Table 1). The yields of protein isolate for the mustard species and the rape-mustard cross were significantly higher than the rapeseed species but none compared to that of B. hirta which provided 31 g of isolate/100 g of seed. Loss of nitrogen in the whey during protein isolation was 16% of the rapeseed meal nitrogen but only 12% of the yellow mustard nitrogen. All Brassica species were found to contain about 6.5% of nonprotein nitrogen in the meal nitrogen which would constitute a substantial portion of the whey nitrogen. Phenolic acids were presumed to be responsible for the brown and tan colors in most isolates. Only B. hirta appeared to be essentially free of these phenolic compounds so that the flours and isolates could be used over a wide range of pH in food products without discoloration.

Except for the high butenyl isothiocyanate content, the B. campestris x B. juncea meal was intermediate between the parental species in its content of isothiocyanates and oxazolidinethione.

The proteins in the rapeseed species were significantly higher in lysine and lower in arginine than the mustard species and the rape-mustard cross. B. hirta protein was particularly low in lysine but rich in arginine (Table 2). The composition of other essential and nonessential amino acids were similar among all Brassica species but the proteins of the rape-mustard cross differed in content of several amino acids.

CONCLUSIONS

Although higher in oil content, the rapeseed species were clearly inferior to mustard species as sources of flour and protein isolate. B. carinata and B. nigra offered no advantage over B. juncea as parents for interspecific crosses to improve the flour characteristics of rapeseed. Due to its large seed size, low hull and pigment contents, B. hirta was the best source of food-grade products in the present study. While B. hirta cannot be intercrossed with the rapeseed species, a partially yellow-seeded cultivar of B. campestris, Candle, has been selected by Dr. R.K. Downey of Agriculture Canada from a B. juncea x B. napus x B. campestris cross. This cultivar, now in commercial production, has high oil content, low crude fiber and low glucosinolate content.

Table 1. Seed characteristics, product yield and composition of *Brassica* species

Brassica species and common name	Seed characteristics: Weight mg	Oil %	Hull %	Protein Product	Yield of product g/100g seed	Protein (Nx6.25) %	Crude fiber %	Ash %	Color of product	Isothiocyanates: p-OH benzyl	Allyl mg/	Butenyl g meal	Pentenyl	Oxazolidinethione
B. napus	4.0	45.4	22	defatted meal	54	40.0	11.5	6.5	grey	-	-	2.1	0.6	7.5
				dehulled flour	32	50.0	3.7	7.2	cream					
Target rape				protein isolate	16	83.0	0.1	2.0	brown					
B. campestris	2.1	41.5	23	defatted meal	56	37.6	11.9	7.1	grey	-	-	2.0	1.5	2.4
				dehulled flour	33	47.5	4.6	8.0	cream					
Echo turnip rape				protein isolate	17	85.2	0.1	2.1	brown					
B. juncea	3.2	37.8	17	defatted meal	60	47.4	6.5	5.5	cream	-	10.0	-	-	-
				dehulled flour	43	54.0	3.7	6.0	cream					
Oriental mustard				protein isolate	22	93.2	0.1	1.5	tan					
B. carinata	2.6	34.9	23	defatted meal	63	45.4	8.8	6.4	grey	-	4.9	-	-	-
				dehulled flour	40	53.7	5.0	7.1	cream					
Abyssinian mustard				protein isolate	22	88.3	0.2	2.0	brown					
B. nigra	1.7	29.3	-	defatted meal	68	46.3	7.7	5.7	cream	-	7.0	-	-	-
				dehulled flour	low	53.4	4.2	5.9	cream					
Black mustard				protein isolate	24	91.7	0.1	2.0	tan					
B. hirta	7.9	26.3	18	defatted meal	73	47.1	7.7	5.6	cream	30.1	-	-	-	-
				dehulled flour	55	56.0	3.4	5.9	cream					
yellow mustard				protein isolate	31	92.5	0.3	2.0	cream					
B. campestris	4.5	29.8	19	defatted meal	68	44.0	8.6	7.4	grey	-	3.3	5.4	1.2	1.5
				dehulled flour	49	50.7	4.4	8.0	cream					
x *B. juncea*				protein isolate	22	89.7	0.1	2.2	tan					

Table 2. Amino acid composition of defatted, dehulled flours of *Brassica* species

Amino acid	g amino acid/16 g nitrogen in sample							Standard deviation
	B.napus	*B.campestris*	*B.juncea*	*B.carinata*	*B.nigra*	*B.hirta*	*B.camp.xjuncea*	
Tryptophan	1.1	1.1	1.0	1.0	1.1	1.0	0.8	.05
Lysine	6.0	5.9	5.1	5.4	5.7	4.6	5.3	.16
Histidine	2.9	2.6	2.8	2.8	2.7	2.5	2.7	.28
Ammonia	3.3	2.8	2.7	3.0	3.0	3.1	3.0	.19
Arginine	6.5	5.9	7.8	7.8	7.0	8.3	6.1	.35
Aspartic Acid	7.2	7.3	7.1	7.0	7.0	7.1	9.0	.14
Threonine	4.2	4.4	4.2	4.0	4.1	4.1	4.4	.11
Serine	4.4	4.4	4.3	4.3	4.2	4.1	4.4	.07
Glutamic Acid	21.7	21.7	22.9	22.5	22.2	22.4	20.9	.28
Proline	6.2	6.8	6.7	6.8	7.0	6.4	6.0	.10
Glycine	5.5	5.5	5.3	5.4	5.4	5.6	6.1	.01
Alanine	4.6	4.7	4.2	4.5	4.8	4.7	4.5	.30
Half Cystine	2.0	2.2	2.2	2.2	2.2	2.3	1.5	.16
Valine	4.8	4.9	4.6	4.6	4.8	4.7	5.0	.07
Methionine	1.7	1.8	1.6	1.5	1.7	1.6	1.5	.05
Isoleucine	3.8	3.8	3.8	3.7	3.9	3.9	4.0	.05
Leucine	7.3	7.3	7.1	7.0	7.1	7.1	7.6	.16
Tyrosine	2.6	2.5	2.4	2.3	2.0	2.2	3.0	.19
Phenylalanine	4.0	3.9	4.0	4.0	4.0	4.1	4.1	.30

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