GENETIC ANALYSIS OF SEED STORAGE PROTEINS OF PEA MUTANTS[1/]

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Genetic variation in the band patterns of pea proteins as expressed in gel electrophoresis is well known for both major storage proteins, vicilin and legumin (6,7). Our earlier investigations (5) in which eight Pisum lines with reciprocal chromosome translocations were compared with the test line 'Proteo' (normal chromosome structure) showed both qualitative and quantitative differences in globulin electrophoretic profiles.

Storage proteins of lines L88 and L114 were further analyzed by SDS electrophoresis. Theasubunit of legumin (40Kd zone) in the two mutant lines showed a single band pattern, while the test line showed a double band (Fig. la,b). In the F1 of Proteo x L88 and of Proteo x L114 a double band pattern occurred. Twenty F2 seeds from the first cross segregated in 15 double : 5 single band ratio ($X^2_{3:1}=0.00$); 39 F_2 seeds from the second cross segregated 32:7 ($X^2_{3:1}$) =1.03).

Line L114 showed in the smaller vicilin subunlt (15Kd zone) (Fig. lb) three bands together in comparison with the two band pattern occurring in the test line; the additional band had a lower molecular weight than the other two. The F1 cotyledons had the same three subunits observed in the parental mutant line. In $F2_7$ 27 seeds with three bands and 12 seeds with two bands were found ($X^2_{3:1}$ =0.69).

Thomson (7) and Casey (1) noticed that both vicilin and legumin band patterns are under genetic control. Our results show that both Vicilin 15Kd subunits and legumin 40Kd subunits are determined by single Mendelian genes. The former result supports similar findings for the major Vicilin subunits by Mahmoud and Gatehouse (3), while the latter result corroborates the genetic analyses of Casey (1), Davies (2), and Matta and Gatehouse (3).

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—^ Contribution no. 12 from Centro di Studio per il Migl ioramento Genetico degli Ortaggi - C.N.R. - Portici (Napoli) - Italy

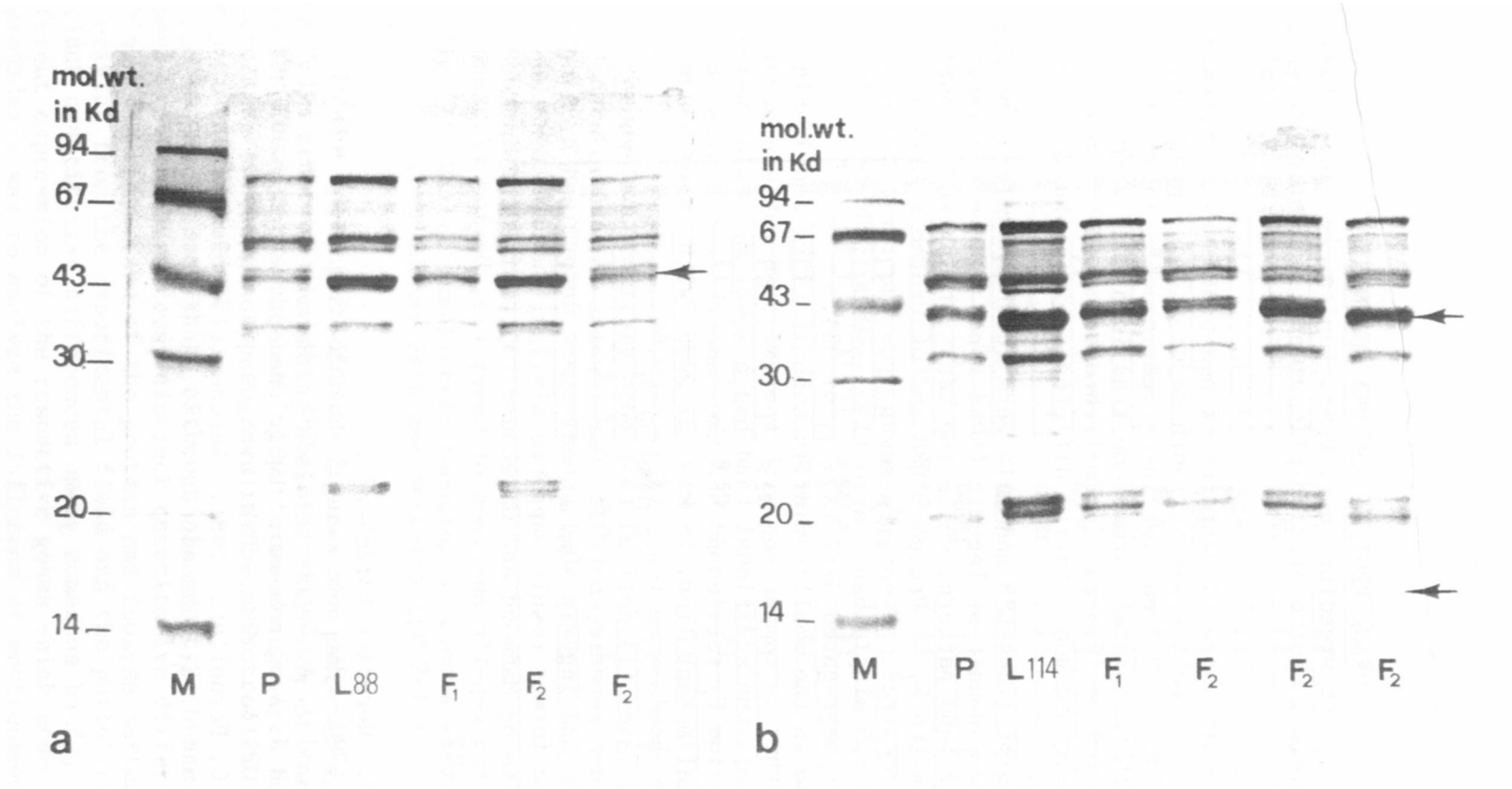

Fig. 1. SDS electrophoregrams of reduced globulins in parental lines, F1 and F2

M=molecular weight markers.

a) Proteo (P) and L88

b) Proteo (P) and L114