Assessment of the Protein Quality of Two New Canadian-Developed Oat Cultivars by Amino Acid Analysis†

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The total protein and amino acid compositions of two newly released spring-type oat cultivars (*Avena sativa* L.), namely Newman and AC Stewart, have been determined by use of analytical chromatographic methods. Mean protein values in the whole oat grains were 10.75% in Newman and 11.93% in AC Stewart, and, dehulled, the protein contents were 13.27 and 12.62%, respectively. These results are in agreement with Robbins et al. (*J. Agric. Food Chem.* **1971**, *10*, 536–539) recalculated results (12.34%), which were based on the sum of the weights of the amino acids present. Both new oat cultivars contained a good balance of essential amino acids, i.e., $EAA_9 = 44.2–45.4\%$, compared to the FAO/WHO reference protein pattern value of 33.9% for a 2–5-year-old child. The whole oat grains were limited only in lysine. They had an amino acid score, adjusted for digestibility, of 58% for Newman and 66.7% AC Stewart. These results suggest that the most accurate evaluation of protein quality in oats, and possibly in other cereals and legumes, is from their amino acid compositional data.

Keywords: *Oats; assessment; protein quality; amino acids; composition*

INTRODUCTION

Breeding oats (*Avena sativa* L.) for high yields and improved protein quality has received increased attention from oat breeders and the milling industry in recent years (Burrows, 1986; Schrickel et al., 1992; Forsberg and Reeves, 1992). Studies have shown that increasing the protein content of cereals results in lower crop yields and, for most cereals and legumes, lower quality protein (Peterson and Brinegar, 1986). Unlike wheat, maize, rye, barley, sorghum, and millet, however, an increase in oat protein concentration through breeding does not cause an appreciable reduction in the essential amino acid profile of the oat proteins (Hischke et al., 1968; Robins et al., 1971; Maruyana et al., 1975; Zarkadas et al., 1982; Peterson and Brinegar, 1986).

The primary storage proteins of oats are the globulins, which are found primarily in the cotyledon and axis of the embryo and which account for between 75 and 80% of the total proteins on a dry weight basis (Peterson and Brinegar, 1986; Luthe, 1987; Shotwell and Larkins, 1989; Peterson, 1992). Prolamins, which constitute the other main storage proteins of oats, are found in the endosperm of the seed and account for approximately 10% of the total protein (Shewry and Tatham, 1990). Like other cereals, the prolamins of oats are practically devoid of lysine and tryptophan, which make them the most limiting amino acids in these crops (Youngs and Forsberg, 1987; Peterson, 1992). Consequently, genetic improvements to increase the lysine levels in oats, either by a reduction of prolamin storage proteins or by an increase of oat globulins, which are considered to have an excellent balance of amino acids, will be required.

In the past oats have been used primarily as feed grain for ruminants and horses (Peterson and Brinegar, 1986). The high crude fiber content and low metabolizable energy of the hulls have made them less suitable for humans and monogastric animals. Newer impact huller equipment for dehulling oats, capable of removing 90–95% of hulls in one pass (Deane and Commers, 1986), has led to expanded usage of oat grain for food and feed purposes. Although world oat production has declined over the past 20 years, total oat consumption by humans increased from 2.4% of production in 1955 to approximately 17% by 1988, and this trend appears to continue (Hoffman and Ash, 1989). The greatest use of oats for human consumption is in breakfast cereals and as ingredient in bakery products and infant formulas (Burnette et al., 1992).

Dehulled oats (groats) contain approximately 15–20% protein (Robbins et al., 1971; Zarkadas et al., 1982; Peterson, 1992) and have an average protein efficiency ratio (PER) of 2.15 (Youngs et al., 1982; Lockhart and Hurt, 1986; Forsberg and Reeves, 1992). Nutritional studies with pigs and chickens have shown that oat groats have total protein digestibility values of 84–89% (Eggum, 1969) and a biological value (BV) equal to 70–73%. Oat groats are now considered to be a good protein replacement for more expensive protein concentrates for chicken and pig diets (Maruyana et al., 1975; Hulan et al., 1981; Maurice et al., 1985; Cave et al., 1989; Friend et al., 1989).

The aims of this study were, first, to compare the levels and variation of total proteins and the amino acid profiles of two newly released spring-type oat cultivars, developed to grow in areas with longer daylengths (>16 h) and northern latitudes (>45° N), Newman and AC Stewart (Burrows, 1990, 1992), and, second, to assess the protein quality of these two cultivars from digestibility and amino acid compositional data (FAO/WHO/UNU, 1985; FAO/WHO Expert Consultation, 1990).

MATERIALS AND METHODS

Materials. Type DC-5A (lot no. 746) cation-exchange spherical resin, sized to 6.0 ± 0.5 μm, was purchased from Dionex Chemical Co., Sunnyvale, CA. The amino acid stan-

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dards and the three highly purified microcolumn citrate buffers (pH 3.283, 0.20 M; pH 4.10, 0.20 M; pH 6.40, 1.0 M) and sample dilution buffer (pH 2.2; 0.20 M) recommended for high-sensitivity single-microcolumn analysis were used as described previously (Zarkadas et al., 1987). All other chemicals and reagents were of the highest purity commercially available and were used without further purification.

Experimental Procedures. *Plant Material and Sample Preparation.* The two new oat varieties, cv. Newman and AC Stewart, selected for this investigation were developed by Burrows (1990, 1992). Newman is very similar to its recurrent parent Donald (Burrows, 1984). The pedigree of Newman is Donald*4/Dumont. The cv. Dumont (McKenzie et al., 1984) contributed the genes for rust resistance. Assessment of agronomic performance was carried out at the Plant Research Centre, Central Experimental Farm, Ottawa, and further tested in three other geographical regions in eastern Canada for 2 years, between 1986 and 1987.

AC Stewart oat is a spring-type cultivar similar in maturity to Newman (Burrows, 1990), the pedigree of which is Ogle*4/Dumont. The recurrent parent Ogle and Dumont (McKenzie et al., 1984) contributed the rust-resistance genes as described previously by Burrows (1992).

Representative samples of seed of the two cultivars were taken from each of the three replicates of the Ontario and Atlantic provinces cereal and protein crop variety trial grown at three different sites at Agriculture Canada's Central Experimental Farm, Plant Research Centre, Ottawa, ON, in 1991.

The oat grains were cleaned and dried to 65–75 g of moisture/kg of seeds. To analyze oats with and without hulls, only half of the oat samples were dehulled before grinding. Samples of seed of the two cultivars taken from each of the three replicates were dehulled by the impact hulling process (Deane and Commers, 1986). In this process, oat grain is fed to the center of a high-speed rotor with fins (1400–2200 rpm), which throws the grain by centrifugal force against a rubber stator. The impact huller frees the hulls and produces a mixture of free groats, free hulls, groat chips, fines, and some unhulled oats (Burnette et al., 1992). The hulls and fines are first removed from the other fractions by air aspiration, and the dehulled oat groats were then subjected to vigorous separation from unhulled oats.

All samples were then pulverized in a standard electrically driven end runner mill (Cyclone Sample Mill, U.D. Corp., Fort Collins, CO), passed through a 0.5 mm mesh sieve, lyophilized, and then stored at −20 °C in polypropylene bottles until used.

Preparation of Tissue Hydrolysates. Duplicate oat samples (50.0 mg) were hydrolyzed in Pyrex (no. 9860) test tubes (18 × 150 mm) under vacuum (below 10 mmHg) with 5.0 mL of triple-glass-distilled constant-boiling HCl (6.0 M) containing 0.2% (v/v) phenol and one drop of octanoic acid at 110 ± 0.5 °C for periods of 24, 48, 72, and 96 h with the usual precautions described by Moore and Stein (1963) and Zarkadas et al. (1988c). Analyses of individual acid hydrolysates were performed on the clear filtrate in duplicate according to methods described previously (Zarkadas et al., 1990).

Procedures for Amino Acid Analyses. Amino acid analyses were carried out on a Beckman Spinco Model 121 NB fully automated amino acid analyzer using single-column methodology (Zarkadas et al., 1986, 1987, 1990). The automated instrument was equipped with a Beckman Model 406 analog interface module, a system Gold (Beckman Instrument, Inc., Altex Division, San Ramon, CA) chromatographic data reduction system, and an IBM (AT series) compatible personal computer to increase the sensitivity of the analysis and enable quantitation of amino acids at the picomole level as described previously (Zarkadas et al., 1986, 1987).

Complete amino acid analyses were carried out on each of three oat replicate samples according to the standard procedures described previously (Zarkadas et al., 1986, 1987). Each of the three replicates with and without hulls was divided into two subsamples, i.e., A and B, which were then hydrolyzed for 24, 48, 72, and 96 h as described previously (Zarkadas et al., 1988a–c). Analyses of individual acid hydrolysates were performed in duplicate. The data reported for serine and threonine in Table 1 represent the average values of 72 determinations extrapolated to zero time of hydrolysis by linear regression analysis of the results. The values for valine, isoleucine, leucine, and phenylalanine are the average of 48 values obtained from the 48, 72, and 96 h of hydrolysis. All others reported are the average values of 72 determinations from 24, 48, 72, and 96 h of hydrolysis.

Methionine and cyst(e)ine were determined separately in triplicate 50.0 mg oat samples with and without hulls according to the perfomic acid procedure of Moore (1963). Norleucine was added in each hydrolysate as an internal standard. Recoveries of cyst(e)ine as cysteic acid and methionine as methionine *S,S*-dioxide were calculated in proportion to the yields obtained by the performic acid treatment of standard solutions of these amino acids. The data were normalized relative to alanine, valine, isoleucine, and leucine present in the sample.

Tryptophan in oat samples (50.0 mg) was also determined separately after alkaline hydrolysis (Hugli and Moore, 1972) on a single column as described previously (Zarkadas et al., 1986), using 3-nitrotyrosine as the internal standard, as described by Zarkadas et al. (1987). The tryptophan data presented in Table 1 represent the average of 24 determinations.

Determination of Total Protein Mass in Oats. Recoveries of amino acids were calculated on the basis of the protein content of individual hydrolysates determined according to the methods described by Horstmann (1979), Nguyen et al. (1986), and Zarkadas et al. (1988a,c) by the following equation:

$$\mathrm{WE} = \sum_{i=1}^{18}(a_i b_i) \tag{1}$$

According to this method, a mean residue weight (WE, in micrograms per nanomole) is calculated for the amino acids constituting the proteins in the oat samples; a_i is the mole fraction of a specific amino acid i found in the analyzed aliquot, and b_i is the molecular weight of amino acid residue i. A conversion factor, CF, which is the apparent average residue molecular weight (in micrograms per nanomole) increased in proportion to the missing tryptophan, methionine, and cyst(e)ine values and is characteristic for the protein mixture in oats, can be used for determining the protein mass in each hydrolysate sample analyzed from the following equation:

$$\mathrm{CF} = \mathrm{WE}/[1 - (a_{\mathrm{Trp}} + a_{\mathrm{Cys}} + a_{\mathrm{Met}})] \tag{2}$$

The protein concentration of each hydrolysate was then calculated by multiplying CF by the total nanomoles (χ_i) of each amino acid found in the analyzed aliquot as follows:

$$P = \mathrm{CF}\cdot\sum_{i=1}^{15}\chi_i \tag{3}$$

Statistical Analysis. Data processing of the results was carried out by a FORTRAN computer program developed for this purpose. Analysis of variance, conducted on the amino acid data, for a completely randomized block design (factorial) was done by the general linear model procedure (SAS, 1991) and represents the average values from three replicates per variety.

RESULTS AND DISCUSSION

Oats are a good-quality plant protein source used in both human and animal nutrition. Improvements in grain yield, disease resistance and other agronomic traits which have been achieved over the past decade through oat breeding, however, have been accompanied by a decrease in total protein but not in protein quality (Youngs and Forsberg, 1987; Peterson, 1992; Forsberg and Reeves, 1992). As a result, the oat breeders and the oat milling industry have shown increased interest

Table 1. Comparison of the Amino Acid Composition and Protein Contents of Two New Canadian-Developed Oat Cultivars, Newman and AC Stewart (Grams of Amino Acid per Kilogram of Total Protein)

	new oat cultivars[a]								
	Newman		AC Stewart		significance levels				
amino acid	oat meal (with hulls) mean ± SEM	groats (dehulled) mean ± SEM	oat meal (with hulls) mean ± SEM	groats (dehulled) mean ± SEM	CV	cultivar	treatment B (with and without hulls)	cultivar × treatment B	oat groats[b] mean levels of 289 cultivars
aspartic acid	75.45 ± 6.48	76.42 ± 0.51	73.32 ± 0.70	69.45 ± 0.15	7.53	2.02^{ns}	0.21^{ns}	0.57^{ns}	88.64
threonine	33.84 ± 1.03	31.54 ± 1.45	33.80 ± 0.84	32.48 ± 0.31	4.67	0.26^{ns}	4.15^{ns}	0.30^{ns}	32.84
serine	47.18 ± 0.15^{a}	43.28 ± 0.73^{a}	47.74 ± 0.76	$45.54 \pm 1.23^{a,b}$	3.22	2.73^{ns}	12.74^{**}	0.99^{ns}	41.84
glutamic acid	219.75 ± 0.82^{b}	223.26 ± 1.64^{b}	220.68 ± 0.61^{b}	229.23 ± 1.75^{a}	1.11	5.87^{*}	17.77^{***}	3.10^{ns}	238.06
proline	57.96 ± 2.83^{a}	56.67 ± 1.56^{a}	46.49 ± 3.04^{b}	47.44 ± 0.95^{b}	6.36	29.18^{***}	0.01^{ns}	0.34^{ns}	46.81
glycine	45.85 ± 1.15	43.28 ± 0.48	44.39 ± 0.74	44.78 ± 0.85	3.70	0.00^{ns}	1.32^{ns}	2.41^{ns}	48.61
alanine	40.74 ± 3.83	42.32 ± 0.33	44.01 ± 0.53	43.89 ± 0.81	7.92	1.53^{ns}	0.14^{ns}	0.19^{ns}	49.79
cysteine	45.88 ± 0.72^{a}	47.29 ± 1.90^{a}	$44.95 \pm 0.44^{a,b}$	41.62 ± 1.21^{b}	5.23	5.91^{*}	0.50^{ns}	3.05^{ns}	31.88
valine	56.06 ± 0.42	55.96 ± 0.27	54.83 ± 1.71	54.60 ± 1.08	3.68	1.21^{ns}	0.02^{ns}	0.00^{ns}	52.77
methionine	16.89 ± 0.51	15.20 ± 0.70	16.21 ± 0.05	16.59 ± 0.50	5.97	0.41^{ns}	1.35^{ns}	3.46^{ns}	24.90
isoleucine	40.72 ± 0.29	40.46 ± 0.39	41.60 ± 1.00	42.21 ± 0.85	3.35	2.71^{ns}	0.05^{ns}	0.29^{ns}	38.84
leucine	77.72 ± 1.32	76.19 ± 0.69	76.06 ± 0.51	77.87 ± 0.74	1.82	0.01^{ns}	0.08^{ns}	3.82^{ns}	73.70
tyrosine	40.69 ± 0.49	40.94 ± 0.12	42.35 ± 0.41^{a}	43.39 ± 0.68^{a}	1.79	22.64^{***}	2.24^{ns}	0.84^{ns}	30.90
phenylalanine	$53.95 \pm 1.17^{a,b}$	51.95 ± 0.67^{b}	57.13 ± 0.34^{a}	57.28 ± 2.01^{a}	3.80	12.37^{**}	0.54^{ns}	0.78^{ns}	52.81
histidine	24.53 ± 0.66	26.85 ± 0.25	25.97 ± 0.75	27.10 ± 1.11	5.25	1.14^{ns}	4.75^{ns}	0.56^{ns}	21.91
lysine	38.78 ± 0.92^{b}	$41.89 \pm 0.90^{a,b}$	44.86 ± 1.81^{a}	$42.43 \pm 0.93^{a,b}$	5.54	6.06^{*}	0.06^{ns}	4.23^{ns}	41.82
arginine	69.92 ± 1.99	71.58 ± 0.58	69.69 ± 0.61	68.04 ± 3.57	4.52	1.08^{ns}	0.00^{ns}	0.83^{ns}	68.75
tryptophan	14.26 ± 0.47^{b}	15.25 ± 0.07^{a}	15.70 ± 0.05^{a}	15.97 ± 0.06^{a}	2.52	27.69^{***}	5.62	4.20^{ns}	
ammonia	16.17 ± 0.57^{a}	14.46 ± 0.52^{a}	10.99 ± 0.64^{b}	7.88 ± 1.09^{c}	9.79	70.43^{***}	11.83^{**}	0.99^{ns}	26.89
WE,[c] μg/nmol	0.113042 ± 0.0004	0.113581± 0.00009	0.113473 ± 0.0001	0.113407± 0.0001	0.37	0.27^{ns}	0.92^{ns}	1.51^{ns}	
CF,[c] μg/nmol	0.114029 ± 0.0004	0.114648± 0.00009	0.114583 ± 0.0002	0.114523± 0.0002	0.37	0.74^{ns}	1.25^{ns}	1.84^{ns}	
total protein g/kg of dry mass	107.49 ± 2.13	132.72 ± 2.42	119.27 ± 0.63	126.16 ± 9.42	4.12	0.82^{ns}	30.87^{***}	10.05^{***}	123.35[c]
total AA N[d] g of AA N/ kg of protein	166.49 ± 0.74	165.81 ± 0.54	162.77 ± 0.57	159.67 ± 0.28	0.67	59.49^{***}	8.68^{*}	3.59^{ns}	177.42
g of AA N/ kg of dry mass	17.74 ± 0.39	21.80 ± 0.40	19.22 ± 0.03	19.95 ± 0.74	4.40	0.14^{ns}	22.88^{***}	11.08^{**}	20.94

[a] Mean values and standard error of measurements (SEM) for $N = 3$ replicates and $N \times 16$ = number of determinations. Significance: F, values from analysis of variance between cultivars. ***, $P < 0.001$, **, $P < 0.01$; *, $P < 0.05$; ns, not significant; CV, coefficient of variation. [b] Robbins et al. (1971) recalculated results according to the methods of Horstmann (1979) and Zarkadas et al. (1988a–c, 1994, 1995), which were based on the sum of the weights of the amino acids present. [c] Computed according to the methods of Horstmann (1979) and Zarkadas et al. (1988a–c), using eqs 1 and 2. [d] Total amino acid nitrogen (AA N) was determined according to the methods of Heidelbough et al. (1975).

in the development of higher protein cultivars, which are required for high-quality cereal products. The two new northern adapted oat cultivars selected for this investigation, Newman and AC Stewart, developed by Burrows (1990, 1992), have proven to have superior traits including high grain yield, large groat (oat seeds without their hulls) size and high groat/hull ratio, and high hectoliter weight, and both are resistant to several races of rust that are prevalent in Ontario.

The results of total protein and amino acid composition of the whole oat grain and dehulled Newman and AC Stewart cultivars, along with the levels of statistical significance obtained from analyses of variance, are presented in Table 1, expressed as grams of anhydrous amino acid per kilogram of fat- and ash-free oat seed protein. The data represent the average values of three replicates ($N = 3$). The results show deviations of less than 2.5% from the average values obtained among the three replicates of each cultivar and corresponding low coefficient of variations.

Protein determinations in each acid hydrolysate from both whole oat grains and groats of the Newman and AC Stewart cultivars were carried out according to the method of Horstmann (1979) as described previously (Zarkadas et al., 1988a–c), and the results are summarized in Table 1. This method of calculating the protein mass in oats is based upon the summation of the weights of the amino acids in oat proteins (grams of amino acids per kilogram of dry sample) and yields accurate estimates of the amount of protein present as determined by eqs 1–3. The mean residue or equivalent weight (WE, micrograms per nanomole) and conversion factor CF (micrograms per nanomole) given in Table 1 are very similar between cultivars and can be used in all subsequent protein quantitation of whole grain or dehulled oats as described by Horstmann (1979) and Zarkadas et al. (1988a–c).

The protein concentration of two new whole oat grain cultivars, Newman and AC Stewart, as presented in Table 1, appeared to be very similar, but when they were compared with the dehulled oat (treatment B) samples, the differences were highly significant ($P < 0.001$). Similarly, treatment B and (cultivar × treatment B) interaction with respect to total protein contents between those two cultivars were both highly significant ($P < 0.01$) and are in accord with the protein content values reported in Table 1 on whole oat kernels and dehulled oats and with reports by others on oat hulls (Young and Forsberg, 1987; Forsberg and Reeves, 1992). Mean protein values of the samples were 107.49 g of protein/kg of dry mass in the Newman cultivar and 119.27 g of protein/kg of dry matter in AC Stewart. The protein contents of the dehulled oats from the Newman and AC Stewart cultivars were 132.72 and 126.16 g of protein/kg of dry sample, respectively. These results are similar to the values reported by Pomeranz et al. (1973) for commercial milled oats, which ranged from 9.6 to 13.4% for light and heavy weight oats, respectively, but are considerably lower than the values found by Robbins et al. (1971) in oat groats. Robbins et al. (1971) conducted a survey on the crude protein contents of 289 oat groat samples representing 228 cultivars and 61 experimental genotypes, and they found a range in groat protein concentration from 124 to 244 g of protein/kg of dry mass, with a mean of 171 g of protein/kg of groats on a dry basis. Peterson (1992) reported more recent data from entries in the U.S. Department of Agriculture uniform nursery trials, which showed an average protein concentration from 164 to 167 g of protein/kg of dry sample for the uniform midseasson and early oats from promising breeding lines and cultivars taken from several locations. The highest protein content reported for oats was about 180 g/kg of oat groat dry mass (Peterson, 1992).

The most likely explanation for the large differences in the protein values from dehulled oats, as presented in Table 1, and those reported by Robbins et al. (1971) and Peterson (1992) for oat groats is the method used for total protein determination in oats by these authors. Robbins et al. (1971) used the conventional Kjeldahl nitrogen method to determine total nitrogen. This method does not differentiate between nitrogen derived from protein nitrogen and that originating from nonprotein nitrogenous compounds, which from the present results appear to be in large amounts in oats. When the Robbins et al. (1971) results were recalculated from their amino acid data according to the methods of Horstmann (1979) and Zarkadas et al. (1988a–c, 1994, 1995), it was found that their oat groats contained only 123.35 g of protein/kg of oat groat samples, on a dry weight basis, which represents a decrease of 38.6% from the 171 g of protein/kg of oat groats (Table 1). Similar differences in protein content have been reported previously among cereals and leguminous seed products (Zarkadas et al., 1988a). Wide differences in protein content have also been reported by Heidelbaugh et al. (1975) for Skylab foods. It appears that the most accurate method of calculating protein content of oat varieties is from the summation of the weights of each of the amino acid residues present in the oat cultivars (Benedict, 1987; Khanizadeh et al., 1992; Zarkadas et al., 1994).

The total amino acid nitrogen values reported in Table 1 were calculated from their respective amino acid composition as described by Heidelbaugh et al. (1975). The mean nitrogen content in whole oat grains was 17.74 g of amino acid nitrogen/kg of dry sample in the Newman cultivar compared to 19.22 g of amino acid nitrogen/kg of dry mass of AC Stewart oats (Table 1). The total amino acid nitrogen contents of the dehulled oats from the Newman and AC Stewart culitvars were 21.80 and 19.95 g of amino acid nitrogen/kg of dry sample, respectively.

The results in Table 1 show that the total protein ratio in oats with and without hulls differed significantly, with the AC Stewart oats having a higher ratio (0.945) in comparison with Newman oats (0.801), suggesting that the groat/hull ratio between these two cultivars must also differ significantly. Groat/hull ratio and test weights have been widely used in the marketplace as reliable indices of oat grain quality, and selection for high groat percentage and test weight is practiced in nearly all oat improvement programs (Bunch and Forsberg, 1989). According to Forsberg and Reeves (1992) groat proportions represents 680–720 g/kg of whole oat kernels.

The amino acid profiles of the two new oat cultivars with and without hulls and levels of statistical significance obtained from analysis of variance, as presented in Table 1, show close similarities in composition. Both of these cultivars were found to contain high levels of glutamic and aspartic acids and when taken together account for almost 29.4–29.9% of all residues. Since Robbins et al. (1971) reported that approximately 69% of the acidic amino acids were amidated, the actual frequency of free carboxyl groups in oats is approxi-

Table 2. Comparison of the Essential Amino Acid (EAA) Composition of Two Oat Cultivars and High-Quality Animal Proteins with the Suggested EAA Pattern of Requirements for Humans

EAA	EAA[a] requirements for preschool child (2–5 year old)	oat genotypes: Newman oat meal (with hulls)	Newman groats (dehulled)	AC Stewart oat meal (with hulls)	AC Stewart groats (dehulled)	oat groats means of 289 cultivars[f]	animal products[b]: egg	animal products[b]: cow's milk
		Milligrams of Amino Acid per Gram of Total Protein						
EAA_9								
histidine	19	24	27	26	27	22	22	27
isoleucine	28	41	40	42	42	39	54	47
leucine	66	77	76	76	78	79	86	95
lysine	58	39	42	45	42	42	70	78
methionine + cyst(e)ine	25	63	62	61	58	61	57	33
phenylalanine + tyrosine	63	95	93	99	101	84	93	102
threonine	34	34	31	34	32	33	47	44
tryptophan	11	14	15	16	16		17	14
valine	35	56	55	55	55	53	66	64
% total protein								
EAA_9	33.9	44.3	44.2	45.4	45.1	42.2	51.2	50.4
EAA index[d]		85.5	86.9	90.2	91.1			
total EAA,[e] mg/g of N		2934	2942	3056	3010	2616	3215	3200
		Percent Protein Digestibility in Man[a]						
		86	86	86	86	86	95	97
		Percent Amino Acid Score[a]						
		67.2	72.4	77.6	72.4	72.4	100	100
		Protein Digestibility Corrected Amino Acid Score[a]						
		58	62.3	66.7	62.3	62.3	95	97
limiting EAA		Lys	Lys, Thr	Lys	Lys, Thr	Lys, Thr		

[a] Data from FAO/WHO/UNU (1985) and FAO/WHO (1990). [b] Data taken from Bodwell (1987). [c] EAA_9: threonine, valine, methionine, isoleucine, leucine, phenylalanine, lysine, tryptophan, and histidine. [d] Calculated according to the methods of Block and Mitchell (1946) and Oser (1961). [e] Computed from reference protein standards (FAO/WHO, 1965). [f] Data taken from Robbins et al. (1971).

mately 9.2–10.5%. Although the frequency of occurrence of the total basic amino acids of oats is considerably lower, and accounts for approximately 13.3–14.1%, it slightly exceeds that of the free carboxyl groups. Leucine, the next most abundant amino acid, accounts for a further 7.6–7.7%. The present mean values for total aromatic amino acids ranged from 9.3–9.5% in Newman to 9.9–10.1% in Stewart oats. The amino acids with hydrophobic side chains account for a further 29.6–30.7% compared to 50.9–51.6% for hydrophilic amino acids. The amino acid residues in smallest amount in these two oat cultivars are lysine (3.9–4.5%), tryptophan (1.4–1.6%), and methionine (1.5–1.7%).

These results are in good agreement with those reported by Hiscke et al. (1968) and Pomeranz et al. (1973, 1976) on covered oat varieties and with those reported by Robbins et al. (1971) for oat groat samples from 289 oat cultivars, but some differences have been noted. The apparent differences noted in the levels of serine, tyrosine, histidine, and tryptophan between cultivars after dehulling were statistically significant ($P < 0.05$). The glutamic acid content of AC Stewart was also significantly higher ($P < 0.05$) than that of Newman and generally increased highly significantly ($P < 0.001$) in the dehulled kernels of both cultivars. The AC Stewart cultivar has a significantly high ($P < 0.001$) content of tyrosine, phenylalanine, and tryptophan compared to that of Newman. There was also significant variation ($P < 0.05$) in the content of lysine and cysteine between cultivars. However, (cultivar × treatment B) interaction, with respect to amino acid composition, was not significantly different except with regard to total protein content.

The essential amino acid (EAA) profiles of the two new oat cultivars with and without hulls are similar and ranged from 2934–2942 mg of EAA/g of nitrogen in Newman to 3010–3050 mg/g of N in AC Stewart. When comparisons of the EAA profiles of both cultivars were made with other proteins (Table 2), it was found that oat proteins were only slightly lower than either hen's whole egg (3215 mg/g of N) or cow's milk (3200 mg/g of N) (FAO/WHO, 1965, 1973). Similar results were obtained from the essential amino acid indices calculated from their amino acid composition (Table 2) according to the methods of Block and Mitchell (1946) and Oser (1951).

The essential amino acid profiles and protein ratings of the oat cultivars investigated are compared in Table 2 with those of the reference protein pattern (FAO/WHO/UNU, 1985; FAO/WHO Expert Consultation, 1990) for a 2–5-year-old child and oat groats values reported by Robbins et al. (1971), with whole egg and cow's milk, which are two high-quality animal proteins. The FAO/WHO Expert Consultation (1990) amino acid scoring method is based on the nine essential amino acids (EAA_9) required for humans, also listed in Table 2. Oats have true protein digestibility of 86 (FAO/WHO Expert Consultation, 1990). The two cultivars evaluated in this study with or without hulls are very similar in their essential amino acid contents and contained adequate amounts of all essential amino acids ranging from 44.2 to 45.4%, which is considerably higher than the 33.9% reference protein pattern value given by FAO/WHO Expert Consultation (1990) for a 2–5-year-old child. The whole oat grains from both cultivars were limited only in lysine compared to dehulled oats, which are limited also in threonine. Mean values for corrected amino acid scores were 58 and 62.3% for Newman oats with and without hulls, respectively, and 66.7 and 62.3% in whole grain and dehulled AC Stewart oats, respectively. These results are in agreement with the Robbins et al. (1971) recalculated amino acid score (62.3%). It

should be noted that while lysine in oats ranged from 39 to 45 mg/g of total oat protein, it is still below the recommended FAO/WHO Expert Consultation (1990) reference standard value of 58 mg of lysine/g of dietary protein for the 2–5-year-old child (Table 2). Similarly, threonine was slightly lower in the dehulled oat cultivars than the FAO/WHO Expert Consultation (1990) recommended levels.

From the foregoing results, it becomes evident that an accurate evaluation of protein quality of oats, with or without hulls, can be made from amino acid compositional data, as recommended by FAO/WHO/UNU (1985) and FAO/WHO Expert Consultation (1990), and by the Expert Work Group (1984), Pellett and Young (1984), and Zarkadas et al. (1992, 1993a,b, 1994, 1995).

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