Amino Acid Composition of Oat Groats

George S. Robbins, Yeshajahu Pomeranz,* and Lee W. Briggle[1]

Protein and 17 amino acids were determined in 289 samples of oat groats covering a wide range of genetic material. The samples contained 12.4 to 24.4% crude protein (average 17.1%). Chemical analyses of the oat hydrolyzates indicated that the amino acid composition was nutritionally superior to that of other cereal grains. Several cultivars with significantly increased levels of limiting amino acids (lysine and threonine) were found. Correlation coefficients between protein content and amino acid composition of the protein, or among the amino acids, were determined and evaluated in light of their significance in plant breeding.

The urgency of the world protein crisis combined with the challenge of both increasing the protein content and improving the nutritional value of cereal proteins have prompted, in recent years, numerous investigations on the amino acid composition of several cereal grains. Investigators have been particularly encouraged by the report of Middleton *et al.* (1954), which has shown that the genetic barrier to protein in wheat can be broken, and by the finding that the opaque-2-mutant gene in corn doubled the lysine and tryptophan contents in corn endosperm (Mertz *et al.*, 1964). There have been many reports on the amino acid composition of corn, wheat, rice, and sorghum, as indicated in literature citations of several recent publications (Bressani and Elias, 1968; Davis *et al.*, 1970; Houston *et al.*, 1969; Johnson *et al.*, 1968; Kasarda *et al.*, 1971; Keeney, 1970; Milner, 1969; Van Etten *et al.*, 1967).

Information on oats is rather limited (Hischke *et al.*, 1968) and often contradictory, as pointed out by Tkachuk and Irvine (1969), with regard to data on tyrosine, lysine, and cystine. There is great interest in the nutritional value of oats as a feed and food. Cultivars grown today in the United States are highest among the common cereals in both protein and the limiting amino acid lysine. The present work is concerned with a survey of the amino acid composition of groats from oat cultivars grown commercially in the United States during the period 1900 through 1970.

MATERIALS AND METHODS

Two-hundred-and-eighty-nine samples of oat groats were obtained from J. C. Craddock, who is in charge of the Oat World Collection maintained by the Crops Research Division, Agricultural Research Service, U.S. Department of Agriculture, Beltsville, Md. Cultivars included were grown under irrigation at Aberdeen, Idaho, in 1965, except for 15 which were obtained from originating Agricultural Experiment Stations. All were selected to represent as wide a range of genetic material as possible, based on known traits such as yield capacity, plant height, straw strength, panicle size and shape, disease resistance, and others. Since little or no information was available on amino acid profile, the group of cultivars was considered a random set of genotypes for this characteristic. Most of the cultivars (228) are registered by the Crop Science Society (Garrison, 1968) and have been grown commercially in the United States and Canada for varying periods, or are at present important cultivars. The other 61 are promising new experimental lines from different breeding programs or are important sources of germ plasm being used by United States and Canada oat breeders.

The samples varied widely in kernel size and shape. Groats contained approximately 12% moisture.

Estimation of Crude Protein. All samples were ground in a micro-Wiley mill to pass a 20-mesh sieve, and nitrogen was determined by the Kjeldahl method on 1.0 g of the whole ground groat. Crude protein was estimated by multiplying the nitrogen concentration by 6.25; crude protein data are given in this report on a moisture-free basis.

Amino Acid Analysis. Amino acid analysis of the ground groat was performed on a Beckman 121 automatic amino acid analyzer. Hydrolysis was carried out by adding 4 ml of 6 *N* HCl to 40 mg of sample in 16 mm borosilicate glass test tubes. The mixture was frozen in an acetone bath and the test tubes were evacuated to less than 50 μ. The contents were then allowed to melt so that any entrapped air bubbles could escape, and after repeated evacuation the test tubes were sealed. Hydrolysis was carried out at 110° C ± 1° C for 22 hr in a forced-draft oven. After removal from the oven and cooling to room temperature, the tubes were opened, the hydrolyzed material was evaporated three times to dryness under reduced pressure, and diluted to 10 ml with citrate buffer 0.20 *N* Na^+ pH 2.2. The insoluble humin in the resulting solution was removed by filtration through glass wool.

Two-hundred-and-fifty microliter aliquots of the hydrolyzate were placed automatically on the short and long columns of the instrument for separation of basic and acidic and neutral amino acids, respectively. The accelerated amino acid analysis at 53.7° C required a total of 133 min for separation on both columns.

Data processing was made by electronic integration and conversion of perforated tape to punched cards which facilitated checking the data. Several computer programs were used to calculate original output in nine forms, prepare summaries, and statistically evaluate the results.

Values are expressed in g amino acid per 100 g amino acid recovered. Recoveries were at least 90% and averaged about 95%.

Generally, a negligible amount of cysteic acid and an appreciable amount of methionine sulfone were found as a result of hydrolysis, and were automatically added to their precursors.

Most results given in this report are rounded off to the first decimal place, though in actual calculations of means, standard deviations, and correlation coefficients, at least three figures after the decimal point were used.

National Barley and Malt Laboratory, Crops Research Division, Agricultural Research Service, U.S. Department of Agriculture, Madison, Wis. 53705

[1] Crops Research Division, Agricultural Research Service, U.S. Department of Agriculture, Beltsville, Md. 20705

Table I. Mean, Maximum Value (Max), Minimum Value (Min), Standard Deviation (s), and Coefficient of Variability (CV) for Crude Protein and Amino Acid Composition of 289 Oat Samples

	Max	Min	Mean	s	CV	Mean + 3s	Mean − 3s
Percent protein (PcP)	24.4	12.4	17.1	2.010	11.7	23.2	11.1
Lysine (Lys)	5.2	3.2	4.2	0.324	7.6	5.2	3.3
Histidine (His)	3.1	1.2	2.2	0.316	14.1	3.2	1.3
Ammonia (NH_3)	3.0	2.5	2.7	0.079	2.9	3.0	2.5
Arginine (Arg)	7.8	6.2	6.9	0.231	3.3	7.6	6.3
Aspartic Acid (Asp)	9.9	8.3	8.9	0.278	3.1	9.8	8.2
Threonine (Thr)	3.5	3.0	3.3	0.098	2.9	3.6	3.1
Serine (Ser)	4.8	3.8	4.2	0.187	4.4	4.9	3.7
Glutamic Acid (Glu)	26.9	21.9	23.9	0.938	3.9	26.8	21.1
Proline (Pro)	5.8	3.8	4.7	0.416	8.7	6.0	3.5
Half Cystine (Cys)	2.6	0.6	1.6	0.442	26.8	3.0	0.3
Glycine (Gly)	5.5	4.4	4.9	0.210	4.3	5.6	4.3
Alanine (Ala)	5.5	4.2	5.0	0.187	3.7	5.6	4.4
Valine (Val)	5.7	4.9	5.3	0.106	2.0	5.7	5.1
Methionine (Met)	3.3	1.0	2.5	0.347	13.9	3.5	1.5
Isoleucine (Ile)	4.1	3.4	3.9	0.088	2.2	4.2	3.7
Leucine (Leu)	7.8	4.8	7.4	0.205	2.8	8.0	6.8
Tyrosine (Tyr)	4.4	2.3	3.1	0.232	7.4	3.8	2.4
Phenylalanine (Phe)	5.7	4.9	5.3	0.138	2.6	5.8	5.0
Sum of Lys + Thr + Met (SLTM)	11.1	8.2	10.0	0.487	4.9	11.5	8.6

Table II. Cultivars with Crude Protein (%) or Amino Acid Values (% in Protein) Differing by More than Three Standard Deviations from the Mean of 289 Oat Samples

C.I. No.[a]	Variety Name	Crude Protein or Amino Acid	Content in Cultivar	Mean of All Samples	C.I. No.[a]	Variety Name	Crude Protein or Amino Acid	Content in Cultivar	Mean of All Samples
1242	Cornellian	Thr	3.00	3.3	7420	Florad	PcP	24.44	17.1
1643	Colorado No. 37	Leu	4.82	7.4	7440	Neal	Val	4.96	5.3
					7454	Santee	Arg	6.25	6.9
1864	Garton Gray	Arg	6.18	6.9	7473	Ortley	Ile	3.36	3.9
					7552	Wyndmere	Asp	9.89	8.9
1912	Fulghum	His	1.16	2.2	7552	Wyndmere	Met	1.01	2.5
1914	Red Texas	Val	4.87	5.3	7552	Wyndmere	SLTM	8.53	10.0
2053	Markton	Tyr	2.32	3.1	7557	Russell	Asp	9.93	8.9
2382	Nortex	Ala	4.15	5.0	7557	Russell	Met	1.14	2.5
3168	Fulwin	Lys	3.20	4.2	7561	Lodi	Asp	9.89	8.9
3522	Landhafer	Tyr	2.41	3.1	7561	Lodi	Met	1.28	2.5
4170	Andrew	Ile	3.65	3.9	7571	Pennfield	Tyr	4.42	3.1
4626	Mo. 0-200	His	1.15	2.2	7595	Colfax	Met	1.46	2.5
4672	Dupree	Arg	6.20	6.9	7596	Goldcrest	Met	1.46	2.5
4672	Dupree	Tyr	2.40	3.1	7597	Goldfield	Met	1.41	2.5
6642	Newton	Glu	26.86	23.9	7597	Goldfield	SLTM	8.19	10.0
6980	Ballard Selection	NH_3	3.02	2.7	7670	AuSable	Phe	4.93	5.3
					7801	Pendek	Tyr	2.31	3.1
7003	Appler	Thr	3.02	3.3	7811	Orbit	Met	1.24	2.5
7107	Portage	Val	5.01	5.3	7976	Ora	Lys	3.28	4.2
7146	Ascencao	NH_3	2.53	2.7	8040	Portal	Arg	7.82	6.9
7266	Goodfield	Val	4.98	5.3	8303	Rapida	Met	1.43	2.5
7266	Goodfield	Met	1.35	2.5	8420	Yancey	PcP	24.19	17.1

[a] Accession number of the Cereal Crops Research Branch of the U.S. Department of Agriculture.

RESULTS AND DISCUSSION

Means, ranges, standard deviations, and coefficients of variations of crude protein and amino acid compositions of the 289 oat samples are given in Table I. On a moisture-free basis, total protein averaged 17.1%, somewhat lower than the average reported for the seven selected oat samples studied by Hischke *et al.* (1968). The amino acid distribution in the oat proteins was similar to that reported by Hischke *et al.* (1968). The samples studied by us covered a wide range in protein contents, as indicated by both the range and the coefficient of variation. Wide ranges were found for the amino acids present in lowest concentrations (cystine, histidine, and methionine). The high variability in the sulfur-containing amino acids is of interest in view of their low concentration in practically all cereal grains. High variability in the sulfur-containing amino acids can be attributed, in part at least, to their low levels in the oat groats and to analytical error resulting from those amino acids yielding, each, two products after hydrolysis. The limiting amino acids lysine, and especially threonine (Bressani and Elias, 1968), showed relatively narrow ranges of values and corresponding low coefficients of variability. A wider range was found for methionine which, under certain conditions is, presumably, the third limiting amino acid in oats (Graham, 1966). A comparison with the FAO amino acid pattern indicates the excellent contents of essential amino acids in oat groats. Biological evaluation to confirm chemical analyses would require animal feeding tests. Assuming that the source of ammonia is mainly from glutamic and aspartic acids, about 69% of those amino acids were in the form of amides.

In view of the large number of samples that were tested, it is impossible to report here on the amino acid composition

Table III. Cultivars with Highest Lysine Contents among 289 Oat Samples

C.I. No.	Variety Name	Protein (%)	Lysine Content (% in Protein)
1242	Cornellian	18.6	5.0
1883	Garton No. 473	20.1	4.8
2194	Gold Rain	17.8	4.8
3417	Ranger	17.1	4.9
3611	Vicland	15.8	4.9
3910	Benton	16.9	4.8
3916	Cody	15.8	4.8
4626	Mo. 0-200	17.1	5.2
6980	Ballard	15.8	4.9
7107	Portage	16.3	4.8
7706	Sierra	14.2	4.8
7769	Blount	16.1	4.9
7811	Orbit	15.4	4.8

of individual samples. Interested plant breeders can obtain such information from one of us (L.W.B.). Cultivars which showed values differing by more than three standard deviations from the mean are listed in Table II. It must be emphasized that the data are based on testing single samples, varying widely in protein content, and grown in one crop year in a single location.

Two cultivars were high in protein (over 24%, compared to a mean of 17.1%); three in aspartic acid (about 1% above a mean of 9.9%); and one each in glutamic acid, tyrosine, and arginine. The two cultivars which were highest in protein content in this series of 289, Florad and Yancey, are not considered high protein oats. They were developed for production in the Southeastern States and are not well adapted to Idaho. They produced in 1965 about one-third less than check cultivars and consequently were abnormally high in protein. It is not known what effect this could have on amino acid balance. There were samples significantly lower than the mean in nearly all amino acids. While few of the samples had values more than three standard deviations above the mean, several cultivars were sufficiently above the mean in lysine and threonine to warrant their listing. Results for lysine are given in Table III. Twenty samples contained 3.5% threonine in the protein (average 3.3%). In interpreting the results, again, the previous limitations concerning the nature and source of the tested material must be considered.

The available information was used to determine correlations among the tested amino acids and the amino acids and protein contents; the results are summarized in Table IV. Correlation coefficients of 0.150 and 0.116 were significant at the 1 and 5% levels, respectively. High correlations between two amino acids might, theoretically, permit predicting the amount of one from analyses conducted on the other; if one of the amino acids can be determined by a simple and specific procedure, a valuable tool for screening is available. Finally, study of correlations can be used to establish the value of increasing the protein content to improve the nutritional value of the grain, and to determine the types of proteins that are synthesized in protein-rich grain.

Several of the amino acids, including glutamic acid and glycine, were significantly correlated, either positively or negatively (as in the study of Hischke *et al.*, 1968), with protein. Additional amino acids that were significantly correlated with protein content included threonine, proline, valine, methionine, phenylalanine, and the sum of lysine, threonine, and methionine (SLTM).

Table IV. Correlations Among Amino Acids and Between Amino Acids and Protein Content of 289 Oat Cultivars

	PcP	Lys	His	NH_3	Arg	Asp	Thr	Ser	Glu	Pro	Cys	Gly	Ala	Val	Met	Ile	Leu	Tyr	Phe	SLTM
PcP	1.000																			
Lys	−.183	1.000																		
His	.137	.379	1.000																	
NH_3	.233	−.071	.177	1.000																
Arg	−.046	.100	.132	.211	1.000															
Asp	−.105	−.079	−.157	−.173	−.085	1.000														
Thr	−.466	−.127	−.266	−.188	−.194	.425	1.000													
Ser	−.133	−.339	−.282	−.085	−.250	.282	.664	1.000												
Glu	.587	−.435	−.151	.092	−.432	−.182	−.337	.061	1.000											
Pro	−.359	−.090	−.160	−.044	−.151	.067	.331	.103	−.197	1.000										
Cys	.049	.304	.205	−.019	.124	−.227	−.274	−.126	−.144	−.638	1.000									
Gly	−.628	−.152	−.377	−.363	−.078	.369	.740	.472	−.435	.522	−.372	1.000								
Ala	−.180	.314	.086	−.214	.031	.024	−.164	−.218	−.387	−.352	.403	−.131	1.000							
Val	−.290	−.181	−.432	−.099	−.006	.066	.115	−.094	−.259	.099	−.241	.260	.328	1.000						
Met	−.392	−.004	−.185	−.086	.158	−.196	.171	−.341	−.387	.418	−.388	.422	−.019	.383	1.000					
Ile	−.028	−.102	−.228	−.124	.078	.105	.111	.013	−.258	−.117	−.051	.087	.273	.559	.141	1.000				
Leu	−.142	−.111	−.280	−.063	−.054	−.106	.006	.046	−.215	−.034	−.147	.091	.273	.475	.145	.321	1.000			
Tyr	−.063	−.057	.001	.043	.555	−.003	−.021	−.068	−.330	−.059	.137	−.008	−.116	−.135	.067	−.105	−.122	1.000		
Phe	.455	−.069	.068	.239	.083	−.216	−.407	−.252	.186	−.488	.211	−.572	.164	.220	−.247	.452	.165	−.068	1.000	
SLTM	−.494	.635	.067	−.148	.138	−.109	.237	−.338	−.633	.303	−.131	.347	.161	.174	.744	.055	.028	.004	−.304	1.000

Degrees of freedom for above correlations (N-2) = 287.

The negative correlation between lysine and protein was much lower than that reported by Hischke *et al.* (1968). This is highly encouraging and indicates the possibility that increased protein in oats need not be accompanied by a decreased lysine concentration in the protein as in many other cereal grains (Shoup *et al.*, 1966). Unfortunately, however, correlations between protein and the other limiting amino acids (threonine and methionine), as well as between protein and SLTM, were highly negative. Consequently, the oat breeder must pay strict attention to not only protein content and percent lysine, but also to the maintenance of a satisfactory level of the second and third limiting amino acids. In fact, levels of threonine and methionine may be more critical than lysine. The rather low coefficient of variation of threonine levels (Table I) indicates that a marked increase in level of threonine through breeding would be difficult to attain. Genetic variability within a population is a prerequisite for progress through selection for that characteristic. Hopefully, *Avena* germ plasm other than that represented in this series may provide more opportunity for increase in threonine.

Several additional correlation coefficients should be mentioned. The concentrations of lysine increased as SLTM increased. The concentration of glutamic acid (the main component of the storage proteins, prolamins and glutelins) increased as the concentration of lysine decreased. This indicates that lysine is probably concentrated (as in other cereals) in the soluble protein fraction. Arginine was correlated negatively with glutamic acid and positively with tyrosine; the correlations of aspartic acid and threonine or glycine were positive. Whereas the correlation between serine and glycine was positive, the concentration in the protein of glutamic acid decreased as the concentration of glycine or SLTM increased. There was a negative correlation between proline and cystine or phenylalanine, but a positive correlation between proline and glycine or methionine. Valine increased as leucine or isoleucine increased; the correlation between isoleucine and phenylalanine was positive. The highest correlations were recorded between glycine and threonine, and methionine and SLTM. In both cases, the correlation coefficients were around 0.74, indicating that about 50% of the variation can be explained by those relationships. All correlation coefficients must be considered in light of the variability of the tested material. Thus, there were small correlation coefficients between ammonia and either glutamic acid or aspartic acid, even though the amides of the latter two amino acids are the main sources of ammonia in the hydrolyzates. The apparent discrepancy is explicable by the fact that the coefficients of variation of ammonia, glutamic acid, and aspartic acid are very low (Table II), and the narrow range of tested values limits obtaining high and significant correlations.

ACKNOWLEDGMENT

The technical assistance of J. T. Gilbertson with the amino acid analyses and R. T. Smith, who dehulled all samples and suggested many of the cultivars included, is gratefully acknowledged. We thank J. J. Schreck for the computer programs.

LITERATURE CITED

Bressani, R., Elias, L. G., *Advan. Food Res.* **16,** 1 (1968).
Davis, L. W., Williams, W. P., Crook, L., J. AGR. FOOD CHEM. **18,** 357 (1970).
Garrison, C. S., (Chairman), *Crop Sci.* **8,** 261 (1968).
Graham, W. R., Quaker Oats Co., Barrington, Ill., private communication, March 15, 1966.
Hischke, H. H., Potter, G. C., Graham, W. R., *Cereal Chem.* **45,** 374 (1968).
Houston, D. F., Allis, M. E., Kohler, G. O., *Cereal Chem.* **46,** 527 (1969).
Johnson, V. A., Schmidt, J. W., Mattern, P. J., *Econ. Bot.* **22,** 16 (1968).
Kasarda, D. D., Nimmo, C. C., Kohler, G. O., "Wheat: Chemistry and Technology," Y. Pomeranz, Ed., American Ass. Cereal Chem., St. Paul, Minn., 1971.
Keeney, D. R., *J. Sci. Food Agr.* **21,** 182 (1970).
Mertz, E. T., Bates, L. S., Nelson, O. E., *Science* **145,** 279 (1964).
Middleton, G. K., Bode, C. E., Bayles, B. B., *Agron. J.* **46,** 500 (1954).
Milner, M., Ed., "Protein-Enriched Cereal Foods For World Needs," American Ass. Cereal Chem., St. Paul, Minn., 1969.
Shoup, F. K., Pomeranz, Y., Deyoe, C. W., *J. Food Sci.* **31,** 94 (1966).
Tkachuk, R., Irvine, G. N., *Cereal Chem.* **46,** 206 (1969).
Van Etten, C. H., Kwolek, W. F., Peters, J. E., Barclay, A. S., J. AGR. FOOD CHEM. **15,** 1077 (1967).

Received for review October 30, 1970. Accepted January 11, 1971. This work was a cooperative investigation of the Crops Research Division, Agricultural Research Service, USDA, and the Wisconsin Agricultural Experiment Station, Madison, Wis. The Barley and Malt Laboratory is supported in part by a grant from the Malting Barley Improvement Association. Mention of a trademark or proprietary product does not constitute a guarantee or warranty of the product by the U.S. Department of Agriculture, and does not imply its approval to the exclusion of other products that may also be suitable.