

ASSESSMENT OF OAT (*AVENA SATIVA* L.) GENOTYPES FOR FORAGE QUALITY BASED ON MORPHOLOGICAL PARAMETERS FOLLOWING DUS GUIDELINE

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ABSTRACT

The present Research was conducted in Livestock Farm, All India Coordinated Research Project on Forage Crop (AICRP), Department of Genetics and Plant Breeding, JNKVV, Jabalpur, Madhya Pradesh, India during *Rabi* season in 2021. This experiment was conducted on 16 Oat genotypes for the identification of morphological traits. The observations were recorded in three randomly selected genotypes of each replication for 9 different characters by using the guideline of distinctiveness, uniformity, and stability. The morphological traits of data were recorded on different genotypes of oat traits like Plant growth habit, Lowest leaves of hairiness of sheaths, Leaf blade-hairiness of margins of leaf below flag leaf, Time of panicle emergence, Stem hairiness of uppermost node, Panicle orientation of branches, Ligule shape, Plant length (cm), Panicle length (cm). The information on genotypic characterization plays a major role in the agronomical and morphological traits for the maintenance of genotypes in gene banks. The maximum number of erect plant growth habits (10) followed by weak leaves sheath hairiness (6), Strong leaf blade hairiness (7), medium time of panicle emergence (10), weak stem hairiness of uppermost node (6), erect type of panicle orientation of branches (6), unilateral type of panicle orientation of branches (6), Broad edged Ligule shape (9), medium plant length (6), long panicle length (6).

Key words : Oats, Morphological characterization, DUS guideline

Oats is (*Avena sativa* L.) an annual crop belonging to the Poaceae family, hexaploid group. Oats most likely evolved from *A. sterilis* (Trabut 1914) instead of *A. fatua* (Zade 1918). *A. sativa* is an allohexaploid have three distinct genomes, named A, B, and C (Nishiyama 1929; Rajhathy 1960). The genome of Progenitor is one of the *strigosas* group (Nishiyama 1929). *A. ventricosa* is a donor of C genome (Thomas 1970). B genome is normally a modified form of A genome (Sada sivaiah and Rajhathy 1968).

Oats play a major role in the cereal fodder crops to use as animal feed and for human consumption. Oats are sixth-ranked worldwide after maize, rice, wheat, barley, and sorghum. In 2012, the annual production of oats worldwide gives 21 million tonnes. 70% production of oats was major used for animal feeding production like horses,

cattle, sheep, and poultry. Other fodder legumes like berseem, lucerne, pea, and vetch grew with oats combination to increase the productivity per unit area.

Oats is the dietary food having physiological and nutritional characteristics of the highest β -glucan, fat-soluble vitamin E, and polyunsaturated fatty acids and other dietary fibre components like high tocopherol and natural antioxidant levels should increase as a demand of human need by using biofortification, represented by Zwer (2004).

MATERIALS AND METHODS

Experimental site

The experiment was conducted under the All India Coordinated Research Project on Forage crops,

Department of plant breeding and genetics at seed breeding form, college of Agriculture, Jawaharlal Nehru Krishi Viswa Vidyalaya, Jabalpur (M.P.).

Experimental materials

Plant materials used in the present experiment comprise 14 oat genotypes along with 2 checks collected from the AICRP project form, Jabalpur. The experiment was conducted in a randomized complete block design with two replication during *the Rabi* season in 2021.

Observation recorded

The following observations were recorded at a specific period of the growth stage. Following genotypes of characters viz., Plant growth habit, Lowest leaves of hairiness of sheaths, leaf blade-hairiness of margins of leaf below flag leaf, Time of panicle emergence, Stem hairiness of uppermost node, Panicle orientation of branches, Ligule shape, Plant length (cm), Panicle length (cm).

RESULTS AND DISCUSSION

Plant growth habit

The plant growth habit develops from specific a genetic pattern that determines growth. Environmental factors are the components that contribute to the physical nature of the plant. Plant growth habit is divided into erect, prostrate, semi prostrate. The plant growth habit was recorded during at juvenile stage angle of the tiller from vertical. Among 16 genotypes 10 genotypes were recorded as erect, 4 genotypes as semi-prostrate, and only 2 genotypes had prostrate-type plant growth. Similar results were identified by Gupta and Mehta (2018).

Hairiness of lowest leaf sheaths

The lower section of the leaf encloses the internode. This character was classified into four parts absence, weak, medium, and strong. This trait was observed in hairiness on the lowest leaves of the plant at 50% flowering stage. Out of 16 genotypes, four genotypes has not lowest leaf sheath, six genotypes were weak and two genotypes have medium, 4 genotypes were grouped into strong lowest leaves similar findings and grouping of genotypes based on

TABLE 1
Different category of morphological traits of oats

Traits	Categories or types	Symbols
Plant growth habit	Erect	E
	Semi prostrate	SP
	prostrate	P
Leaves sheaths hairiness	Absent	A
	weak	W
	medium	M
	strong	S
Leaf blade hairiness	Absent	A
	weak	W
	medium	M
	strong	S
Panicle emergence	Very early	VE
	Early	E
	Medium	M
	Late	L
	Very late	VL
Stem hairiness	Absent	A
	weak	W
	medium	M
	strong	S
Panicle orientation of branches	Erect	E
	unilateral	U
	sub unilateral	SUL
Ligule shape	Pointed	P
	Broad edged	BE
Plant length	Very short	VS
	Short	S
	medium	M
	Long	L
	Very long	VL
Panicle length	Very short	Vs
	Short	S
	medium	M
	Long	L
	Very long	VL

the hairiness of lowest leaf sheath were made by Sumathi *et al.*, (2004), Gupta and Mehta (2018), Ravi *et al.* (2021).

Leaf blade hairiness

The leaf blade is parts of the leaf above the sheath it's also referred to as the lamina. This character was recorded during at the time of the flowering stage. Found the margin of the leaf blade was hairiness below the flag leaf. This trait was classified into four parts absence, weak, medium, and strong. Five genotypes were grouped into an absence of hairiness, 4 genotypes had weak, and One genotype had only medium. The remaining 6 genotypes were divided into strong leaf blade hairiness. The result was supported by Sumathi *et al.*, (2004), Gupta and Mehta (2018), and Ravi *et al.*, (2021).

TABLE 2
Morphological Characterization of Oat

Characters	Genotypes															
	NDO 1	JMO 42	JMO 248	JMO 259	JMO 271	JMO 276	JMO 304	JMO 310	JMO 316	JMO 239	KENT	JO 1	JO 5	JHO 822	OS-6	UPO 212
Plant growth habit	E	SP	E	E	E	E	E	E	E	E	p	SP	E	SP	SP	P
Leaf sheath hairiness	A	W	M	W	W	M	S	S	S	S	A	A	W	W	A	W
Leaf blade hairiness	W	W	M	W	S	S	S	S	S	S	A	A	A	A	A	W
Time of panicle emergence	M	M	M	M	M	M	M	L	L	VL	E	M	VL	M	E	M
Stem hairiness of uppermost node	S	S	M	M	S	S	S	W	W	A	W	W	W	W	M	M
Panicle orientation of branches	SUL	SUL	U	E	U	SUL	U	SUL	U	U	E	U	E	E	E	E
Ligule shape	P	BE	BE	P	BE	BE	BE	BE	BE	BE	P	P	P	BE	P	P
Plant length (cm)	M	M	M	M	L	L	M	L	L	VL	VS	M	S	S	VS	S
Panicle length (cm)	M	M	L	L	L	L	L	L	VL	VL	S	M	M	S	S	M

**Stages of observation: 50% flowering time.

Panicle emergence

The time of flower initiation is a growth stage that represents the reproductive phase in oats development. Flower initiation is divided into early, medium, late emergence, and the very late emergence of the panicle. This attribute was recorded during 50% flower initiation stage. Observed the panicle emerged at the time of flower initiation. Two genotypes were recorded as early, 10 genotypes were found in medium and 2 genotypes were late emergences of panicle and the remaining 2 genotypes had a very late time of panicle emergence. Similar results were reported by Sumathi *et al.*, (2004), and Gupta and Mehta (2018).

Stem hairiness of uppermost node

The link region between a leaf and stem is called a node. The connection between the two nodes' regions is called an internode. This trait was classified into weak, medium, strong, and very strong. This trait was observed during 50% flowering time. Found the hairiness of the node. The 6 were classified as weak, 4 classified as medium stem followed by 5 as strong stem, and only one had absent hairiness uppermost

node. They do not have very strong stem hairiness uppermost node. The result was identified by Sumathi *et al.*, (2004), and Gupta and Mehta (2018).

Panicle orientation of branches

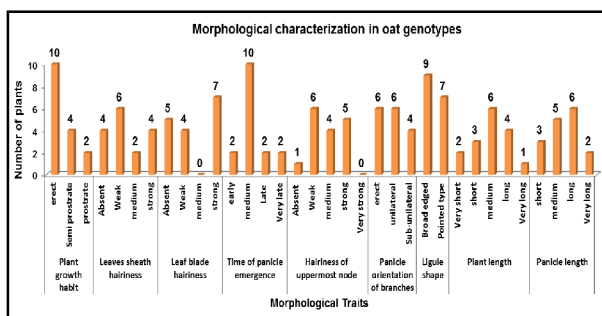
Panicle attitude character was observed at the time of 50% flowering time stage. Found the different attitude branches of the panicle. Out of 16 genotypes, 6 were grouped found as erect panicle attitude type. 6 genotypes are classified as unilateral type, and 4 genotypes were classified as sub-unilateral type. Sumathi *et al.*, (2004) reported similar results.

Ligule shape

The ligule shape is the outgrowth at the inner junction of the leaf sheath and leaf blade. The ligule shape was observed during at the time of 50% flowering time stage. The papery shape of the membrane is positioned between the leaf sheath and the leaf blade. Based on ligule shape 16 genotypes were classified 9 genotypes were pointed type 7 genotypes were found to be broad-edged type. Ravi *et al.*, (2021) and Gupta and Mehta (2018) identified similar results.

Plant length (cm)

The plant height was observed during at the time of 50% flowering time stage. Among the 16 genotypes, two were found as very short, 3 only divided as short, 6 genotypes were grouped as medium, 4 genotypes were grouped into long plant lengths and only one had as very long. Found similar results from Sumathi *et al.*, (2004), Gupta and Mehta (2018), and Ravi *et al.*, (2021).



Graph 1. Morphological Characterization in Forage Oat genotype.



Classification of plant growth habit

Plate 1. Unilateral panicle.

Plate 2. Semi-prostrate type plant growth.

Plate 3. Semi-erect type plant growth.

Plate 4. Semi-erect type plant growth.

Panicle length (cm)

The panicle length was observed during at the time of harvesting stage. The panicle length was observed with scale. Based on panicle length, 16 genotypes were grouped into 3 genotypes were divided into short, 5 genotypes were recorded as medium and 6 genotypes had long, only 2 genotypes were divided as very long. Sumathi *et al.*, (2004), Gupta and Mehta (2018), and Ravi *et al.*, (2021) reported similar results.

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