Heredity analysis of radiation induced semidwarf mutants in Tartary buckwheat (*Fagopyrum tataricum* Gaertn.)

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Recently, heavy-ion beams have been regarded as a good mutagen for plant breeding, and as such various varieties have been developed by using heavy-ion beams. We previously reported the biological effects and mutation induction by ion beams in Tartary buckwheat[1) 2)]. We obtained semidwarf mutants named IRBFT-45, 63, 67 and 77. The semidwarf type is important for improving the lodging resistance and yielding ability in buckwheat breeding. These semidwarf mutants were obtained by irradiating dry seeds of Tartary buckwheat (var. Rotundatum) with 40 Gy of carbon (^{23} keV/μm, $^{12}C^{6+}$), 100 Gy of carbon (^{39} keV/μm, $^{12}C^{6+}$), 30 Gy of iron (624 keV/μm, $^{56}Fe^{24+}$) and 20 Gy of argon (280 keV/μm, $^{40}Ar^{17+}$) ions[3)]. On the other hand, we obtained similar semidwarf lines named IRBFT-6 and 20 by irradiating dry seeds with 50 and 500 Gy of gamma rays (^{60}Co, 44.4TBq) at the Institute of Radiation Breeding, and IRBFT-38 by irradiating dry seeds with 40 Gy of helium ions (^{16} keV/μm, $^{4}He^{2+}$) at JAEA. The plant height of all of these semidwarf lines was 50-60% of the original varieties. We performed heredity analysis on these semidwarf mutants.

All of the F_1 plants obtained by crossing among IRBFT-6, 20, 45 and their original varieties showed wild type like phenotype. The phenotypes in the populations of F_2 were segregated into wild type like and semidwarf, and the appropriate segregation ratio was found to be 3:1 by a chi square test (Table 1). This suggests that the trait of semidwarf in IRBFT-6, 20, and 45 was controlled by a nuclear single recessive gene.

To classify these semidwarf lines, a half diallel cross was performed (Fig. 1). When F_1 plants showed a semidwarf phenotype, the causal gene of the parents was considered to be the same. When F_1 plants showed wild-type like phenotype, the causal genes of the parents were considered to be different. From the phenotype in F_1, it was estimated that these 7 lines were classified into 2 groups. One consisted of IRBFT-6, 20 and 45, which had a common semidwarf gene termed *sdA*. The other consisted of IRBFT-38, 63, 67 and 77, which had another semidwarf gene termed *sdB*.

Because a crossing test with original varieties was not performed in *sdB* lines (IRBFT-38, 63, 67 and 77), the number of *sdB* gene(s) was not determined. Instead, we investigated the segregation ratios in the F_2 plants generated by crossing *sdB* lines with IRBFT-20 (*sdA*) (Table 2). The phenotypes in the populations of F_2 were segregated into wild type like and semidwarf. Their segregation ratios were then fitted to the two recessive gene model (Table 2). These results indicated that *sdB* was controlled by a single recessive gene different from *sdA*.

Table 1. Segregation patterns of plant type crossing between semidwarf lines and the original variety in the F_2 population

Cross combination	No. of plants		χ^2	p
	Wild type	Semidwarf	3:1	
Pontivy×IRBFT-6	21	9	0.4	0.53
Hokkai T8×IRBFT-20	54	17	0.04	0.84
Rotundatum×IRBFT-45	60	13	2.01	0.16

♀ \ ♂	IRBFT-20	IRBFT-38	IRBFT-45	IRBFT-63	IRBFT-67	IRBFT-77
IRBFT-6	SD 6	WT 3	SD 4	WT 5	WT 4	WT 4
IRBFT-20		WT 4 (SD 1)	SD 5	WT 4	WT 7	WT 5
IRBFT-38			WT 2 (SD 1)	SD 5	SD 3	SD 1
IRBFT-45				WT 3	WT 4	WT 4
IRBFT-63					SD 17	SD 14
IRBFT-67						SD 16

Fig. 1. Phenotypes of F_1 plants by a half diallel cross. SD means semidwarf type, and WT means wild-type like. Numbers in parentheses are the numbers of research plants.

Table 2. Segregation patterns of plant type crossing between semidwarf lines in the F_2 population

Cross combination	No. of plants		χ^2	p
	Wild type	Semidwarf	9:7	
IRBFT-20×IRBFT-38	109	85	0.01	0.99
IRBFT-20×IRBFT-63	64	56	0.41	0.52
IRBFT-20×IRBFT-67	137	103	0.07	0.79
IRBFT-20×IRBFT-77	130	109	0.33	0.56

References

1) T. Morishita et al.: RIKEN Accel. Prog. Rep. 36, 137 (2003)
2) T. Morishita et al.: RIKEN Accel. Prog. Rep. 40, 255 (2007)
3) T. Morishita et al.: RIKEN Accel. Prog. Rep. 41, 232 (2008)

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