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# LINKAGES IN *PISUM* L.
# IV. THE GENE *DET* (DETERMINATE GROWTH)[1]

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Summary. In $M_2$-generation obtained as a result of the seed treatment of the line Wt 3527 with a combined dose of fast neutrons — Nf (200 r) and N-nitroso-N-aethylurea — NEU (0.014 per cent) a mutant characterized by terminal inflorescence has been selected.

Segregation in the $M_2$-family as well as in the $F_2$-generation (mutant × initial line) showed the recessive inheritance. The name *determinate growth* was given for the mutation type, the symbol *det* for gene and the catalogue number Wt 16 100 for the mutant in the Pea Gene Bank at Wiatrowo.

The locus identity test showed that the trait with a similar phenotype in the line JI 1358 is determined by an allele of the same locus *det*.

The observations of dihybrid segregation in $F_2$ plants after crossing the testerline Wl 1238 to the mutant Wt 16 100 showed linkages of the gene *det* with the markers *r* and *tl* (Cr-0 values: *Tl-Det*=18,6; *R-Det*=18,7). So, it may be concluded that the gene *det* controlling the terminal inflorescence in pea is localized in chromosome 7.

A characteristic feature of the growth and development of legumes is the lack of clear barrier between the vegetative and generative phase. Most of the species from this group have the indeterminate type of growth — their inflorescences are formed on the consecutive nodes. In view of that, in the breeding programmes of different legume crops (e.g. field bean, lupins) the ideotype of "the self-completing" variety has been worked out (Starzycki 1981, Święcicki sr. 1984). The broad sense of this term means a plant model with a clear end of the vegetative growth. From this phase assymilates should be transported for filling grains only — resulting in early and more uniform maturing. Such an ideotype can "self-complete" the vegetation in different ways — even in the species with terminal inflorescence. E.g., in white lupin the cv. Wat, in which leaves shed (like in trees) in the stage of full, green pods, has been released. Moreover, in white lupin, as well as in yellow and narrow-leaved lupins unbranched genotypes have been selected with only a single main inflorescence. Single flowers appear on the nodes, instead of secondary branches (Święcicki sr. 1984).

In the field bean (*Vicia faba*) the single gene controlling terminal inflorescence

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has been found (Starzycki 1981) and the variety TJ-nova has been released (Steuckardt, Dietrich 1986).

The same gene was found in pea in 1980 as a result of seed treatment of the line Wt 3527 with a combined dose of 200r Nf+0.014 per cent NEU (Święcicki 1983, 1984a). It was presented for the first time on the Symposium of the EUCARPIA Section for Gene Resources (Święcicki 1986). This paper deals with the genetic tests of a mutant gene *determinate growth* for origin, identity and linkage resulting in mapping the new gene *det* in chromosome 7.

## MATERIALS AND METHODS

The wild type of pea has an indeterminate growth. But in the $M_2$ — population of the cv. Paloma=Wt 3527 (after seed treatment with a combined dose of 200r Nf+0.014 per cent NEU) a mutant with the terminal inflorescence has been found. The mutant plants are characterized by the inflorescence on the top of the stem (Fig. 1) and by a smaller number of flowering nodes. Sometimes the apical flowers are abnormal — open but fertile (Fig. 2). The mutant was included into the Pea Gene Bank at Wiatrowo under the catalogue number Wt 16100.

The mode of inheritance has been investigated in the origin test cross between the mutant Wt 16100 and its initial line Wt 3527.

For the locus identity test the mutant Wt 16100 was crossed with a phenotypically similar line from the John Innes Institute collection (JI 1358).

The linkage test was performed between the mutant Wt 16100 and the testerline Wl 1238 — from the Weibullsholm Pea Collection of the Nordic Gene Bank. The genotype of the both lines is as follows: Wl 1238 — *A, d, i* — chromosome 1; *k, s, wb,* — chromosome 2; *b* — chromosome 3; *cp-1, gp, te,* $U^{st}$ — chromosome 5; *r, tl* — chromosome 7 and normal for mutant gene. Wt 16100 — *a, D, I, K, S, Wb, B. Cp-1, $G_p$, Te, u, R, Tl* and *determinate growth* — terminal inflorescence.

The phenotypic expression of gene markers mentioned above was described previously (Święcicki 1984 b, 1985).

Observations of $F_2$ generation and dihybrid segregation provided data for linkage studies (*chi*-square and crossing-over values). Statistical calculations were performed on the IBM PC-computer at Wiatrowo.

## RESULTS AND DISCUSSION

The pea mutant with terminal inflorescence was found at Wiatrowo in 1980. The segregation of the mutant plants in the $M_2$-family (2 mutated: 8 normal) suggested the monogenic, recessive inheritance. The origin test cross confirmed this suggestion. Plants of $F_1$ — generation of Wt 16100 — mutant × Wt 3527 — initial line (and reciprocal) were normal and fully fertile (sown in a greenhouse, 1980).

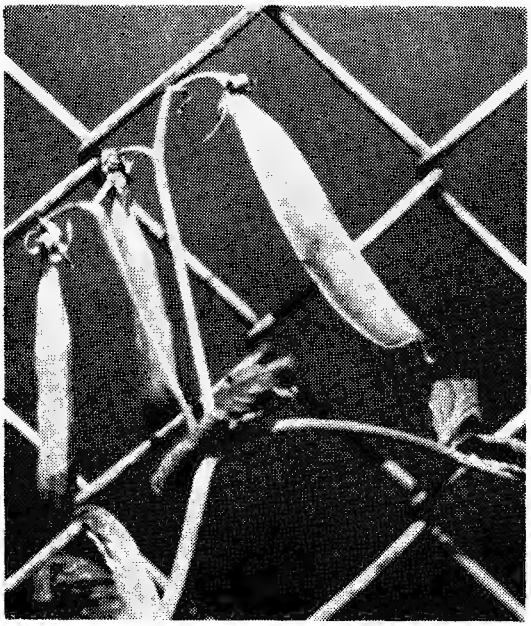

Fig. 1. *Determinate growth* (the gene *det*) in *Pisum*

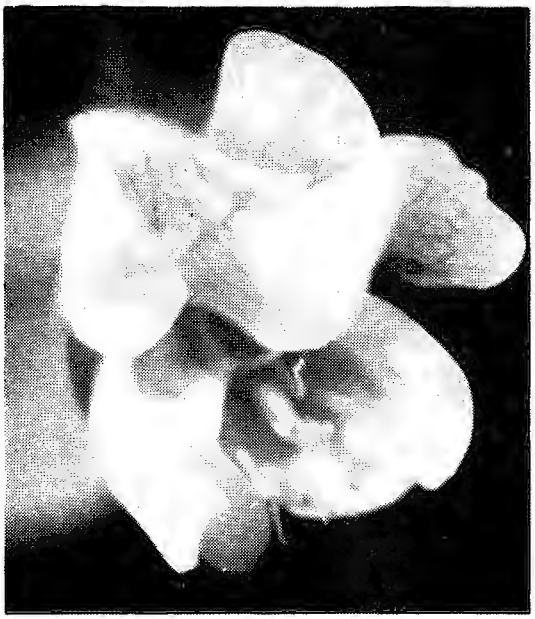

Fig. 2. Open flower of terminal inflorescence in *Pisum*

Because of the same chromosomal structure of the line Wt 3527 and Wl 110 (from the Weibullsholm Pea Collection) it indicates the normal karyotype of *Pisum* for the mutant Wt 16100. The $F_2$ generation (sown in a field, 1981) segregated into 240 normal: 107 mutant plants (260,25 : 86,75 expected; *chi*-square=6.3). The above information allows to accept the symbol *det* for the recessive gene/character of the determinate growth.

All the pea accessions in the world gene banks have the normal type of developing their inflorescences. The only exception is the line JI 1358 (variety Mummy pea) which, according to Matthews (personal communication) has a similar, determinate phenotype like the line Wt 16100. The locus identity test was, therefore, necessary (Blixt 1972). The $F_1$ plants of the cross Wt 16100 ×JI 1358 were of the determinate growth type, showing that the feature in the both lines is controlled by the allele from the same locus.

Table 1. Monohybrid segregation for gene markers in chromosome 7 observed in $F_2$ population of the linkage test — Wl 1238 (testerline) × Wt 16 100 (*determinate growth*)

| Gene | Allele | | Total | $\chi^2$ (3 : 1) |
|---|---|---|---|---|
| | dominant | recessive | | |
| *R* | 333 | 123 | 456 Found | |
| | 342.00 | 114.00 | 456 Expected | 0.95 |
| *Tl* | 361 | 133 | 494 Found | |
| | 370.50 | 123.50 | 494 Expected | 0.97 |
| *Det* | 378 | 111 | 489 Found | |
| | 366.75 | 122.25 | 489 Expected | 1.38 |

For the linkage test the testerline Wl 1238 (with markers in chromosomes 1,2,3,5,7) was crossed with the mutant of the determinate growth — Wt 16100 (the cross number K. 279-Wt). The $F_1$ generation was sown in a greenhouse in 1983. The fertility without disturbances confirmed the normal karyotype of the mutant. The $F_2$ generation (499 plants) was grown in the field in 1984.

Table 2. Distribution of phenotypes in $F_2$ population of the linkage test — Wl 1238 (testerline) × Wt 16 100 (*determinate growth*). Joint segregation of gene markers in chromosome 7

| Pair of gene | Phase [1] | Phenotypes | | | | Total | Joint $\chi^2$ | Cr-O value (per cent) |
|---|---|---|---|---|---|---|---|---|
| | | DD | Dr | rD | rr | | | |
| *Tl-R* | C | 321 | 17 | 12 | 106 | 456 Found | | |
| | | 247 | 91 | 86 | 32 | 456 Corrected expected segregation | | |
| *Chi*-square | | 22.17 | 60.18 | 63.67 | 171.12 | | 317.14 | 6.35±1.18 |
| *Tl-Det* | R | 253 | 107 | 125 | 4 | 489 Found | | |
| | | 278 | 82 | 100 | 19 | 489 Corrected expected segregation | | |
| *Chi*-square | | 2.25 | 7.62 | 6.25 | 21.55 | | 37.67 | 18.61±4.33 |
| *R-Det* | R | 231 | 102 | 119 | 4 | 456 Found | | |
| | | 256 | 77 | 94 | 29 | 456 Corrected expected segregation | | |
| *Chi*-square | | 2.44 | 8.12 | 6.65 | 21.55 | | 38.76 | 18.66±4.48 |

[1] C — coupling phase
R — repulsion phase

Observations of the monohybrid segregation showed no disturbances for the gene markers (Table 1). The segregation for the mutant gene *det* also showed the Mendelian nature of the character.

The dihybrid segregations (*chi*-square and crossing-over values) did not reveal linkages of the mutant gene *det* with the markers in chromosome 1, 2, 3 and 5. But linkages were found between the gene *det* and the genes *r* and *tl* in chromosome 7 (Table 2). According to the last issue of the *Pisum* map not too many genes (only 12) were localized in this chromosome (Blixt 1977), and few of them are good markers with a stable phenotypic expression, e.g. *wsp*, *r*, *tl*, *coch*. In the following years there were only exceptional, short reports in the Pisum Newsletter dealing with linkages in chromosome 7. Two isozyme loci — *Acp-2* and *Est-4* were described by Weeden (1985). So, the gene *det* seems to be important from the theoretical point of view as well as for, the applied plant breeding. Further studies on gene mapping and combinations with genes controlling stem growth and development (e.g. *fas*, *bif*) should give additional information on linkages with other markers in chromosome 7 (*wsp*, *coch*, *Est-4*) and on the influence of the genotypic background on *de* expression before including the new gene into breeding projects. Rare combinations of alleles are specially important for gene banks (Święcicki 1982, Marx 1985).

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## SPRZĘŻENIA GENÓW U GROCHU (*PISUM* L.)
## IV. GEN *DET* (DETERMINATE GROWTH)


### Streszczenie

W pokoleniu $M_2$ uzyskanym w wyniku traktowania nasion linii Wt 3527 kombinowaną dawką szybkich neutronów (200 r) i N-nitrozo-N-etylomocznika (0,014%) wyselekcjonowano mutanta grochu charakteryzującego się terminalnym kwiatostanem.

Na podstawie segregacji w $M_2$, jak również w pokoleniu $F_2$ uzyskanym ze skrzyżowania mutanta z linią wyjściową stwierdzono, że terminalny typ kwiatostanu uwarunkowany jest genem recesywnym. Mutacji nadano nazwę: *determinate growth*. Gen oznaczono symbolem *det*, natomiast mutant otrzymał w Banku Genów w Wiatrowie numer katalogowy Wt 16 100.

Test identyczności loci wykazał, że w linii JI 1358 cecha o podobnym fenotypie uwarunkowana jest allelem tego samego locus.

Obserwacje segregacji dwugenowej u roślin pokolenia $F_2$ otrzymanego ze skrzyżowania linii testowej Wl 1238 z mutantem Wt 16 100 wykazały występowanie sprzężenia genu *det* z markerami *r* oraz *tl* (Cr-0: *Tl-Det*=18,6; *R-Det*=18,7). Można zatem stwierdzić, że gen *det* warunkujący tworzenie terminalnego kwiatostanu u grochu zlokalizowany jest w chromosomie 7.


## СЦЕПЛЕНИЯ ГЕНОВ У ГОРОХА (*PISUM* L.)
## IV. ГЕН *DET* (ДЕТЕРМИНИРОВАННЫЙ ТИП РОСТА)


### Резюме

В поколении $M_2$, полученным в результате обработки семян линии Wt 3527 комбинированной дозой быстрых нейтронов (200 г) и N-нитрозо-N-этилмочевины (0,014%), был выселектирован мутант гороха, характеризующийся терминальным цветостаном.

На основании сегрегации в поколении $M_2$, а также в поколении $F_2$, полученном от скрешивания мутанта с исходной линией, обнаружено, что терминальный тип цветостана обусловлен рецессивным геном. Мутация была названа детерминированным типом роста. Ген был обозначен символом *det*, а мутант получил номер каталогу Wt 16100 в Банке Генов в Вятрове.

Тест идентичности локусов показал, что в линии JI 1358 признак с подобным фенотипом обусловлен аллелью этого же самого локуса.

Наблюдения сегрегации двугенной у растений поколения $F_2$ после скрешивания тестовой линии Wl 1238 с мутантом Wt 16100 показали появление сцепления гена *det* с маркерами *r* и *tl* (Cr-0: *Tl-Det*= =18,6; *R-Det*=18,7). Можно, следовательно, заключить, что новый ген *det*, обуславливающий образование терминального цветостана у гороха, находится в хромосоме 7.