The Pharma Innovation Journal 2022; 11(11): 413-417

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(11): 413-417

www.thepharmajournal.com
Received: 01-09-2022
Accepted: 07-10-2022

Priyanka Kumari
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Jenny Priya
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Ekka, Swapnil
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Krishna Prasad
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Ekhlaque Ahmad
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Manigopa Chakraborty
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Corresponding Author:
Ekhlaque Ahmad
Department of Genetics & Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand, India

Inheritance pattern of awn characteristics in f_7 generation of rice (*Oryza sativa* L.) cross pusa-1174 and BPT-5204

Priyanka Kumari, Jenny Priya Ekka, Swapnil, Krishna Prasad, Ekhlaque Ahmad and Manigopa Chakraborty

Abstract
The present investigation was executed at the experimental plot of Birsa Agricultural University, Kanke under the rainfed conditions of Jharkhand, India during *kharif* 2021 in the F7 generation seeds of the cross Pusa-1176 x BPT-5204 sown as panicle to progeny rows at two different dates as set I and set II with the interval of 15 days in order to study the influence of environment on the traits under study. The research has been chiefly emphasized on the study of genetic behaviour and segregation pattern of the awn characters in rice which includes presence of awns and awn colour. The observations were recorded morphologically in the F_7 generation families of the cross Pusa-1176 and BPT-5204and thereafter, expected genetic ratios have been computed based on the observations recorded using chi-square test. The genetic ratios obtained from the segregating families were monogenic as well as digenic for both the awn characters concluding that it is governed by single gene or two genes depending on the segregation pattern. Hence, the results showed that family no. 42, 44, 62, 83 and 84 for the trait presence of awns and family no. 42, 44, 62, 72, 211, 288 and 309 for awn colour showed varied segregation pattern in set I and set II revealing the effect of changes in temperature and photoperiod. But the respective segregation ratio was found similar in the family no. 84 and 230 for the presence of awns and family no. 83, 84, 230 and 275 for awn colour in both the sets concluding that the behaviour and expression of genes were persistent and remained unaffected by the environmental fluctuations.

Keywords: Inheritance, segregation, chi-square, gene action, dominant, recessive

Introduction
Rice (*Oryza sativa* L.) is a monocot plant that belongs to Poaceae family. It is one of the major staple food crops for approximately 3.5 billion people who depends on this crop for nearly 20% of their regular calorie intake and thereby considered as a lifeline for food and nutritional security (Ricepedia, 2020) [21]. It is basically cultivated under diverse ecosystems ranging from irrigated to rainfed upland to rainfed lowland to deep water. At the end of fiscal year 2020, India had approximately 44 million hectares of land area for cultivation of rice out of which the total area under rainfed lowland and upland rice is 14.4 and 6.3 million ha, respectively. This area under rice had been relatively consistent over during the past three years and it was the most produced food grain across the south Asian nation (Anonymous, 2021) [1]. The production of rice in India was estimated to be approximately 2.7 thousand kilograms per hectare. Although a consistent increase in the yield of rice was noted since fiscal year 1991 (Anonymous, 2021) [1], the production and productivity is still thought to be enhanced in order to meet the demands of expected global population in future and perform better in reduced cultivable land. Therefore, the need of the hour is to increase the rice grain yield per unit area that is essentially crucial for ensuring food security, particularly in developing countries in Asia, such as in China and India. Nevertheless, yield of rice is contributed by several yield attributing traits such as traits number of plants per unit area, number of panicles per plant, grain number per panicle (GNPP) and grain weight etc. the present research work has been emphasized on the genetic studies of awn characters in rice plants that plays the least role in yield improvement.
Awn is a characteristic of various plants and present in the species of poaceae family such as rice, wheat, and barley as well as for many forage grass species (Gu, *et al*. 2005) [8]. It is either a hair- or bristle-like appendage that typically extends from the lemmas of spikelets and varies in their rate of development, length, diameter and bristle length.

It is generally considered as a wild trait that has been reduced in the domesticated plants. In earlier period, presence of awns contributed to seed dispersal by wind and by sticking to animal's fur promoting range expansion. Moreover, it protected the crop from predators thereby safeguarding the produces. Therefore, quality aspects associated to awn characteristics have been of interest primarily during domestication where short-awned or awnless species have been preferred because they were easier to handle and process (Yuo *et al.* 2012) [29].

Morphologically, awn is a triangular-shaped at its cross-section, with the base oriented towards the rachis and containing vascular bundles and chlorenchyma cells with the potential to improve the photosynthetic capacity of the canopy (Yuo *et al.* 2012) [29]. The positive correlation between awns and yield-related traits such as grains per plant, grain size, and kernel weight has been reported in some cereal crops such as wheat and barley (Ntakirutimana *et al.* 2020) [19], whereas the contribution of awns to grain yield of rice is almost negligible. Awns are considered less important trait in rice crop for yield potential because through many studies it has been revealed that there were no significant differences between awned and awnless genotypes (Furuta *et al.* 2015; Jin *et al.* 2009) [6, 11]. However, the correlation between yield and development is not clearly recognized in rice. The genetic basis of the effect of awns on yield-related traits and their influence on grain yield is not well understood although several pathways involved in the development of awns have been characterized on molecular level in rice crop (Ntakirutimana *et al.* 2019) [18]. Recent studies have provided an overview on genes involved in the awn development (Mach *et al.* 2015; DeWitt *et al.* 2020) [14, 20] and several genes were identified that are involved in the development of awns in rice such as An-1 (Luo *et al.* 2013) [13], An-2 (Gu *et al.* 2015) [7], Laba1 (Hua *et al.* 2015) [9], Gad1 (Jin *et al.* 2016) [12] and RAE3 (Furuta *et al.* 2015) [6]. However, the current knowledge regarding interaction of these genes with yield and yield attributing traits such as grain number per panicle and kernel size and weight etc. is not satisfactory and the debate is still going on among scientists. (Huang *et al.* 2020, Bessho-Uehara *et al.* 2016) [10, 2]. But the effect of the genes An-1, An-2, and Laba1 etc. was found to be neutral on grain yield and several molecular studies on these genes indicated that these genes were associated with reduced total grain yield as compared to their mutant alleles.

The negative impact of awn development in rice on its yield have been reported by many researchers (Luo *et al.* 2013; Gu *et al.* 2015; Jin *et al.* 2016) [13, 12]. The reason behind the undesirable effect of awns in rice is lack chlorenchyma cells or contain only one vascular bundle (Luo *et al.* 2013) [13] and this explains why rice awns are not photo synthetically active and cannot contribute to photosynthesis (Toriba *et al.* 2010) [27]. However, in some landraces of rice (e.g., Tipakhiya, Sathi), the presence of awns helps in preventing water loss and moreover, the consequences of awn removal in these varieties leads to spikelet sterility and uneven or arbitrary distribution within the panicles (Singh *et al.* 2009) [25]. Therefore, the objective of the present research programme is to study the genetic behaviour of awn characters in rice crop i.e. presence of awns and awn colour and computation of the expected Mendel's ratios in order to know the segregation pattern of the traits under study that would also illustrate that how many genes govern the traits.

Materials and Methods

The present investigation was carried out at the experimental plot of Birsa Agricultural University, Kanke under the rainfed conditions of Jharkhand, India during kharif 2021. The F7 generation seeds of the cross Pusa-1176 x BPT-5204 was sown as panicle to progeny rows on the seed bed nursery and thereafter transplanted into the field. Sowing was done in at different dates as set I and set II with the interval of 15 days in order to study the influence of environment on the traits under study. However, to understand the genetic behaviour and to reveal out the gene action of awn characters in rice, observations were recorded based on the morphology of awn characters such as presence of awns and awn colour in progeny rows grown in the field. The variations in awn characters among the segregants were noticed due to the awning feature of one of the parents of the cross i.e. from Pusa-1176. Both the characters related to awns were classified into two distinct classes on the basis of presence of awns (awn present/awn absent) and colour of awns (awn coloured/awn colourless). From the first set of progeny rows that was sown, only 12 out of 43 families were observed to be segregating for the presence of awns and rest 31 families were found to be fixed. Furthermore, 22 families showed segregation for awn colour and the rest 21 were fixed. In the other set that was sown late i.e. after the interval 15 days, 13 out of 29 families were found to be segregating and rest seemed to be fixed for the presence of awns in progeny rows. However, 14 families segregated for awn colour and rest of the them were found to be fixed.

Thereafter, expected genetic segregation ratio was calculated for both the traits i.e. presence of awns and awn colour in each of the segregating families and was tested for goodness of fit by using chi-square test (Pearson, 1900) with the formula given below.

$$\chi^2 = \Sigma (O - E)^2 / E$$

Where, 'O' is the Observed frequency and
'E' is the Expected frequency

Results

The genetic ratios obtained after testing the goodness of fit have been presented in the table given below representing the genetic behaviour and the scenario of gene interactions for the awn characters i.e. presence of awns (Table I) and awn colour (Table II) of the F7 generation families sown in the first set and the second set sown after the interval of 15 days.

For the trait presence of awns (Table I), first set of families sown revealed that family no. 95 and 230 exhibited 3:1 (awned/awnless). The families that showed digenic ratio of 9:7 (awned/awnless) were family no. 44, 84,455 and 323 but family no. 168 revealed reverse ratio i.e. 7:9 (awned/awnless). Family no. 42, 62 and 156 exhibited 15:1 (awned/awnless) and family no. 4 was observed to show the ratio of 1:15 (awned/awnless). In the other set, 3:1 (awned/awnless) ratio was computed in the family no. 44, 72, 230 and 322 and the ratio of 9:7 (awned/awnless) was exhibited in the family no. 82, 83, 84, 92, 309, and 321 but family no. 95 showed reverse ratio i.e. 7:9 (awned/awnless). The family no. 42 and 62 was found to be fit in the ratio of 13:3 (awned/awnless).

The results of the trait awn colour (Table 2) for the first set of families sown showed 3:1(coloured /colourless) monogenic ratio in the family no. 42, 288 and 301 and 1:3 (coloured

/colourless) was observed in the family no. 168, 230, 286, 309 and 359. The ratio of 9:7 (coloured /colourless) was obtained only in the family no. 62 but 7:9 (coloured /colourless) ratio was computed in the family no. 44, 323 and 455. The family no. 156, 211 and 392 exhibited the ratio of 15:1 (coloured /colourless) and the genetic ratio of 1: 15 (coloured /colourless) was found to be observed in the family no. 4, 72, 83, 84, 92, 95 and 275. The other set of the families revealed that family no. 71, 211 and 322 was found to be fit in the ratio of 3:1 (coloured /colourless) and family no. 72 and 230 showed reverse of it i.e. 1:3 (coloured /colourless). The ratio of 9:7 (coloured /colourless) was computed for the family no. 44, 309 and 321 and the ratio of 13:3 (coloured /colourless) was found to be obtained in the family no. 42, 62 and 288 but reverse ratio of 1:15 (coloured /colourless) was observed in the family no. 83, 84 and 275.

Furthermore, number of families that showed segregation for the trait presence of awns (fig. 1) and awn colour (fig. 2) has been represented graphically according to their expected genetic ratios computed through chi-square test.

Table 1: Expected genetic segregation ratios computed for the awn character (presence of awns) in F_7 families of the cross Pusa-1174 and BPT-5204

Set I								Set II						
S/ No.	Family No.	Observed values		Total population	Expected genetic ratio	Chi-square value	P-value	Family No.	Observed values		Total population	Expected genetic ratio	Chi-square value	P-value
		Awn present	Awn absent						Awn present	Awn absent				
1	95	109	49	158	03:01	3.046	0.081	44	50	24	74	03:01	2.18	0.140
2	230	15	5	20	03:01	0	1.000	322	4	2	6	03:01	0.222	0.638
3	44	6	4	10	09:07	0.057	0.811	72	2	1	3	03:01	0.111	0.739
4	84	33	24	57	09:07	0.063	0.802	230	2	1	3	03:01	0.111	0.739
5	455	13	11	24	09:07	0.042	0.838	83	73	58	131	09:07	0.015	0.903
6	323	7	4	11	09:07	0.244	0.621	92	3	2	5	09:07	0.029	0.865
7	168	2	3	5	07:09	0.029	0.865	309	1	1	2	09:07	0.032	0.858
8	83	121	27	148	13:03	0.025	0.874	84	53c	37	90	09:07	0.255	0.614
9	42	56	4	60	15:01	0.018	0.893	82	58	44	102	09:07	0.016	0.899
10	156	25	1	26	15:01	0.256	0.613	321	8	6	14	09:07	0.005	0.944
11	62	37	1	38	15:01	0.849	0.357	95	72	87	159	07:09	0.152	0.697
12	4	2	25	27	01:15	0.062	0.803	62	8	1	9	13:03	0.345	0.557
13	-	-	-	-	-	-		42	30	5	35	13:03	0.458	0.499

Table 2: Expected genetic segregation ratios computed for the awn character (awn colour) in F_7 families of the cross Pusa-1174 and BP-T5204.

Set I								Set II						
S/ No.	Family No.	Observed values		Total population	Expected genetic ratio	Chi-square value	P-value	Family No.	Observed values		Total population	Expected genetic ratio	Chi-square value	P-value
		Awn coloured	Awn colourless						Awn coloured	Awn colourless				
1	42	103	37	140	03:01	0.152	0.697	211	3	1	4	03:01	0.000	1.000
2	301	8	2	10	03:01	0.133	0.715	322	4	2	6	03:01	0.222	0.638
3	288	15	5	20	03:01	0.000	1.000	71	3	1	4	03:01	0.000	1.000
4	309	25	59	84	01:03	1.016	0.313	72	1	2	3	01:03	0.111	0.739
5	230	3	17	20	01:03	1.067	0.302	230	1	2	3	01:03	0.111	0.739
6	359	3	7	10	01:03	0.133	0.715	309	49	25	74	09:07	2.987	0.084
7	286	4	21	25	01:03	1.080	0.299	44	18	15	33	09:07	0.039	0.843
8	168	1	4	5	01:03	0.067	0.796	321	8	6	14	09:07	0.005	0.944
9	62	25	13	38	09:07	1.405	0.236	62	47	6	53	13:03	1.920	0.166
10	44	11	14	25	07:09	0.001	0.975	42	20	7	27	13:03	0.913	0.339
11	455	10	14	24	07:09	0.042	0.838	288	14	4	18	13:03	0.142	0.706
12	323	4	7	11	07:09	0.244	0.621	83	3	41	44	01:15	0.024	0.877
13	392	39	4	43	15:01	0.684	0.408	275	1	12	13	01:15	0.046	0.830
14	156	25	1	26	15:01	0.256	0.613	84	6	76	82	01:15	0.159	0.690
15	211	17	1	18	15:01	0.015	0.903	-	-	-	-	-	-	
16	95	2	63	65	01:15	1.117	0.291	-	-	-	-	-	-	
17	275	1	14	15	01:15	0.004	0.950	-	-	-	-	-	-	
18	83	2	17	19	01:15	0.593	0.441	-	-	-	-	-	-	
19	84	6	134	140	01:15	0.922	0.337	-	-	-	-	-	-	
20	4	2	25	27	01:15	0.062	0.803	-	-	-	-	-	-	
21	72	1	39	40	01:15	0.960	0.327	-	-	-	-	-	-	
22	92	1	12	13	01:15	0.046	0.830	-	-	-	-	-	-	

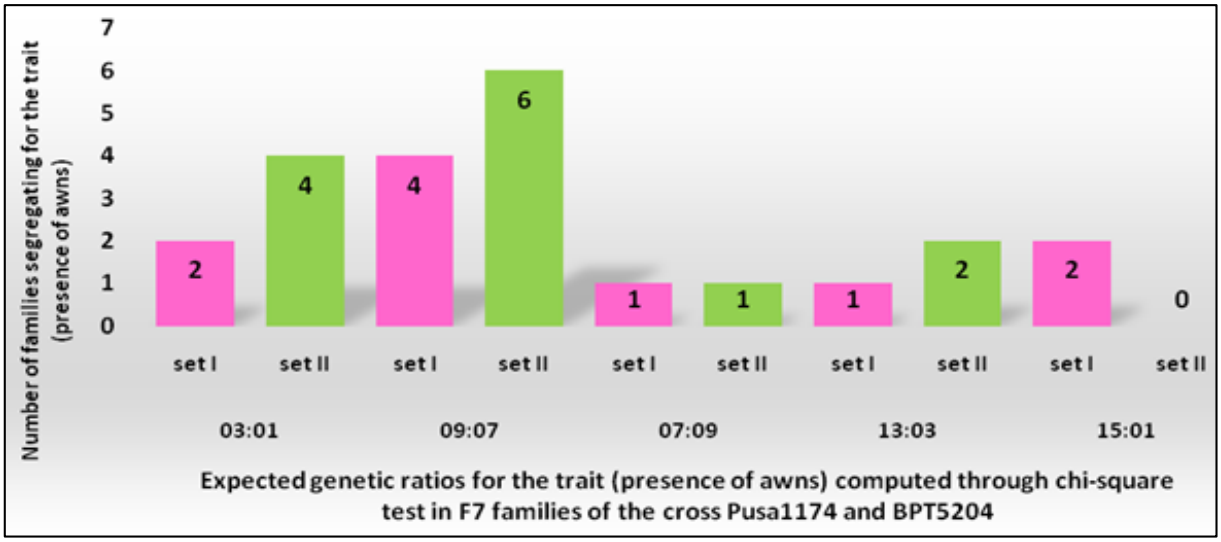

Fig 1. Graphical representation of number of families segregating for the trait (presence of awns) and expected genetic ratios for the trait (presence of awns) computed through chi-square test in F_7 families of the cross Pusa-1174 and BPT-5204.

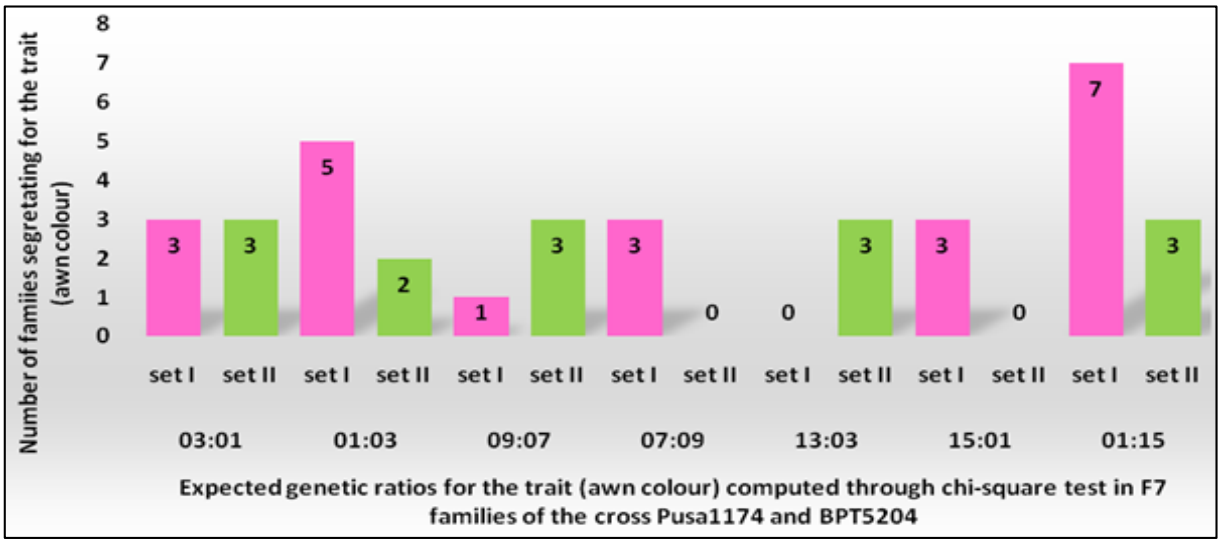

Fig 2. Graphical representation of number of families segregating for the trait (presence of awns) and expected genetic ratios for the trait (presence of awns) computed *through* chi-square test in F_7 families of the cross Pusa-1174 and BPT-5204.

Discussion

The study of genetic ratios was accomplished in the segregating families by using chi-square test and discovered both monogenic as well as digenic ratio among the F7 families. Expected genetic ratios have been computed for each segregating family in order to know the segregating pattern in terms of Mendel's ratio which would determine the interaction of two or more genes that controls the trait under study i.e. presence of awns and awn colour. Several kinds of genetic ratios have been obtained among the F7 generation families for both the traits. Monogenic ratio of 3:1(awned/awnless) indicated that the trait is governed by single dominant gene and reverse of this ratio i.e. 1:3 indicated that the trait is governed by recessive gene. Similar results which showed awn development as dominant trait were reported by Bharadwaj *et al.* (2007) [3], Tomar *et al.* (2000) [26] and Deepak *et al.* (2016) [4] for the awn character. It is also supported by Hoshino (1915), Nagao (1936) [17] and Yamaguti (1926) [28]. However, Nadaf *et al.* (1995) [16] reported awning behaviour as recessive trait. The results in the present research work also exhibited several forms of digenic ratios such as 9:7, 15:1, 13:3 and even reverse of these ratios which indicated that the trait under study is governed by two genes. Among the digenic ratios mentioned, the ratio 9:7 indicated complementary gene action in which recessive alleles at either of the two loci can mask the expression of dominant alleles at the two loci, the ratio 15:1 indicated duplicate gene action in which a dominant allele at either of two loci can mask the expression of recessive alleles at the two loci and the ratio 13:3 indicated inhibitory gene action in which a dominant allele at one locus can mask the expression of both dominant as well as recessive alleles at second locus. These results were supported by Shobha Rani *et al.* (2005) [24] and showed that expression of awned trait was governed by complementary genes with a dihybrid segregation ratio of 9:7 (awned/awnless) in F2 generation. The genetic ratio of 15:1 was reported by Mitra and Ganguli (1992) [15]. Sahu *et al.* (2018) [22] reported that segregation ratio of awn closely fitted with 13: 3 digenic ratio. For the awn character, trigenic ratios (63:1) have also been reported by Deepak *et al.* (2016) [4] and Sethi (1997) [23] but it was not found in the present study.

Conclusion

Thus, the above obtained results exhibited that family no. 42, 44, 62, 83 and 84 for the trait presence of awns and family no. 42, 44, 62, 72, 211, 288 and 309 for awn colour showed varied segregation pattern in set I and set II that displayed the influence of changes in temperature and photoperiod. But the respective segregation ratio was found similar in the family no. 84 and 230 for the presence of awns and family no. 83, 84, 230 and 275 for awn colour in both the sets concluding that the behaviour and expression of the concerned genes were found persistent in both the sets sown and remained unaffected by the environmental fluctuations.

Acknowledgement

Authors are grateful to Birsa Agricultural University, Ranchi, Jharkhand for providing assistance and various facilities required for conducting the research programme.

References

1. Anonymous. Statista Research Department; c2021.
2. Bessho-Uehara K, Wang DR, Furuta T, Minami A, Nagai K, Gamuyao R *et al*. Loss of function at RAE2, a previously unidentified EPFL, is required for awnlessness in cultivated Asian rice. Proc. Natl. Acad. Sci. USA, 2016;113:8969-8974.
3. Bharadwaj C, Mishra R, Sathyavathi CT, Rao SK. Dominant gene for awn character in rice (*Oryza sativa* L.). Indian Journal of Agricultural Sciences. 2007;77(9):61-62.
4. Deepak P, Laxmi PS, Sharma RC. Inheritance of growth habit, awnedness and spikelet shattering in interspecific cross of rice (*Oryza sativa* L. × *O. rufipogon* Griff). Azarian Journal of Agriculture. 2016;3(4):82-85.
5. DeWitt N, Guedira M, Lauer E, Sarinelli M, Tyagi P, Fu D, *et al*. Sequence-based mapping identifies a candidate transcription repressor underlying awn suppression at the B1 locus in wheat. New Phytol. 2020;225:326-339.
6. Furuta T, Komeda N, Asano K, Uehara K, Gamuyao R, Angeles-Shim RB, *et al*. Convergent loss of awn in two cultivated rice species *Oryza sativa* and *Oryza glaberrima* is caused by mutations in different loci. G3 Genes Genomes Genet. 2015;5:2267-2274.
7. Gu B, Zhou T, Luo J, Liu H, Wang Y, Shangguan Y, *et al*. An-2 Encodes a Cytokinin Synthesis Enzyme that Regulates Awn Length and Grain Production in Rice. Mol. Plant. 2015;8:1635-1650.
8. Gu XY, Kianian SF, Foley ME. Phenotypic selection for dormancy introduced a set of adaptive haplotypes from weedy into cultivated rice. Genetics. 2005;171:695-704.
9. Hua L, Wang DR, Tan L, Fu Y, Liu F, Xiao L, *et al*. LABA1, a domestication gene associated with long, barbed awns in wild rice. Plant Cell. 2015;27:1875-1888.
10. Huang D, Zheng Q, Melchkart T, Bekkaoui Y, Konkin DJF, Kagale S, *et al*. Dominant inhibition of awn development by a putative zinc-finger transcriptional repressor expressed at the B1 locus in wheat. New Phytol. 2020;225:340-355.
11. Jin FX, Kim DM, Ju HG, Ahn SN. Mapping quantitative trait loci for awnness and yield component traits in isogenic lines derived from an *Oryza sativa/O. rufipogon* cross. J Crop Sci. Biotechnol. 2009;12:9-15.
12. Jin J, Hua L, Zhu Z, Tan L, Zhao X, Zhang W, *et al*. GAD1 encodes a secreted peptide that regulates grain number, grain length and awn development in rice domestication. Plant Cell. 2016;28:2453-2463.
13. Luo J, Liu H, Zhou T, Gu B, Huang X, Shangguan Y, *et al*. An-1 encodes a basic helix-loop-helix protein that regulates awn development, grain size, and grain number in rice. The Plant Cel. 2013;25:3360-3376.
14. Mach J. Domesticated versus wild rice? Bring it awn! Am. Soc. Plant Biol; c2015.
15. Mitra SK, Ganguli PM. Some observations on the characters of wild rice hybrids. Indian Journal of Agricultural Science. 1992;32:271-279.
16. Nadaf SK, Goud JV, Parameshwarappa R. Genetic studies in rice (*Oryza sativa* L.): inheritance of four spikelet characters. Indian Journal of Genetics and Plant Breeding. 1995;55(4):351-636.
17. Nagao S. Genetics and Breeding in Rice (in Japanese), Tokyo; c1936. p. 72.
18. Ntakirutimana F, Xie W. Morphological and genetic mechanisms underlying awn development in monocotyledonous grasses. Genes. 2019;10:573.
19. Ntakirutimana F, Xie W. Unveiling the actual functions of awns in grasses: From yield potential to quality traits. Int. J Mol. Sci. 2020;21:7593.
20. Pearson K. On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. Philos Mag Ser. 1900;50:157-75.
21. Rice Pedia, http://ricepedia.org/rice-as-food/, accessed on 15 June 2020.
22. Sahu GR, Burman M, Nair SK, Sarawgi AK, Rao RK. Genetic Behaviour of Awning Character in Rice (*Oryza sativa* L.). Int. J Curr. Microbiol. App. Sci. 2018;7(5):490-493.
23. Sethi BL. Annual report of rice. Rice Research Station, Nagina; c1996-1997.
24. Shobha Rani N, Pandey MK, Prasad GSV, Kumar D. Inheritance of hull colour and awns in short grain aromatic rices: In 5th International Rice Genetic Symposium and 3rd International Rice Functional Genomic Symposium 19-23 Nov, IRRI, Manila, Philippines; c2005.
25. Singh S, Singh TN, Chauhan JS. Architectural engineering of rice panicle for increased productivity: A powerful Biological Tool for Combating Agricultural Water Crisis. J Crop Improv, 2009;23:451-466.
26. Tomar JB, Prasad SC, Madhukumari. Genetics of morphological characters in rice (*O. sativa* L.). Indian J Agril. Sci. 2000;7(11):736-740.
27. Toriba T, Suzaki T, Yamaguchi T, Ohmori Y, Tsukaya H, Hirano HY. Distinct regulation of adaxial–abaxial polarity in anther patterning in rice. *Plant Cell*. 2010;22(604:1452-1462.
28. Yamaguti Y. Kreuzungsuntersuchugen an Reispflanzen. I. Genetische Analyse der Granne der Sorten des Reis. Ber. Ohara Inst. 1926;3:1-120.
29. Yuo T, Yamashita Y, Kanamori H, Matsumoto T, Lundqvist U, Sato K, *et al*. A short internodes (SHI) family transcription factor gene regulates awn elongation and pistil morphology in barley. J Exp. Bot., 2012;63:5223-523.