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New sources of tasselless mutation

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A very large diversity of genes was described and located in maize, including genes that determine the structure and functioning of generative system. One of these systems, based on CMS and fertility restoring genes is used in hybrid seed production. An alternative to the androsterility type is the tasselless mutation, first described more than four decades ago (Micu V.E., 1970, Genetica, v.6:2, p.21-27).

In order to highlight possible sources of tasselless mutation during 2010-2012 we have conducted an observational research in the collection of lines, that include 720-1000 patterns of 293 lines, descending from 80 distinct genetical sources which contain a wide diversity of biological and morphological traits. All observed material consists of inbred lines at S_7 - S_9 . In previous generations no similar mutations were noticed.

The results of the research made in 2011-2012 is summarized in the table. In 2011 the tasselless mutation was observed in source HM 77. In 2012 the tasselless mutation was observed in 4 other sources. In order to determine the genetical character of tasselless mutation the mutants from each source were pollinated with normal plants from their source. The tasselless mutation from source HM 77, observed in 2011 and 2012, proves to be hereditary. For further research of this mutation we have obtained 59 inbred crosses $tls\ X\ normal$. Morphological expression of this character is gradual – from partial reduction to total absence of tassels (figures 1 and 2). Revealing mutant plants in S_7 - S_9 (and not earlier) indicates to a possible polygenic hereditary base of tasselless mutation in studied sources.

Table 1. Sources of tasselless mutation

Nr.	Source	Number of patterns	Number of plants
		, p	total / tasselless
1	HM 13 (S ₉)	3	44/11
2	HM 47 (S ₉)	3	52/16
3	HM 75 (S ₉)	1	15/11
4	HM 77 (S ₇ -S ₉)	2	118/37
5	Descendent from B73 line (S ₇)	1	25/16

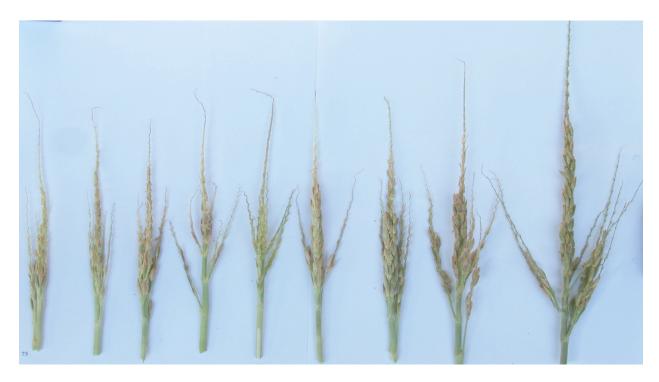


Figure 1. Gradual expression of tasselless mutation (source HM 77)



Figure 2. Tasselless mutation (Source HM 77)