et Spach ($2n$=14=S^bS^b) and *Secale cereale* L. ($2n$=28=RRRR) was produced under the collective idea of 'adding genetic variability'. The *Aegilops* x *Secale* hybrid is of interest because it offers a unique opportunity to study how *Aegilops* and *Secale* nuclear genomes interact in *Aegilops* cytoplasm. Further, because the chromosomes of *S. cereale* are markedly larger than those of *A. bicornis* this hybrid also provides an excellent material to study the biosystematic relationships between the two genera.

The F_1 hybrid plants were vigorous, well spiking and completely male sterile, with dominant rye characters, but the spikes lacked awns (Figure 1). Attempts were made to produce amphidiploids by treating F_1 hybrid plants at 3–4 tiller stage with 0.25% colchicine solution. However, the treated plants remained self-sterile and no viable pollen was observed in any of the anthers. Further, one cultivar each of bread wheat (Chinese Spring) and hexaploid triticale (TL 2396) was crossed onto the intergeneric hybrid and only two seeds, one per cross, were obtained. The seed set also confirmed the partial viability of female gametes.

At the meiotic metaphase-I in the F_1 hybrid, majority of the PMCs studied revealed the preponderance of univalents, though up to three (maximum) atypical rod bivalents were also recorded. On the basis of distinctly larger size and morphology of the chromosomes, it could be inferred that the observed bivalents were autosyndetic in nature, and were from the rye genome. Occurrence of autosyndetic paring between the chromosomes of R genome conforms to that reported earlier[1]. Meiotic configurations (MI) further suggest as if *Aegilops* cytoplasm is less congenial for bivalent formation. Had there been no effect(s) of *Aegilops* cytoplasm, RR genome from tetraploid rye should have formed seven bivalents at metaphase-I as against three (maximum) observed autosyndetic bivalents (T. Tsuchiya, pers. commun.). Since the reciprocal crosses were not available, the probable implication of *Aegilops* cytoplasm in the suppression of autosyndetic pairing could not be confirmed. This inference, however, merits further investigation.

Absence of heteromorphic bivalents(s) on the other hand, is indicative of non-homology existing between the chromosome complements of the parental genome.

A. bicornis and *S. cereale* are known for their high degree of resistance to different pathogens. A few desirable traits include; powdery mildew resistance in *A. bicronis*, and rust resistance coupled with high protein content in *S. cereale* [2]. Intergeneric hybrid under report was basically produced for reciprocal transfer of desirable traits from *A. bicornis* to the cultivar(s) of *S. cereale*. However, the failure of chiasmata associations between the chromosome complements of the parental genomes suggests that an effective isolation barrier does exist which, unless some specialized techniques[3–5] allowing the breaking and fusion of chromosomes are employed, would not permit the recombination and transfer of genetic information between the two genera.

Figure 1. Three spikes of the hybrid between *Aegilops bicornis* and *Secale cereale* (left) and two spikes of *Secale cereale* (right).

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Some biochemical changes in the shoots of pearl millet infected by downy mildew

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In order to probe into certain biochemical changes in the pearl millet shoots infected with downy mildew pathogen (*Sclerospora graminicola* (Sacc.) Schroet), total leaf chlorophyll, total phenol and total free amino acid contents in the shoots and the specific activity of the enzyme nitrate reductase in both shoots and roots of the host were analysed. The estimations revealed that the total leaf chlorophyll, total phenol and total free amino acid contents were found low whereas the nitrate reductase activity was found to be high in both the diseased shoots and roots of pearl millet (*Pennisetum americanum* L. Leek).

PEARL millet (*Pennisetum americanum* L. Leek) downy mildew (*Sclerospora graminicola* (Sacc.) Schroet.) is a national problem. Various biochemical alterations take place during pathogenesis but these have not been studied systematically. This communication reports changes in the

Table 1. Biochemical changes in diseased leaves, shoots and roots of pearl millet infected by downy mildew.

Parameters (units)	Healthy			Diseased		
	Leaves	Shoots (L+S)	Roots	Leaves	Shoots (L+S)	Roots
Total chlorophyll (mg/g, dry wt)	1.36×10^{-3}	—	—	0.49×10^{-3}	—	—
Total phenols (mg/g, fresh wt.)	—	2.584	—	—	3.876	—
Total free amino acids (mg/g, fresh wt.)	—	—	0.686	—	0.294	—
Nitrate reductase (moles of NO_3 transfored/ min/mg protein)	—	0.0090	0.0503	—	0.0140	0.01416

(L = Leaves; S = Stem.)

total chlorophyll in leaves, total phenols and total free amino acids in the shoots and roots of healthy and diseased plants.

Downy mildew sporangia were sprayed on 7-day-old plants of NHB-3 variety raised in 12" pots. Total leaf chlorophyll[1], total phenols[2], total free amino acids[3], nitrate reductase[4], and enzyme-protein[5] were estimated 15 days after appearance of symptoms.

The loss in total chlorophyll confirmed the earlier findings in pearl millet[6] and sorghum[7] during pathogenesis (Table 1). The present results for the total phenols also agree with those in downy mildew-infected plants[8-11].

Lower contents of total free amino acids during pathogenesis support earlier findings with pearl millet[10] and cowpea infected with mosaic virus[12].

Our observations on the activities of nitrate reductase, during pathogenesis, in both roots and shoots of pearl millet are contrary to those observed in rice leaves infected with bacterial blight[13] and the resistant and susceptible cowpea varieties infected with mosaic virus[12]. The possible reasons for the high nitrate reductase activities in the diseased plant-parts could be due to a greater induction of the enzyme during pathogenesis. It may also be possible that the pathogen generates this enzyme in order to utilize the free nitrate present in the host tissues. The roots might be absorbing more nitrate from the soil to meet the demands of both the host and pathogen. In turn, nitrate transformed into nitrite and further into ammonia might be getting incorporated rapidly into the amino acids, thereby enhancing protein metabolism and also helping the host photosynthetic processes to speed up in spite of the loss in total chlorophyll content.

These possibilities remain to be investigated to understand overall biochemical changes during pathogenesis.

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Natural selection in varietal mixtures of greengram (*Vigna radiata* (L.) Wilczek)

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The competitive ability of eight greengram genotypes/ varieties in relation to their respective yield, disease reaction and pod traits was studied. Initial sowing was done by mixing the seed of each variety in equal proportion (12.5%). Single pod from each plant was plucked, identified and number of plants of each variety was counted at harvest. Successive sowing for four seasons was done by taking a large random sample from the