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Germplasm Characterization for Biochemical Parameters in Oats (*Avena sativa* L.)

R. Premkumar[1*], A. Nirmalakumari[2] and C. R. Anandakumar[3]

[1]Assistant Professor, RVS Agricultural College, Thanjavur, Tamil Nadu – 613 402, India

[2]Professor, Plant Breeding and Genetics, Centre of Excellence in Millets, Athiyandal, Thiruvannamalai, Tamil Nadu – 606 603, India

[3]Registrar, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu – 641 003, India

*Corresponding Author E-mail: premmelb@gmail.com

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ABSTRACT

The present investigation was carried out using 29 grain and dual purpose genotypes of oats based on yield and yield contributing characters along with one check variety, Kent and these genotypes were used for biochemical analysis viz., crude protein, crude fibre, crude fat and amylose content. Mean values were worked out for those genotypes using descriptive statistics. Based on the results, there was a significant differences between the genotypes were observed for all the biochemical characters. The genotypes namely TNAs 17, TNAs 9, Kent and TNAs 4 were found to possess high crude protein, crude fibre, crude fat and amylose content respectively. Breeding for high yielding varieties is the primary objective of the breeders. The improvement of nutritional quality of the grains should also be given an important consideration. Genotypes with high grain nutrient content and high single plant kernel yield would be used for direct selection or hybridization. In contrast, high grain nutrient content genotypes with low yield potential would be useful for trait specific breeding improvements.

Key words: *Genotypes, Yield, Amylose, Kernel, Nutrient.*

INTRODUCTION

Oat (*Avena sativa* L.) is a small coarse cereal used all over the world for food, feed and fodder, and it is frequently grown as a dual-purpose crop[22]. Despite an important cereal, the area under cultivation of oat has been continuously decreasing during the past few decades[3]. However, recent demand of oats for human consumption has been gradually increased, particularly owing to its nutritional benefits. Oat has been shown to be a nutritious source of protein, carbohydrate, fibre, vitamins and minerals as well as of some compounds (polymers of fructose and antioxidant molecules, *etc*.) with beneficial effects on health[11,18]. Compared to other cereal crops, oat is reputed to be better suited for production under marginal environments, including cool-wet climate and soils with low fertility[13].

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Oats have long been recognized as having superior quality among cereals with respect to protein and lipid composition, as well as soluble dietary fibre (ß-glucan). The starchy endosperm, which is the primary storage site of starch, protein, lipid, and ß-glucan, occupies the highest proportion of the oat kernel. The largest single component in the groat is starch, which is present in compound grains composed of several multifaceted individual granules similar to those found in rice[1]. Starch content is variable among varieties (43 to 64 % of the groat)[16]. The second most abundant component in the oat kernel is protein. Oats have higher protein than many of the other commonly consumed grains, and the amino acid profile of oats is generally superior to other cereals, containing higher levels of most of the essential amino acids than other major domestic cereals[24].

Oats are also higher in lipid compared to other cereals, and the lipid has a favourable ratio of unsaturated to saturated fatty acids[23]. The soluble fibre in oats is almost entirely mixed linkage ß-glucan, the main component of the oat endosperm cell wall. Nutritionally favourable attributes of oats, such as high protein, fat and fibre content, have aroused considerable interest in increasing utilization of oats for human consumption[14]. Protein concentration in oat groats is high typically ranging between 15 to 20 per cent.

Hussain *et al*[8]., reported that '*Fatua*' oats harvested at various intervals produced more fodder and less crude protein with plant age or during crop maturity.

The crop should be harvested at a stage that provides an optimum compromise between forage yield and quality. Maximum green fodder and dry matter yield and crude protein content were recorded when oats was harvested at 50 per cent flowering.

MATERIALS AND METHODS

The experiment was conducted during *Rabi*, 2013-2014 at Indian Agricultural Research Institute, Regional Station, Wellington. A total of 48 genotypes received from IARI, Regional Station, Wellington and Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore and Indian Grassland and Fodder Research Institute, Jhansi were evaluated under field condition using randomized complete block design with three replications. Out of 48 germplasm accessions, 29 grain and dual purpose oat germplasm accessions were selected based on yield and yield contributing traits for biochemical analysis. The selected germplasm accessions along with check variety were used for biochemical analysis *viz*., crude protein, crude fiber, crude fat and amylose content (Table 1). The nitrogen content estimated by conventional Micro-Kjeldahl method[7] and the estimated value of nitrogen was multiplied by 6.25 to obtain the crude protein per cent. Crude fibre content was determined according to the method adopted by Goering and Vansoest[6]. Crude fat was determined according to the method of AOAC. Simplified procedure of Juliano[12] was used for the estimation of amylose content.

RESULTS AND DISCUSSION

The most important aspect of oat kernel is its quality as a food or feed. It is good source of protein, fibre, fat and amylose content. Among all cereals, it possesses an excellent source of β-glucan, a dietary fiber with blood glucose stabilizing and cholesterol lowering properties. Hence, in this study, 29 grain and dual purpose oat genotypes were selected based on yield and yield contributing characters along with one check variety, Kent and these genotypes were analysed for crude protein, crude fibre, crude fat and amylose content. Mean values were worked out for those genotypes using descriptive statistics. Based on the results, there was a significant differences between the genotypes were observed for all the biochemical characters (Table 2).

Crude protein content varied from 12.17 to 20.30 with a mean of 15.50 per cent. The genotypes, TNAs 17 (20.30 %), TNAs 20 (19.57 %), TNAs 24 (18.24 %), TNAs 15 (17.71 %) and TNAs 5 (17.61 %) had the highest crude protein content. Robbins *et al*[19]., Yeoh and Watson[24], McMullen[14], Miller *et al*[15]., and Saidi *et al*[20]., also reported highest protein content in oats. The crude protein value of ideal fodder oat is 12.42 per cent. The quality of fodder oat is greatly influenced by plant age and crude protein content[4]. They concluded that forage yield, dry matter yield and crude fibre increased while seed yield and crude protein declined with advancing maturity.

Hussain *et al*[9]., conducted trials during 1990 and 1991 to evaluate yield and quality of fodder at different harvesting stages of oats and barley. Maximum crude protein content in oats and barley was 14.93 and 14.37 per cent,

respectively. The crude protein content is 10.33 per cent at booting stage of oats which had been mainly for fodder purpose.

Crude fibre content ranged between 10.58 and 22.66 with a mean of 16.29 per cent. The genotypes *viz*., TNAs 9 (22.66 %), TNAs 3 (22.34 %), TNAs 4 (20.34 %), TNAs 18 (20.25 %), TNAs 19 (19.75 %) and TNAs 8 (19.75 %) had recorded highest crude fibre content. Hussain *et al*[10]. also observed highest amount of crude fibre content. In contrast, Biel *et al*[2]., observed lowest amount for this trait in oats.

Crude fat content varied from 2.47 to 6.85 with a mean of 3.54 per cent. The genotypes namely Kent (6.85 %), TNAs 43 (5.18 %), TNAs 21 (5.14 %), TNAs 22 (4.93 %) and TNAs 17 (4.63 %) had the highest crude fat content. Southgate[21], Welch[23] and Biel *et al*[2]., also reported highest value of crude fat content in oats. Southgate[21] also reported that lipids are only a minor component of cereals and it ranges from 5-10 percent in oats, on a dry-matter basis. Oats contain higher levels of lipid than any other cereal grain, and most of it is found in the bran and starchy endosperm. The embryo contains the highest concentration of lipid of all the tissues of the oat, but it represents only a small proportion of the total groat by weight. Over 40 per cent of the total lipid in oats is triglyceride[25].

Amylose content ranged between 11.89 and 30.27 with a mean of 17.45 per cent. The genotypes namely TNAs 4 (30.27 %), TNAs 14 (25.83 %), TNAs 19 (23.35 %), TNAs 12 (22.39 %) and TNAs 6 (21.58 %) had recorded highest amylose content. Paton[17] also found highest rage for the above said trait. The amylose content of oat starch ranges from a low of 16-18 per cent[17] to a high of 26-29 per cent[5]. A relatively large amount of intermediate starch fraction having properties of both amylose and amylopectin was reported. Oat starch, in contrast to those of wheat and maize contains a relatively large amylose lipid complex.

Table 1: List of 30 genotypes selected for biochemical analysis in oats

S.No	Genotype	Source	Pedigree
1	TNAs 1	IARI, RS, Wellington	V1
2	TNAs 2	IARI, RS, Wellington	V2
3	TNAs 3	IARI, RS, Wellington	V3
4	TNAs 4	IARI, RS, Wellington	V4
5	TNAs 5	IARI, RS, Wellington	V5
6	TNAs 6	IARI, RS, Wellington	V6
7	TNAs 7	IARI, RS, Wellington	V7
8	TNAs 8	IARI, RS, Wellington	V8
9	TNAs 9	IARI, RS, Wellington	V9
10	TNAs 10	IARI, RS, Wellington	V10
11	TNAs 11	IARI, RS, Wellington	V11
12	TNAs 12	IARI, RS, Wellington	V12
13	TNAs 13	IARI, RS, Wellington	V13
14	TNAs 14	IARI, RS, Wellington	V14
15	TNAs 15	IARI, RS, Wellington	URS/FAPA
16	TNAs 16	IARI, RS, Wellington	EC 705556
17	TNAs 17	IARI, RS, Wellington	URS/GUAPA
18	TNAs 18	IARI, RS, Wellington	URS 22
19	TNAs 19	IARI, RS, Wellington	URS TORENA
20	TNAs 20	IARI, RS, Wellington	UFRGS 078030-2
21	TNAs 21	IARI, RS, Wellington	URS GORIA
22	TNAs 22	IARI, RS, Wellington	UFRGS 077026
23	TNAs 23	IARI, RS, Wellington	EC 705561
24	TNAs 24	IARI, RS, Wellington	URS TARIMBA
25	TNAs 43	IGFRI, Jhansi	JMO-2000-4
26	TNAs 44	IGFRI, Jhansi	JMO-99-2
27	TNAs 45	IGFRI, Jhansi	JMO-851
28	TNAs 46	IGFRI, Jhansi	JMO-99-1
29	TNAs 47	IGFRI, Jhansi	JMO-822
30	Kent (Check)	Australia	-

Table 2. Biochemical analysis in selected 30 oat genotypes

Genotypes	Crude protein (%)	Crude fibre (%)	Crude fat (%)	Amylose content (%)
TNAs 1	12.17	13.28	2.56	15.34
TNAs 2	15.40	18.01	3.45	16.94
TNAs 3	15.33	22.34	3.70	21.29
TNAs 4	14.77	20.34	4.53	30.27
TNAs 5	17.61	15.69	2.89	12.46
TNAs 6	14.10	12.20	3.50	21.58
TNAs 7	15.86	17.43	3.70	19.44
TNAs 8	17.47	19.75	2.67	15.16
TNAs 9	13.27	22.66	4.15	13.72
TNAs 10	12.49	11.04	2.93	16.19
TNAs 11	14.63	12.17	2.79	12.85
TNAs 12	16.80	15.11	3.06	22.39
TNAs 13	16.49	19.17	2.88	18.30
TNAs 14	14.42	18.01	3.13	25.83
TNAs 15	17.71	13.36	3.95	18.59
TNAs 16	14.23	19.75	2.98	20.31
TNAs 17	20.30	13.36	4.63	13.15
TNAs 18	16.21	20.25	3.28	14.97
TNAs 19	15.68	19.75	3.16	23.35
TNAs 20	19.57	17.19	3.00	11.89
TNAs 21	14.93	12.20	5.14	12.75
TNAs 22	17.46	15.11	4.93	16.37
TNAs 23	12.48	17.63	2.93	14.76
TNAs 24	18.24	13.79	3.77	18.67
TNAs 43	13.29	16.85	5.18	16.23
TNAs 44	16.31	16.85	2.67	18.19
TNAs 45	14.81	19.17	2.58	14.38
TNAs 46	14.77	10.46	2.88	14.15
TNAs 47	12.25	12.20	2.47	15.79
Kent	16.15	13.63	6.85	18.26
Mean	**15.50**	**16.29**	**3.54**	**17.45**
SE	**0.37**	**0.62**	**0.18**	**0.77**
Minimum	**12.17**	**10.58**	**2.47**	**11.89**
Maximum	**20.30**	**22.65**	**6.85**	**30.27**

CONCLUSION

Breeding for high yielding varieties is the primary objective of the breeders. The improvement of nutritional quality of the grains should also be given an important consideration. Genotypes with high grain nutrient content and high single plant kernel yield would be used for direct selection or hybridization. In contrast, high grain nutrient content genotypes with low yield potential would be useful for trait specific breeding improvements.

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