Protein Quantity and Quality and Trypsin Inhibitor Content of Sweet Potato Cultivars from the Highlands of Papua New Guinea

James H. Bradbury,* Brendon Hammer, Tue Nguyen, Merle Anders,[1] and John S. Millar[2]

Crude protein, trypsin inhibitor, and amino acid analyses on 30 sweet potato cultivars (10 were studied across five different environments) showed that variabilities of these parameters between roots from the same plant are as great as variabilities across roots from different plants of the same cultivar. Within a cultivar, protein and trypsin inhibitor contents are correlated across different environments, but there is no overall correlation over 60 samples. The range of results for particular amino acids was 2–3-fold, for protein nearly 6-fold, and for trypsin inhibitor 167-fold. Amino acid analyses on 33 samples showed that leucine, lysine, and S-containing amino acids are most often limiting. The mean chemical score is 0.73 (SD = ±0.12), but the imbalance of essential amino acids is less than that indicated by the chemical score. The cultivars Simbul Sowar and Takion have high protein combined with moderate variabilities across environments, which may be useful for selection/breeding for high protein.

It has been found that sweet potatoes contain a wide range of crude protein content, viz., 1.3 to >10% on a dry weight basis (Purcell et al., 1972; Li, 1974; Splittstoesser, 1977), which amounts to about 0.4 to >3.3% on a fresh weight basis. Results on a fresh weight basis for sweet potato cultivars from Papua New Guinea fall within this range, 0.8–1.4% (Oomen et al., 1961) and 0.5–2.0% (Bradbury et al., 1984). Work in the United States has shown that the variability of crude protein content between roots of the same cultivar from one hill is slightly less than between hills within fields for Centennial and Jewel sweet potatoes (Purcell et al., 1978). We report pertinent crude protein and amino acid analysis data on variations between (1) roots from the one plant, (2) roots from the same cultivar grown in the same environment, and (3) different environments, for a range of cultivars from Papua New Guinea.

Lin and Chen (1980) have reported a correlation between crude protein content and the amount of trypsin inhibitor present in sweet potato, but the results of Bradbury et al. (1984) and Dickey et al. (1984) have shown no such correlation. Since the presence of trypsin inhibitor has been implicated in the onset of *Enteritis necroticans*, a fatal disease among children in the Highlands of Papua New Guinea (Lawrence, 1979), it is important that further data be obtained on this point. In this paper we report data on contents of crude protein, amino acids, trypsin, and chymotrypsin inhibitors for sweet potato cultivars from the Southern Highlands Province of Papua New Guinea.

MATERIALS AND METHODS

Sweet Potato. Roots were obtained from 10 representative cultivars grown in the Upper Mendi region and 10 cultivars grown in the Erave region (Bradbury et al., 1984) and 10 representative cultivars from Tari. The cultivars from Upper Mendi and Erave were vegetatively reproduced from individual parents and grown in several different locations. In many cases multiple roots were obtained from the same plant. The skin color was recorded for each cultivar (red, brown, or white) and the color of the flesh (orange, yellow, or white) was recorded. Cultivars at Upper Mendi in 1983 were grown in the absence and the presence of added gypsum (S enrichment) at the rate of 500 kg/ha. Their fresh weight was determined and the weight loss on transport to Canberra recorded. The skin was removed by peeling, and the root was cut into small pieces in a blender and dried to constant weight at 40 °C for 4–5 days. The dry chips were powdered, and the moisture content of each sample was calculated from the total weight lost during transport and on subsequent drying.

Nitrogen and Crude Protein. Total nitrogen was determined by using a Carlo Erba 1106 CHN analyzer by the Analytical Group, Research School of Chemistry, Australian National University. Results for % N are the mean of triplicate analyses (mean standard deviation 0.10). Crude protein content was calculated by multiplying the % N by 6.25 (Bradbury et al., 1984).

Amino Acid Analysis. Samples (25 mg) of sweet potato were hydrolyzed under nitrogen gas in autoclavable vials in 6 M HCl at 110 °C for 22 h, the HCl was removed by rotary evaporation, and the sample was dissolved in starting buffer (0.1 M citrate buffer, pH 2.2) and made up to 25 mL. One-milliliter samples were loaded on the column of an LKB 3201 amino acid analyzer, fitted with an automatic integrator. The amount of each amino acid in mg of amino acid/g of N sample was calculated from a knowledge of the N content of the sweet potato and the weight of the hydrolyzed sample (1 mg) loaded. Results are the average of duplicate analyses; mean deviation is ±4%. Cystine was determined in a separate analysis as cysteic acid (Moore, 1963). Tryptophan was obtained by hydrolysis of the protein in $Ba(OH)_2$ and colorimetric determination using *p*-(dimethylamino)benzaldehyde and sodium nitrite (Piombo and Lozano, 1980). No corrections were made for losses of other amino acids by decomposition during hydrolysis. The percent recovery of nitrogen from the column was calculated as described previously (Bradbury et al., 1984). The amino acid score of each essential amino acid was recorded as a ratio of the values obtained for a reference protein as follows: Thr 250, Val 310, (Cys + Met) 220, Ileu 250, Leu 440, (Tyr + Phe) 380, Lys 340, and Trp 60 mg of amino acid/g of N (Food and Agriculture Organization/World Health Organization, 1973).

Trypsin Inhibitor Assay. The method follows that described previously by Bradbury et al. (1984).

Chymotrypsin Inhibitor Assay. The activity of α-chymotrypsin (Sigma Chemical Co., 44 units/mg enzyme, where units = micromoles of substrate reacted per minute)

Department of Chemistry, Australian National University, Canberra, A.C.T. 2600, Australia (J.H.B., B.H. and T.N.), and the World Bank Southern Highlands Rural Development Project, Mendi, Southern Highlands Province, Papua New Guinea (M.A. and J.S.M.).

[1]Present address: Honolulu, HI 96816.

[2]Present address: Rabaul, New Britain, Papua New Guinea.

0021-8561/85/1433-0281$01.50/0

Table I. Crude Protein Content (% Fresh Sweet Potato) of Ten Cultivars from Upper Mendi Grown in Different Environments

	growth conditions									
name of cultivar	Kiburu, 1982 season[a]		Erave, 1982 season[b]		Upper Mendi, 1981 season[c]	Upper Mendi, 1983 season	Upper Mendi, 1983 season, gypsum added[d]	mean	SD	gradient (see text)
Hopomehene (HO)	1.87	1.97	2.31	2.34	0.50	1.19	1.06	1.41	0.74	1.61
	2.06		2.37							
Takion (TA)	2.37	2.69	1.87	2.06	2.06	1.00	1.25	1.81	0.68	1.14
	3.00		2.25							
Soii (SO)	1.12	1.28	2.56	1.97	1.38	0.88	1.13	1.33	0.41	0.93
	1.44		1.37							
Sapel (SA)	1.81	1.88	1.69	1.38	0.75	1.06	1.69	1.35	0.46	0.31
	1.94		1.06							
Kariap (KA)	1.62	1.50	1.94	1.91	2.00	0.81	0.88	1.42	0.56	0.94
	1.37		1.87							
Pulupuri (PU)	1.12	1.34	2.12	1.97	1.00	1.31	0.81	1.29	0.45	1.00
	1.56		1.81							
Kariko (KO)	0.94	0.91	2.19	2.32	1.63	0.94	1.06	1.37	0.60	1.10
	0.87		2.44							
Simbul Sowar (SI)	1.69	1.60	1.87	1.94	1.69	1.31	1.50	1.61	0.23	0.51
	1.50		2.00							
Wanmun (WA)	2.37	2.22	2.31		0.88	1.94	1.19	1.71	0.64	1.12
	2.06									
Tomun (TO)	1.44	1.48	2.81		1.56	1.56	1.31	1.76	0.60	1.33
	1.69									
	1.31									
mean	1.60		2.10		1.35	1.20	1.19	1.51	0.54	

[a] Two (or three) roots from same plant and mean. [b] Roots from two different plants and mean. [c] From Bradbury et al. (1984). [d] Gypsum added to soil at a rate of 500 kg/ha.

was measured by using the specific substrate benzoyl-L-tyrosine ethyl ester (BTEE, Sigma Chemical Co.) by the method of Hummel (1959). The chymotrypsin inhibitor was extracted from the sweet potato sample by the method described by Bradbury et al. (1984) for trypsin inhibitor. In the enzyme assay there was a linear increase in absorbance A at 256 nm for 5 min from which $\Delta A/\Delta t$ was determined. Following Bergmeyer (1974), the residual activity of α-chymotrypsin was given by

$$\text{units/mg of chymotrypsin} = V\Delta A/\epsilon dvc\Delta t = (1.56 \times 10^3)\Delta A/\Delta t$$

where V (assay volume) is 3 mL, ϵ is the extinction coefficient of BTEE product = 0.964 $cm^2/\mu mol$, d is path length of the cuvette (1 cm), v is the volume of the enzyme solution sampled (0.100 mL), and c is concentration of enzyme in the sample solution (0.02 mg/mL). The residual chymotrypsin activity (units/mg) was graphed against the concentration of chymotrypsin inhibitor from which the extract concentration required to give 50% inhibition of a 20 μg/mL solution of α-chymotrypsin was obtained. We define a chymotrypsin inhibitor unit (CIU) as the amount of sweet potato chymotrypsin inhibitor required to cause 50% inhibition of α-chymotrypsin (100 μg) under the conditions of the experiment. The final result was expressed as the number of chymotrypsin inhibitor units per gram of fresh sweet potato (CIU/g).

RESULTS

Thirty sweet potato cultivars [20 of which had been studied previously (Bradbury et al., 1984)] were subjected to analyses for crude protein, trypsin inhibitor and amino acids. Ten of the cultivars were vegetatively reproduced from individual parents and grown in five different environments over three growing seasons. Crude protein and trypsin inhibitor results for these cultivars are given in Tables I and II. Nine sweet potato cultivars were assayed for chymotrypsin inhibitor but none was detected; the minimum level of detection was 0.5 CIU/g. Amino acid analyses are summarized in Table III.

DISCUSSION

Crude Protein. In Table I, column 2, crude protein results are given for multiple roots from the same plant. The average standard deviation for the 10 sets of data in column 2 is 0.20, and that for a similar set of data (three roots per plant) from 10 cultivars from Tari (data not given) is 0.27. The average standard deviation for eight sets of data for roots of the same cultivar from different plants in the same location (Table I, column 3) is 0.27. The standard deviation contains contributions from the reproducibility of the method of analysis for nitrogen [standard deviation for N (dry basis) of 0.075 when converted to crude protein (wet basis) gives a standard deviation of 0.15] and from variabilities between roots within one plant and across roots between different plants of the cultivar. The major contribution to the variability is clearly due to the experimental method of analysis, with possibly a small additional contribution from analysis of different roots within one plant and across different plants of the same cultivar. The variability is about the same as that found by Purcell et al. (1978) for Centennial and Jewel sweet potatoes, after allowance is made for the fact that their results were for percent protein on a dry basis. The observed standard deviation is much less than the standard deviation between the same cultivar grown in different environments (mean value 0.54, column 8, Table I).

Genotype/environment interactions have been treated by the method of Finlay and Wilkinson (1963), which involves graphing protein content for the particular cultivar against the mean protein content for the five different environments (bottom row, Table I). The gradient of the line produced (Table I, column 9) gives a measure of the variability across environments of the particular cultivar. Thus, a gradient of 1 would indicate the expected average variability, while a gradient of 0 would show 0 variability with environment. For each cultivar the gradient may then be graphed against the mean protein content for that cultivar (Table I, column 7) as shown in Figure 1. Clearly, the region on the right side of Figure 1 represents cultivars with a high protein content and the lower right side would

Table II. Trypsin Inhibitor Content (TIU/g of Fresh Sweet Potato) of Ten Cultivars from Upper Mendi Grown in Different Environments

	growth conditions							
name of cultivar	Erave, 1982 season[a]		Kiburu, 1982 season	Upper Mendi, 1981 season	Upper Mendi, 1983 season	Upper Mendi, 1983 season, grypsum added	mean	SD
Hopomehene	2.4	2.8	4.9	0.33	1.5	0.55	2.02	1.88
	3.2							
Takion	17.6	16.1	12.8	12.7	6.1	4.6	10.5	4.89
	14.5							
Soii	3.8	4.2	5.8	0.80	0.49	0.31	2.32	2.52
	4.6							
Sapel	43.6	36.3	23.0	9.1	15.6	11.9	19.2	10.9
	29.0							
Kariap	13.8	16.4	5.1	5.2	3.3	0.83	6.2	6.0
	18.9							
Pulupori	24.5	17.2	9.5	0.43	4.6	1.22	6.6	6.9
	9.9							
Kariko	6.2	5.9	3.7	6.4	4.8	0.26	4.2	2.44
	5.5							
Simbul Sowar	10.7	10.8	10.1	8.2	4.5	7.2	8.2	2.50
	10.9							
Wanmun	3.3	3.1	5.2	0.64	3.1	2.1	2.8	1.67
	2.8							
Tomun	18.9		21.1	10.8	14.3	11.3	15.3	4.6
mean	13.2		10.1	5.5	5.8	4.0	7.7	4.4

[a] Roots from two difference plants and mean. [b] From Bradbury et al. (1984).

Table III. Amino Acid Analyses (mg of Amino Acid/g of N Sweet Potato) and Amino Acid Scores for Upper Mendi (UM) Cultivars Grown in Five Different Environments

	Hopomehene						Takion						Kariko					
amino acids and scores	UM, 1981[a]	Kiburu, 1982	Erave, 1982	UM, 1983	UM, 1983[b]	mean	UM, 1981[a]	Kiburu, 1982	Erave, 1982	UM, 1983	UM, 1983[b]	mean	UM, 1981[a]	Kiburu, 1982	Erave, 1982	UM, 1983	UM, 1983[b]	mean
nonessential amino acids																		
alanine	378	326	258	429	410	360	252	304	316	311	346	306	287	282	388	317	341	323
arginine	208	273	231	341	459	302	220	248	286	280	296	266	134	316	287	321	217	255
aspartic acid	751	1195	1013	904	660	905	649	779	1091	1129	1149	959	1012	789	1178	1076	1061	1023
glutamic acid	1336	568	496	706	597	741	688	533	553	693	634	620	505	523	732	621	585	593
glycine	405	273	225	333	266	300	134	263	263	308	291	252	227	241	346	259	269	268
histidine	114	116	185	156	149	144	56	199	185	118	195	151	92	95	161	141	176	133
proline	185	238	286	252	220	236	176	205	280	219	257	227	168	218	227	194	285	218
serine	288	356	290	349	334	322	204	290	274	346	261	275	188	272	319	262	232	255
S-containing and aromatic amino acids																		
cystine	52	120	115	114	105	101	31	136	111	117	88	97	54	132	107	126	78	99
methionine	60	71	64	129	40	73	64	64	88	90	101	81	91	68	99	122	137	103
phenylalanine	303	390	260	454	346	351	207	306	237	351	366	293	331	298	357	289	340	323
tyrosine	82	173	147	157	242	160	144	202	175	189	340	210	80	190	159	150	296	175
amino acid scores[c]																		
S-containing (Cys + Met)	0.51[1]	0.87[1]	0.81	1.10	0.66[1]	0.79	0.43[1]	0.91	0.90	0.94	0.86	0.81	0.66[1]	0.91	0.94	1.13	0.98	0.92
isoleucine	1.25	1.00	0.90	0.87[1]	0.85	0.97	0.83	0.84[1]	0.84	0.98	1.03	0.90	0.86	0.80	0.98	0.85	1.08	0.91
leucine	1.23	1.10	0.56[1]	0.93[1]	0.62[1]	0.89	0.58	0.99	0.78[1]	1.00	0.72[1]	0.81	0.85	0.78	0.79[1]	0.70	0.72[1]	0.76
lysine	1.33	1.17	0.85	1.59	1.55	1.30	0.75	1.89	0.97	0.88[1]	0.79	1.06	0.64[1]	0.53[1]	1.09	0.65[1]	1.24	0.83
aromatic (Phe + Tyr)	1.01	1.48	1.07	1.61	1.55	1.34	0.92	1.33	1.08	1.42	1.86	1.32	1.08	1.28	1.36	1.16	1.67	1.31
threonine	1.10	1.28	1.06	1.36	0.99	1.16	0.77	1.11	1.00	1.13	0.85	0.97	0.99	0.90	1.21	0.75	0.92	0.95
tryptophan	2.08	1.98	1.78	2.93	3.31	2.42	1.63	1.43	1.28	1.35	2.12	1.56		2.05	1.05	2.67	2.85	2.16
valine	1.38	1.28	0.98	0.99	1.06	1.14	0.88	0.98	1.26	1.28	0.97	1.07	1.11	0.97	1.33	0.88	0.83	1.02
% N recovery	81	76	63	83	75	76	52	73	68	79	82	71	58	65	77	72	72	69

[a] From Bradbury et al. (1984). [b] S enrichment of soil by addition of 500 kg/ha gypsum. [c] The number 1 refers to the first limiting amino acid. In those cases where the difference between the amino acid score of the first limiting amino acid and the score of one or more other amino acids are within experimental error (say 0.05), it would be preferable to score these amino acids equally. This has been done here.

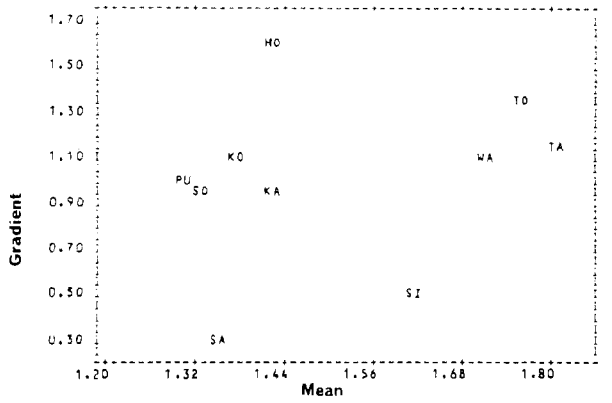

Figure 1. For each cultivar (two letter abbreviation, Table I), the slope (see the text and Table I) is plotted against the mean protein content (Table I, column 7).

be particularly advantageous for selection of cultivars of high and relatively invariable protein content. The cultivar Simbul Sowar combines a relatively high protein content with little variability between different environments whereas Takion has the highest mean protein content, with a variability between environments that is only slightly above the average.

Trypsin Inhibitor. The mean standard deviation of trypsin inhibitor content between two different plants (same environment) of the one cultivar (column 2, Table II) is 3.2, which is similar to the mean standard deviation over each cultivar across different environments (4.4, column 8, Table II). A similar value (4.2) is obtained for roots from the same plant for six Tari cultivars (data not shown). This variability is much larger than that due to experimental errors of measurement. The results show that the variability is the same between roots within one plant and across roots between different plants of the same cultivar and across environments for the same cultivar. There are some cultivars (Hopomehene and Soii) with low values of trypsin inhibitor content and some cultivars (Sapel and Tomun) with consistently high values. The range of trypsin inhibitor contents in Table II is very large, from 0.26 to 43.6. Recent studies have shown that the trypsin inhibitor is very largely destroyed by boiling or baking sweet potato until it is cooked (Hammer and Bradbury; 1984).

Correlation between Protein and Trypsin Inhibitor Contents. Lin and Chen (1980) reported a low positive correlation but Bradbury et al. (1984) and Dickey et al. (1984) found no correlation between the amount of protein and trypsin inhibitor in sweet potato. In this paper we have extended the study to more than 60 samples over more than 30 different cultivars, and across all these samples, there is no correlation between crude protein content and trypsin inhibitor content ($r = 0.005$).

By combining the data of Tables I and II, it is possible to make a correlation between protein and trypsin inhibitor for each cultivar across the five different environments. The correlation coefficients r_1 for each of the different cultivars range between 0.46 and 0.96, which shows better correlation within any particular cultivar than that obtained by Lin and Chen (1980). Correlation coefficients r_2 of about 0.5 were obtained over the 10 varieties grown in the same environment. The relative values of r_1 and r_2 show that correlation is better within one cultivar than within one environment. However, if cultivar and environment are both allowed to vary widely as expressed by analysis of all the data for over 60 samples, then there is a lack of correlation between crude protein and trypsin inhibitor.

Skin and Flesh Color. It was suggested that it may be possible to identify useful traits such as high protein content by visual inspection of skin and flesh color. The skin color (white, brown, red) and flesh color (white, yellow, orange) were recorded for 29 cultivars, but no correlation was found between the color of skin and/or flesh with crude protein or trypsin inhibitor content.

Protein Quality: Amino Acid Analyses. For three different cultivars, two or three roots from the same plant were analyzed and also two roots from different plants of the same cultivar grown in the same location were analyzed. These data are not shown. The variability between these analyses amounted to 15.7% (mean standard deviation) and was due to experimental errors in the technique (mean deviation ~4%), including variable recovery of nitrogen from the amino acid analyzer column (see Table III) and real differences between the composition of the roots. The variability was the same between roots from the same plant as compared with roots from different plants of the same cultivar grown in the same location. The effect of five different environments for three different cultivars are given in Table III. The mean percent standard deviations for all amino acids over the five samples of Hopomehene, Takion, and Kariko are 24.2, 23.4, and 20.6, respectively, which is considerably larger than the mean value of 15.7% for different roots from the one plant or across roots from different plants of the same cultivar. Clearly, environmental effects cause the increased variability of the former results.

The S-enrichment experiment involved 10 cultivars grown at the one site in the absence and presence of gypsum. Amino acid analyses were carried out on four cultivars, Wanmun and the three for which results are given in Table III. There was no change in crude protein content (Table I), and the amount of S-containing amino acids decreased but not significantly, as a result of S enrichment; the average amino acid score over the four cultivars decreased from 0.94 without to 0.78 with S enrichment. This result is in agreement with Purcell and Walter (1982).

Protein quality, measured by the amino acid score of the first limiting amino acid (chemical score), is given for 15 samples in Table III, and other results not in the paper have been included to allow analyses from 33 sweet potato roots altogether. The mean value of the chemical score is 0.73 (SD = ±0.12), which is significantly greater than the value of 0.65 for 33 results of various workers summarized by Bradbury et al. (1984). Results not shown indicate that the first limiting amino acid is variable even between roots from the same plant, and as shown in Table III there is considerable variability between roots of the one cultivar grown in different environments. For these 33 roots lysine is found limiting in 34% of the cases, leucine in 32%, S-containing amino acids in 21%, isoleucine in 11%, and other amino acids occasionally limiting. The percentages differ widely from the earlier results on 33 cultivars worldwide in which S-containing amino acids were limiting in 65% of the cases, lysine in 23%, and leucine in 6% (Bradbury et al., 1984). Some of the difference may result from improved methods for determination of cystine, which has increased the cystine contents of more recent results and reduced the percentage of cases in which the S-containing amino acids (cystine and methionine) are limiting. If this is correct, it would seem likely that lysine and leucine are most often limiting for sweet potatoes from the Highlands of Papua New Guinea with S-containing amino acids in third place.

Nutrition and Selection/Breeding. The fact that (1) the first limiting amino acid may vary even between roots from the same plant and (2) it varies between three different amino acids (leucine, lysine, and the S-containing amino acids) has important nutritional consequences. Thus, the well-known complementarity of amino acids that exists in a diet of rice (lysine limiting), combined with legumes (limiting in S-containing amino acids), is attained within a diet of sweet potato, because of the variability between the different roots. Clearly, the combination of a reasonably good chemical score (0.60–0.73) with internal compensation of three first limiting amino acids within different roots (even from the same plant) means that there is less imbalance of essential amino acids than is indicated from the chemical score. Unfortunately, the quantity of protein present in sweet potato (0.5–3%) (and other tropical root crops) is greatly inferior to that of rice (~6%) and legumes (peas, beans) (Paul and Southgate, 1978).

For a particular amino acid, results over all samples in Table III differ by about 2–3-fold which agrees with previous results (Bradbury et al., 1984). This range is very much less than the 5.6-fold range of protein contents (0.5–2.81%) in Table I and the 167-fold range of trypsin inhibitor contents in Table II. Because of (1) the greater variability in protein content than in protein quality and (2) the likely small loss of essential amino acids due to amino acid imbalance (see above), improvements may be made in protein quantity rather than protein quality by selection/breeding. As indicated earlier and shown in Figure 1, the best cultivars identified in this work for high and only moderately variable protein content over different environments in the Highlands of Papua New Guinea are Simbul Sowar and Takion.

ACKNOWLEDGMENT

We thank R. B. Cunningham and Dr. B. Stevenson, both of Australian National University, for statistical advice and determinations of nitrogen, respectively. Dr. M. Quin is thanked for useful discussions.

Registry No. Trypsin inhibitor, 9035-81-8; chymotrypsin, 9004-07-3.

LITERATURE CITED

Bergmeyer, H. U. "Methods of Enzymatic Analysis"; Academic Press: New York, 1974; Vol. 1.
Bradbury, J. H.; Baines, J.; Hammer, B.; Anders, A.; Millar, J. S. *J. Agric. Food Chem.* **1984**, *32*, 469.
Dickey, L. F.; Collins, W. W.; Young, C. T.; Walter, W. M. *Scientia (Milan)* **1984**, in press.
Finlay, K. W.; Wilkinson, G. W. *Aust. J. Agric. Res.* **1963**, *14*, 742.
Food and Agriculture Organization/World Health Organization. "Energy and protein requirements"; FAO/WHO: Rome, 1973; No. 522.
Hammer, B.; Bradbury, J. H., Chemistry Department, Australian National University, unpublished results, 1984.
Hummel, B. C. W. *Can. J. Biochem. Physiol.* **1959**, *37*, 1393.
Lawrence, G. W. *Papua New Guinea Med. J.* **1979**, *22*, 39.
Li, L. *J. Agric. Assoc. China* **1974**, *88*, 17.
Lin, Y. H.; Chen, H. L. *Bot. Bull. Acad. Sin.* **1980**, *21*, 1.
Moore, S. *J. Biol. Chem.* **1963**, *238*, 235.
Oomen, H. A. P. C.; Spoon, W.; Heesterman, J. E.; Reinard, J.; Luyken, R.; Slump, P. *Trop. Geogr. Med.* **1961**, *13*, 55.
Paul, A. A.; Southgate, D. A. T. "McCance and Widdowson's The Composition of Foods", 4th ed.; HMSO: London, 1978.
Piombo, G.; Lozano, Y. F. *J. Agric. Food Chem.* **1980**, *28*, 489.
Purcell, A. E.; Swaisgood, H. E.; Pope, D. T. *J. Am. Soc. Hortic. Sci.* **1972**, *97*, 30.
Purcell, A. E.; Walter, W. M. *J. Am. Soc. Hortic Sci.* **1982**, *107*, 425.
Purcell, A. E.; Walter, W. M.; Giesbrecht, F. G. *J. Agric. Food Chem.* **1978**, *26*, 362.
Splittstoesser, W. E. *Hort Science* **1977**, *12*, 294.

Received for review August 17, 1984. Accepted November 30, 1984. Financial support was obtained from the World Bank Southern Highlands Rural Development Project.

Characterization of Polysaccharides from White Lupin (*Lupinus albus* L.) Cotyledons

Bernard Carré,[1] Jean-Marc Brillouet,* and Jean-François Thibault

Cell wall material (CWM) was isolated from defatted white lupin cotyledon flour by Pronase and α-amylase treatment. The main sugar component of CWM was galactose, followed by arabinose and uronic acids. Small quantities of rhamnose, fucose, xylose, and glucose were also present. Methylation analysis of CWM showed that galactose units were mainly (1→4) linked. Only small numbers of branched points were present on galactose units. Arabinose was included in a highly branched structure. Xylose was present mainly as nonreducing terminal units and glucose as (1→4)-linked units. CWM was fractionated into pectic substances, hemicelluloses A and B, and α-cellulose. Pectic substances (the largest fraction) were further separated, by ion-exchange chromatography, into a neutral fraction and several acidic polysaccharides. Gel filtration of the neutral fraction produced a polysaccharide primarily composed of galactose.

The development of alkaloid-free mutants of several lupin species (*Lupinus albus*, *Lupinus angustifolius*, *Lupinus luteus*) has allowed the exploitation of their pulses as a protein source both for animals and for humans (Gladstones, 1970; Pompei and Lucisano, 1976a,b). In particular, the white lupin (*L. albus*), which has seeds rich in both protein and oil, appears to have considerable potential as a crop for circummediterranean countries (Hill, 1977). However, the cotyledons of white lupin seeds have a high cell wall material (CWM) content, and this might limit their nutritional value. The CWM content of lupin seed cotyledons varies greatly among species, ranging from

Laboratoire de Biochimie et Technologie des Glucides, INRA, 44072 Nantes Cedex, France.
[1]Present address: Station de Recherches Avicoles, INRA, Nouzilly, 37380 Monnaie, France.

0021-8561/85/1433-0285$01.50/0