Protein and Amino Acid Content of Sweetpotato Cultivars[1]

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Abstract. Protein content of sweetpotatoes from a North Carolina root collection was determined. Protein content ranged from 1.73% dry basis to 9.14%. The amino acid composition of protein extracted from 6 selected cultivars was determined. Tryptophan and total sulfur amino acids were limiting by comparison with the FAO reference protein. Other essential amino acids were in excess suggesting that sweetpotato protein may be useful in supplementing other plant proteins.

The sweetpotato is generally regarded as a high-energy, low-protein food, but can serve to maintain N balance in humans (1) and sustain populations for multiple generations (11). Protein content of over 9% is reported for United States and Japanese cultivars, but world-wide reports vary from 2.46 to 11.8% dry basis (2, 3, 4, 6, 9) depending upon cultivar and growth conditions. A report of complete amino acid analysis of sweetpotato by Nagase suggests that the protein is well balanced nutritionally (10). Other analyses indicate the presence of essential amino acids but the values vary from those reported by Nagase (3, 5, 13). Thus it is possible that higher protein cultivars may be obtained. A high-yielding, high-protein cultivar could become important in eliminating marasmus and reducing the ravages of kwashiorkor in some areas of the world.

In this study we report the protein content, and amino acid composition of 6 selected cultivars of sweetpotatoes from a

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North Carolina root collection.

Materials and Methods

Sweetpotatoes. Roots were obtained from a maintenance collection grown in Norfolk sandy loam near Clayton, North Carolina. Plots were planted May 29 and June 17, 1970, and harvested October 7 and October 28, respectively. At the time of planting, 450 lb./acre of 6-12-12 N:P:K fertilizer was applied and at the last cultivation the plots were side dressed with 450 lb./acre of 8-0-24 N:P:K. In late August 30 lb./acre of N was applied. Diazonon was applied in late July to control wireworm.

Protein and dry matter analyses. Samples for analyses were obtained by cutting 3 mm diam plugs from the equator of 3 to 5 roots with a cork borer. Kjeldahl N was determined on 4-6 samples weighed to 0.1 mg and reported as protein after multiplying by 6.25. Dry matter was determined by drying 6-8 g samples in a vacuum oven at 60°C for 16-18 hr.

Extraction of protein. Representative roots of selected cultivars were peeled and diced, and 300 g were blended in a Waring Blendor with 600 ml cold water for 4 min at high speed. The slurries were filtered through pelon to remove cell walls and fibers. Most of the starch granules were sedimented by centrifugation at 300 x g for 25 min at 4°C. The starch pellets

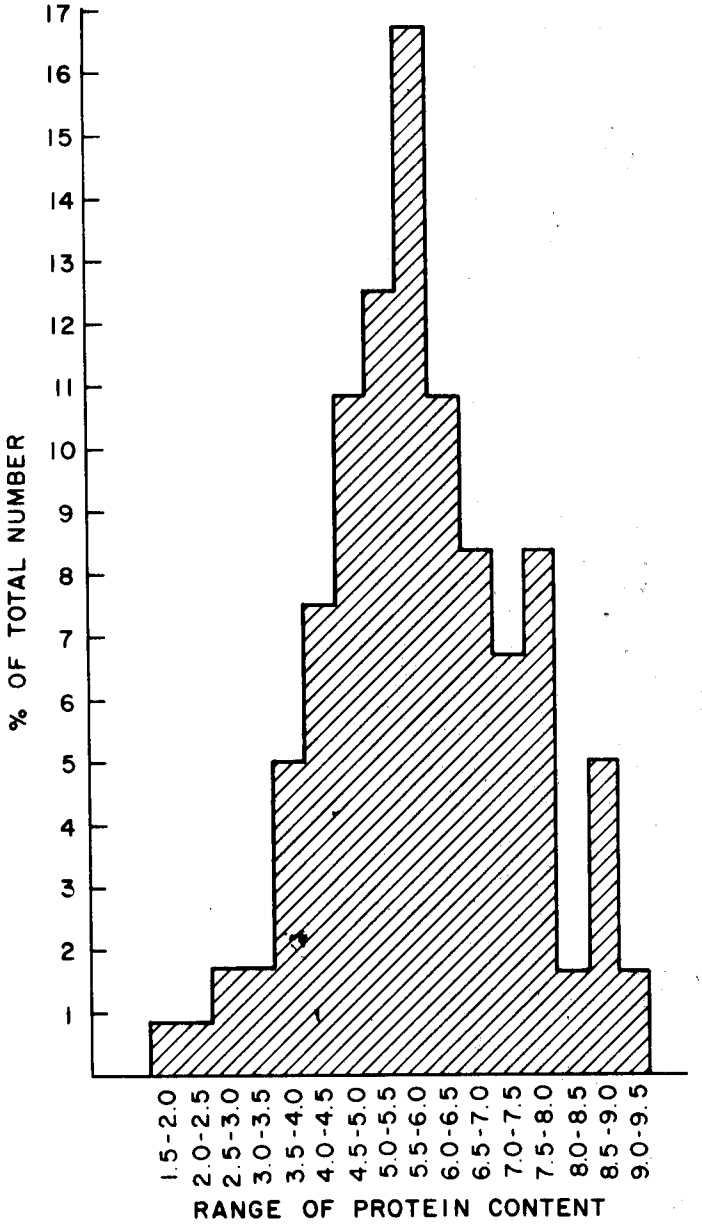

Fig. 1. Frequency of various levels of protein in the North Carolina root collection.

Table 1. Protein and dry matter content of roots of the North Carolina sweetpotato root collection.

Cultivar	% Protein		% DM
	Dry basis	Wet basis	
Porto Rico	9.14	2.24	24.5
Centennial H-26 M[1]	8.75	2.06	23.5
NC 139	8.75	2.19	25.0
219x196-1	8.72	2.37	27.2
P.R. Mutant	8.63	2.37	27.5
Centennial W-1	8.17	2.31	28.3
Centennial H-29M	8.07	2.10	25.9
Acadian	7.99	2.13	26.6
Leeland Bunch	7.90	2.13	26.9
Centennial H-3M	7.78	2.15	27.6
P.I. 286623[2]	7.72	2.12	27.5
Centennial H-19M	7.45	2.09	29.7
195x198-2	7.42	1.62	21.9
Centennial	7.38	1.97	26.9
Jewel Mutant	7.34	1.75	24.2
P.I. 31530	7.18	1.94	27.0
Heartogold	7.18	1.69	23.5
213x221-2	7.17	2.12	29.6
Carogold	7.01	2.06	29.4
NC 246	6.94	1.62	23.4
Centennial W-5 M	6.80	2.37	34.9
NC 193	6.79	2.13	31.3
171X196	6.75	1.57	23.1
NC 221	6.75	2.00	29.6
Centennial W-3 M	6.72	2.31	34.4
Redcliff	6.71	1.56	23.3
NC 232	6.71	1.81	27.0
Julian	6.70	1.78	26.8
Centennial H-11 M	6.62	1.79	25.5
Coastal Sweet	6.56	1.94	29.5
P.I. 308208	6.45	2.00	31.0
Gem	6.31	1.25	19.8
NC 204	6.30	1.37	21.8
P.I. 315347	6.29	2.56	40.7
Earlyport	6.27	1.75	27.9
NC 184	6.23	1.88	30.1
236x221-1	6.27	1.69	26.9
Jewel	6.17	1.44	24.1
217x228-4	6.16	1.69	27.4
NC 218	6.10	1.50	24.6
P.I. 315343	6.09	2.15	35.3
NC 263	6.03	1.75	29.0
P.I. 318846	5.99	2.13	35.5
Centennial H-15 M	5.98	1.81	30.3
Kandee	5.92	1.69	28.5
Gem Mutant	5.87	1.41	24.6
P.I. 324889	5.87	1.56	26.6
Centennial H-10 M	5.80	1.66	28.6
Centennial W-1 M	5.79	2.00	34.5
NC 234	5.78	1.55	26.9
P.I. 324885	5.75	1.87	32.6
NC 282	5.71	1.31	23.0
Nemagold	5.66	1.62	28.7
P.I. 153908	5.66	1.56	27.6
NC 279	5.60	1.62	29.0
P.I. 318851	5.54	1.87	33.8
NC 215	5.54	1.50	27.1
NC 247	5.52	1.37	24.9
NC 217	5.40	1.31	24.3
195x182-1	5.35	1.50	28.0
NC 259	5.28	1.44	27.2
NC 252	5.23	1.44	27.5
NC 257	5.23	1.44	27.5
NC 102	5.21	1.88	36.0
NC 226	5.19	1.31	25.3
219x196-6	5.15	1.44	27.9
NC 238	5.15	1.50	29.1
171x213	5.13	1.31	25.7
NC 253	5.15	1.50	29.1
Southern Queen	5.09	1.94	38.1
White Star	5.06	1.87	37.0
P.I. 308199	5.05	1.69	33.4
NC 267	5.00	1.38	27.5
P.I. 315345	4.94	1.75	35.4
NC 228	4.79	1.50	31.3
NC 250	4.73	1.25	26.4
NC 237	4.73	1.50	31.7
185x195-1	4.54	1.31	28.9
NC 198	4.55	1.19	26.1
Australian Canner	4.50	1.50	33.3
217x228-2	4.49	1.37	30.6

Table 1 continued.

Cultivars	% Protein Dry basis	% Protein Wet basis	% DM
NC 219	4.40	1.50	34.1
Nugget	4.35	1.16	29.4
P.I. 318852	4.34	1.44	33.1
NC 277	4.24	0.94	22.1
221x213-1	4.22	2.00	47.4
P.I. 296116	4.12	1.56	37.9
NC 249	4.10	1.18	28.9
NC 216	3.99	1.12	27.4
NC 273	3.90	1.12	28.8
NC 195	3.86	1.00	25.9
Gold Rush	3.54	1.06	30.0
NC 321	3.51	0.81	23.1
233x171-2	3.32	0.81	24.5
NC 212	3.14	0.56	17.9
NC 241	2.99	0.88	29.3
171x213-5	2.54	1.25	49.3
102x241-3	2.41	0.69	28.5
NC 235	1.73	0.49	28.5

[1]Mutant.

[2]Plant Introduction.

were resuspended and centrifuged at 16,000 x g for 10 min. The centrifugal supernatants of each sample were combined and proteins were coagulated by adding trichloroacetic acid to 12% concn and heating to 50°C. The coagulum was precipitated at 10,000 x g for 25 min and extracted with a mixture of acetone and ether 1:1 until the extracts were colorless. The protein powders were dried overnight at 18-20°C in a hood and stored over mineral oil in an evacuated desiccator; Kjeldahl N analyses were run on the various residues.

Hydrolysis of protein. Samples of the protein (about 6.0 mg) were weighed to 0.1 mg into ampoules and dissolved in 6N HCl. The ampoules were flushed with N, frozen in liquid N, evacuated to about 3 mm Hg and sealed. Samples were hydrolyzed 18 hr by heating in refluxing toluene. The tops were broken off the ampoules and the samples dried over sodium hydroxide pellets in an evacuated desiccator. Since tryptophan is known to be destroyed by this hydrolysis, another set of samples was weighed and hydrolyzed as before except 0.17 ml thioglycholic acid was added [personal communication, H. Robert Horton, based on a report by Matsubura and Sasaki (8)].

Table 2. Protein content of replicated cultivars.

Cultivar	High	Low
H-19	9.08	5.81
Jewel Mutant	8.89	5.79
H-26	8.77	8.73
H-29	8.40	7.75
Centennial	8.00	6.75
H-3	7.96	7.67
Jewell	7.55	4.79
Julian	7.36	6.03
171x196	7.10	6.40
H-10	5.85	5.74
171x213	5.61	4.64
184x234	5.22	5.00
Nugget	5.00	3.70
NC 216	4.24	3.74

Amino acid analysis. The amino acids were measured with a Beckman Model 116 amino acid analyzer according to the method of Spackman (12). Norleucine was added to the sample dilution buffer as an internal standard. Recovery of the norleucine, 98% to 104%, was used to correct recovery of the other amino acids.

Amino acids were measured as micro moles per sample and reported as moles per 100 kg based upon the Kjeldahl protein content of the protein powder.

Table 3. Amounts of total protein left in various residues during extraction and isolation of sweetpotato proteins.

Residue	% of Total protein
Fiber	9.1
Starch	1.4
Supernatant after precipitation	9.9
Protein pellet	79.6

Results and Discussion

Protein content of the various cultivars ranged from 1.73 to 9.14% (Table 1). Most cultivars contained between 4.5-7% protein, which is the range most frequently reported world-wide. The frequency distribution of 0.5% protein increments resembles a normal distribution curve (Fig. 1).

The planting from which root samples were taken was mostly single entries but 14 of the cultivars were replicated without blocking in the field. An estimate of variation was attempted from these (Table 2).

The standard deviation computed from the replicates is 1.121 with 14 degrees of freedom giving LSDs of 3.40% for comparing single entries, 2.40% for comparing multiple entries and 2.95% for comparing a single entry to a double entry.

In Table 1 very high dry matter contents are shown for 221x213-1, P. I. 296116 and 171x213-5. The significance of these data are suspect because the roots collected for assay were small and had wilted significantly by the time of collection and subsequent assay.

In extraction and isolation of proteins, the method used could not be improved by adjusting pH or salt concn. Nearly 80% of the protein was isolated in the protein pellet (Table 3). Since such a large portion of the protein was isolated, it is considered that the amino acid content of the isolated protein is representative of the amino acid content of the sweetpotato per se.

All amino acid values in Table 4, except tryptophan, were obtained from the hydrolysate without added thioglycholic acid (TGA). The tryptophan values were obtained from the samples hydrolyzed in the presence of TGA. The presence of TGA did not change the values for other amino acids except half cystine, which was not found after hydrolysis in the presence of TGA. As a measure of the recovery of tryptophan, a sample of chicken egg white lysozyme was assayed. The tryptophan values were 93% of theoretical.

The molecular wt of each amino acid multiplied by the no. of residues of the amino acid accounted for about 90% of the estimated wt of protein in each sample. The discrepancy between this and 100% may indicate the inaccuracy of 6.25 as a factor for converting N to this particular protein.

The data obtained by Nagase (1957) are shown in Table 4 to compare an unnamed Japanese cultivar with North Carolina sweetpotatoes. The Japanese cultivar shows differences in histidine, glycine, cystine, tyrosine, and tryptophan. The differences are such as to increase the nutritional value.

The essential amino acids of all cultivars are present in such amounts as to suggest good nutritional quality. The reports of Kao, Adolph, and Liu (7), Adolph and Liu (1) and Ruinard (11) suggest that the proteins of sweetpotato are readily utilized by humans, giving reason to believe that sweetpotatoes with higher protein content would be a more useful food.

In Table 5 the amino acid values are compared to the Food and Agricultural Organization of the United Nations (FAO) reference protein. All North Carolina cultivars analyzed are limiting in respect to total sulfur containing amino acids and tryptophan. In the case of 'Centenial', the major commercial sweetpotato, most other essential amino acids are present in sufficient excess to supplement other plant proteins. The chemical score of 'Centenial' protein is 64 based on tryptophan and 74 based on total sulfur containing amino acids.

So far as is known, no effort has been made to obtain higher protein cultivars through breeding programs. The data presented

Table 4. Amino acid content of different sweetpotato cultivars.

Amino acid	Moles / 100 kg						
	Porto Rico 9.14% protein	Jewel Mutant 8.89% protein	Centennial 8.00% protein	Jewel 7.55% protein	Jewel 736% protein	171x196-3 7.10% protein	Japanese[1]
Lysine	28.93	36.28	49.27	46.76	35.91	39.85	44.46
Histidine	7.93	11.10	14.64	15.72	11.19	11.41	27.06
Arginine	23.39	31.64	36.92	34.66	26.39	37.26	36.73
Aspartic Acid	152.54	122.41	109.85	107.89	124.80	134.43	98.42
Threonine	47.70	47.60	51.30	45.82	49.19	52.99	38.63
Serine	50.92	57.68	56.71	48.91	54.76	60.61	52.33
Glutamic Acid	61.56	65.12	67.98	58.85	64.96	75.65	80.20
Proline	42.73	43.16	43.31	47.03	37.50	45.04	37.37
Glycine	73.91	67.21	65.84	57.24	67.42	74.48	34.63
Alanine	61.60	61.89	62.17	58.58	62.36	72.46	68.47
Half Cystine	.00	5.41	3.87	3.49	5.23	7.95	13.20
Valine	66.76	66.60	60.04	57.64	66.36	70.58	67.48
Methionine	18.55	18.29	17.42	17.47	18.58	19.09	16.76
Isoleucine	42.65	32.10	42.57	40.44	77.32	45.28	40.40
Leucine	63.54	63.24	64.35	59.65	63.35	70.06	66.32
Tyrosine	34.23	29.56	29.18	28.89	31.15	31.36	19.86
Phenylalanine	45.04	44.33	42.47	40.44	42.40	43.45	36.32
Tryptophan	5.28	4.94	4.42	5.27	5.69	4.15	8.81

[1]Negase (10).

Table 5. Comparison of the essential amino acids of sweetpotato cultivars with the FAO reference protein.

Amino acid	G amino acid /100 g protein							
	FAO	Porto Rico	Jewel mutant	Centenial	Jewel	Julian	171x196-3	Japanese[1]
Isoleucine	4.2	5.6	4.2	5.6	5.3	10.1	5.9	5.3
Leucine	4.8	8.3	8.3	8.4	7.8	8.3	9.2	8.7
Lysine	4.2	4.2	5.3	7.2	6.8	5.3	5.8	6.5
Methionine	2.2	2.8	2.7	2.6	2.6	2.8	2.8	2.5
Total sulfur	4.2	2.8	3.4	3.1	3.0	3.4	3.8	4.1
Phenylalanine	2.8	7.4	7.3	7.0	6.7	7.0	7.2	6.0
Threonine	2.8	5.7	5.7	6.1	5.5	5.9	6.3	4.6
Tyrosine	2.8	6.2	5.4	5.3	5.2	5.6	5.7	3.6
Tryptophan	1.4	1.1	1.0	.9	1.1	1.2	.8	1.8
Valine	4.2	7.8	7.8	7.0	6.8	7.8	8.3	7.9
Chemical Score based on:								
Total sulfur	100	67	81	74	71	81	90	98[2]
Tryptophan	100	79	71	64	79	86	57	

[1]Nagase (10).
[2]Not limiting.

here, by Juritz (6) and by Murthy and Swaminathan (9) show a wide range of protein levels in various sweetpotatoes suggesting the possibility of further increases in new clones by hybridization and selection for this character.

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