Densinodosum - a new gene on linkage group III

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Among numerous mutation types following treatment of dry seeds of Wt 3527 (cv. Paloma) with a combined dose 200 *r Nf* + 0.014 % NEU the *densinodosum* mutant gene was selected in the M_2 generation (2). After multiplication the line was included to the *Pisum* Gene Bank at Wiatrowo with the catalogue number Wt 11242. The name *densinodosum* is justified by a phenotype—mutant plants in comparison to the initial line have shorter stem with a larger number of nodes (Table 1). Number of nodes to the first flower remains unchanged.

Table 1. Selected, morphological characters of *densinodosum* mutant plants and initial line Wt 3527.

Line	Stem length (cm)	Number of nodes	Number of nodes to the 1st flower
Wt 3527 (Paloma) -initial	**41.0**	**18.2**	**13.8**
Wt 11 242 (*dnd* – mutant)	**33.1**	**21.5**	**13.9**

After multiplication of mutant plants, aspects of dry seed yield were also compared (Fig. 1). It appeared that the *densinodosum* mutant produced higher yield thanks to a larger number of pods and seeds per plant. Thousand grain weight is smaller.

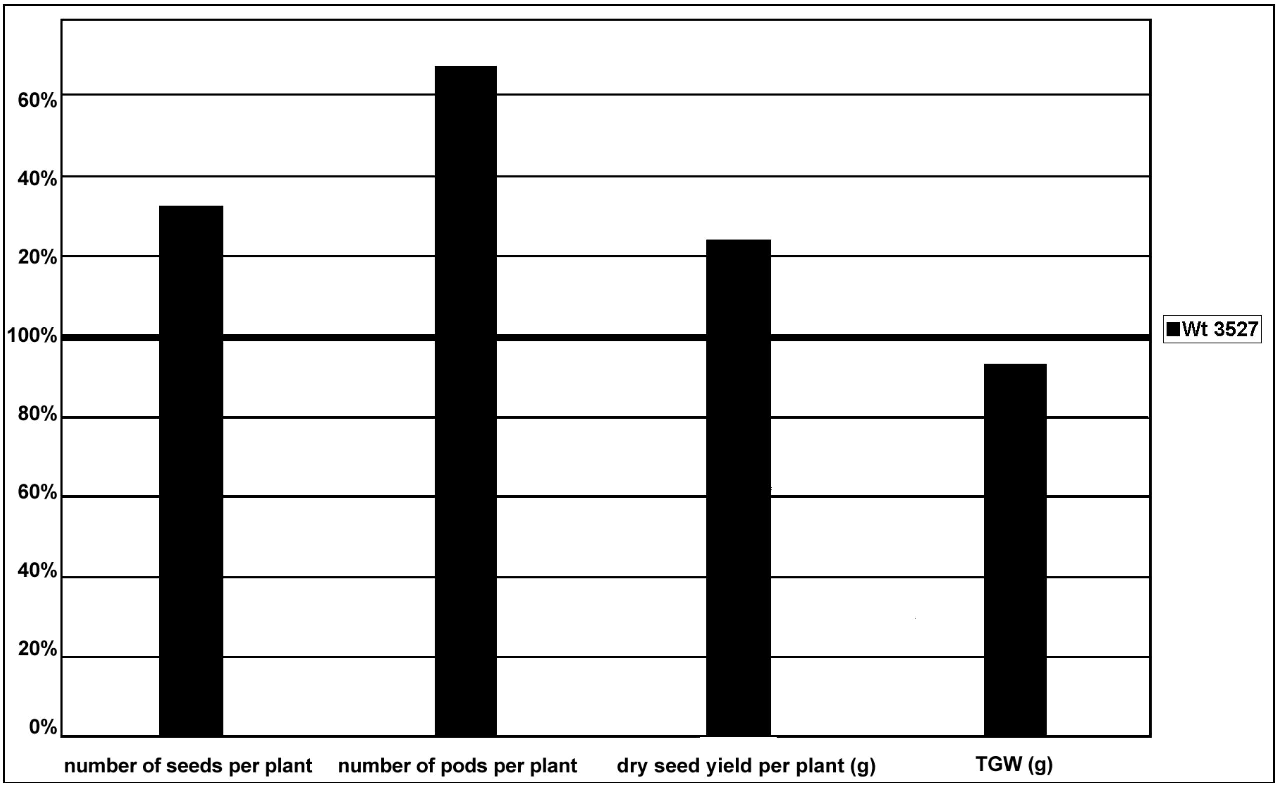

Fig. 1. Aspects of dry seed yield of densinodosum *mutant plants related to the initial line Wt 3527 = 100%.*

The locus identity test cross for the *densinodosum* and two genes with a similar phenotype, *art*1 and *art*2, was conduced (3). F_1 plants of all cross combinations were normal, suggesting that *densinodosum* (Wt 11242) and *arthritic* mutants (Wt 16126 - *art*1 and Wt16125 - *art*2) are not allelic.

For mapping the new mutant gene the line Wt 11242 was crossed with the set of tester lines with markers for seven linkage groups. An analysis of a monohybrid segregation in F_2 generations showed Mendelian, recessive nature of the new gene (Table 2.). The symbol *dnd* is suggested. Undisturbed, monohybrid segregation of most of observed markers was also observed.

Table 2. Monohybrid segregation for the investigated gene *dnd* and gene markers in the linkage group III observed in F_2 populations of the following linkage test crosses: K. 1140 = Wt 11242 x Wt 11540; K. 1139 = Wt 11242 x Wt 11538; K. 1137 = Wt 11242 x Wt 11777; K. 1135 = Wt 11242 x Wt 11238; K. 1136 = Wt 11242 x Wt 11288; K. 1864 = Wt 10357 x Wt 11242; K. 1866 = Wt 11242 x Wt 15327; K. 1973 = Wt 11242 x Wt 15298.

Cross combination	Gene	Allele		Total	*Chi* square* (3:1)
		dominant	recessive		
K. 1140	*Dnd*	80	27	107	0.00
K. 1139	*Dnd*	80	25	105	0.08
K. 1137	*Dnd*	84	19	103	2.36
K. 1135	*Dnd*	107	36	143	0.00
K. 1136	*Dnd*	140	50	190	0.18
K. 1864	*Dnd*	97	19	116	4.60
K. 1866	*Dnd*	211	52	263	3.83
K. 1973	*Dnd*	268	71	339	2.97
K. 1136	*B*	106	30	136	0.63
	St	148	47	195	0.08
	M	99	39	138	0.78
K. 1864	*Uni*	93	25	118	0.92
	Apu	87	31	118	0.10
K. 1866	*M*	69	22	91	0.03
	Chi 32	197	64	261	0.03
K.1973	*Lum2*	285	65	350	7.71
	M	173	56	229	0.04

* $\chi^2 = 3.84$

Observations of plants in F_2 generations gave undisturbed dihybrid segregations for gene pairs *dnd*—gene marker for linkage groups I, II, IV, V, VI and VII. Disturbed, dihybrid segregation was found in the cross combination K. 1136 for *dnd-M* from linkage group III with *Cr-O* value 15.8 (Table 3). However, *dnd* did not show linkage with either *b* or *st* in K. 1136 or with uni^{tac} or *apu* in the cross combination K. 1864.

Two chlorophyll genes–*chi*32 and *lum*2–were previously mapped in our laboratory near *M* on linkage group III (1, 4). Therefore the type line for *dnd* was crossed to the lines Wt 15327 (*chi*32, *M*) and Wt 15298 (*lum*2, *M*). *Dnd* showed clear linkages with both *Lum*2 and *Chi*32, confirming its location in the *M*-segment. At this stage of mapping studies it is impossible to state on which side of *M Dnd* is located, although the absence of linkage with *Uni* suggests that *Dnd* may be on the opposite side of *M* from *Uni*.

Table 3. Distribution of phenotypes in F_2 populations and the linkage tests for the investigated gene *dnd*. Joint segregation of gene pairs in the linkage group III (K. 1136 = Wt 11242 x Wt 11288, K. 1864 = Wt 10357 x Wt 11242, K.1866 = Wt 11242 x Wt 15 327, K. 1973 = Wt 11242 x Wt 15298

Cross Combination	Pair of genes	Phase	Phenotype				Total	Joint chi square	Cr-O value + SE (per cent)
			DD	Dr	rD	rr			
K. 1136	*Dnd - M*	C	89	11	10	28	138	53.4	15.8 ± 3.4
	Dnd - B	R	78	21	28	9	136	0.2	52.5 ± 6.2
	Dnd - St	R	104	36	41	9	190	1.2	43.6 ± 5.8
	B - St	C	90	16	12	18	136	25.1	23.9 ± 4.3
	B - M	R	69	35	26	4	134	4.7	33.6 ± 7.6
	St - M	R	68	34	31	5	138	5.0	34.4 ± 7.4
K. 1864	*Uni*[*] *- Dnd*	R	74	18	23	1	116	3.3	27.2 ± 8.5
	Uni - Apu	C	72	21	15	10	118	3.1	38.7 ± 6.0
	Dnd - Apu	R	67	30	18	1	116	5.3	23.2 ± 8.7
K. 1866	*Dnd - M*	C	64	12	5	10	91	17.7	21.7 ± 5.0
	Dnd - Chi 32	R	145	63	50	1	258	20.0	14.8 ± 6.0
	M - Chi 32	R	47	22	19	1	89	5.8	22.3 ± 10.0
K. 1973	*Dnd - Lum2*	R	204	64	71	1	339	20.9	14.6 ± 5.3
	Dnd - M	C	149	28	23	28	228	32.6	26.5 ± 3.5
	Lum2 - M	R	133	55	40	1	229	13.1	16.8 ± 6.4

*** The fertile allele *uni*^{tac} was included.**

1. Czerwinska, St. and Wolko B. 1991. Pisum Genetics 23: 14-15.
2. Swiecicki, W.K. 1984. PNL, 16: 84-86.
3. Swiecicki, W.K. 1986. Genet. Pol. 27: 73-80.
4. Swiecicki, W.K. and Wolko, B. 1991. Pisum Genetics 23: 40-41.