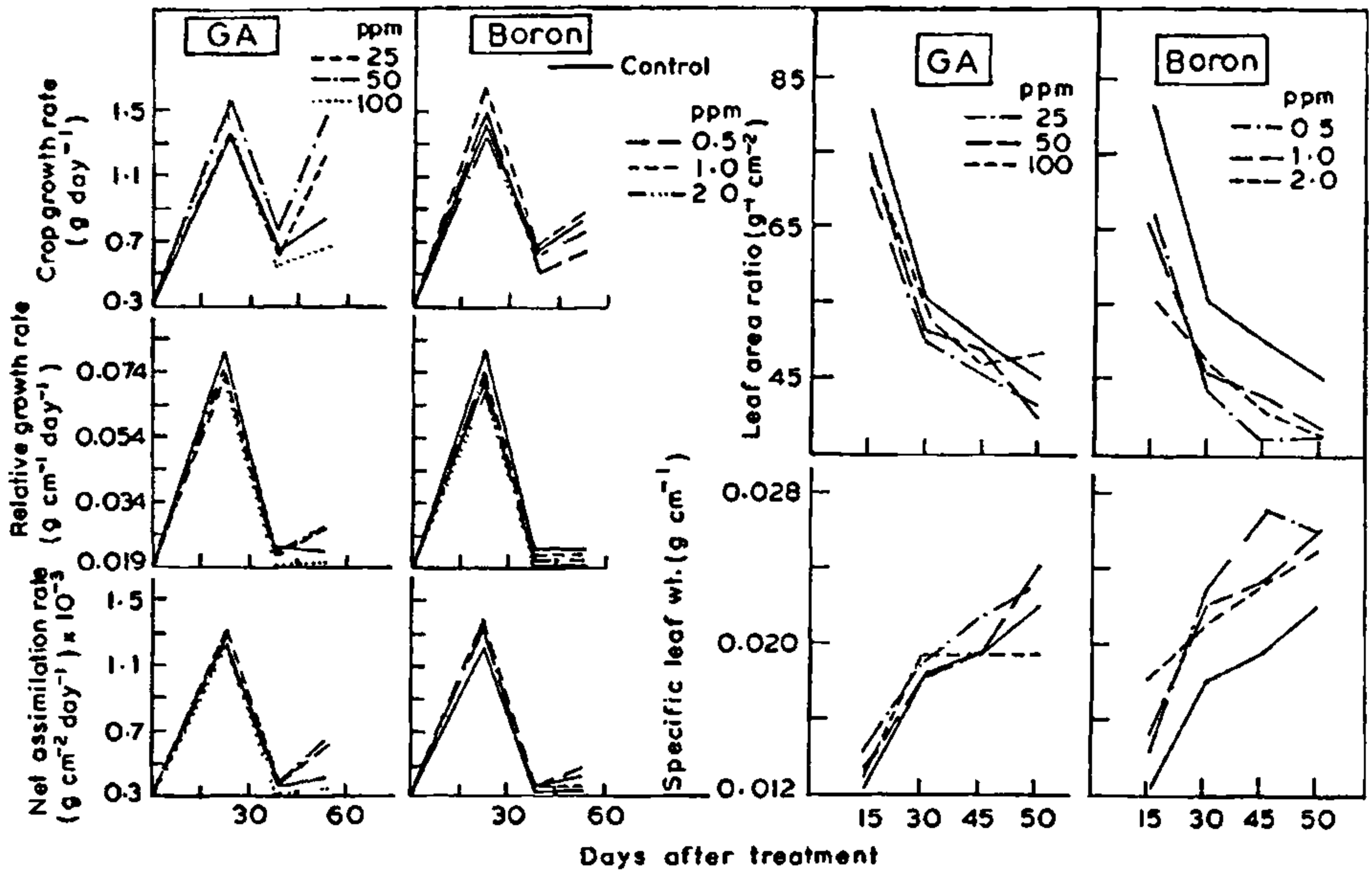

Figure 1. Effect of GA and boron on growth parameters of Siratro.

Specific leaf weight (SLW) increased with age, and was maximum at 50 ppm GA and 1 ppm boron. SLW has been shown to be related to NAR activity[4]. The present results are also supported by the findings of Dong and Arteca[5] on tomato plants treated with phytohormones.

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RESPONSE OF DIFFERENT RICE CULTIVARS TO *AZOSPIRILLUM* INOCULATION

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AZOSPIRILLUM is known to fix atmospheric nitrogen and increase the yield of several crops such as rice, wheat, maize, sorghum and pearl millet[1,2]. *Azospirillum* is a microaerophilic bacterium and survives well and fixes nitrogen in rice rhizosphere[3]. The bacterium promotes plant growth also by mechanisms other than nitrogen fixation in rice[4,5]. It produces auxins in culture and in its natural habitat[2,6]. Differential varietal response to *Azospirillum* has been reported in wheat and sorghum[7]. Hence we assessed the responses of different rice varieties to *Azospirillum lipoferum* Tarrand *et al.*

Peat-based *Azospirillum* inoculum containing approximately 10^8 cells/g was used. Inoculation was by three methods. Seeds were first treated with 2 kg of inoculum by soaking the seeds in water containing the inoculum for 24 h. For 60 kg of seed required for

Table 1 *Effect of Azospirillum inoculation on straw and grain yield of different rice cultivars*

Cultivar	Straw yield (t/ha)			Grain yield (t/ha)		
	Without *Azospirillum*	With *Azospirillum*	Per cent increase	Without *Azospirillum*	With *Azospirillum*	Per cent increase
Dry-season						
ADT 36	4.7±0.2	5.9±0.5	25.5	4.0±0.1	5.0±0.2	25.0
ADT 37	4.6±0.3	5.8±0.2	26.1	3.9±0.2	4.8±0.2	23.1
IR 50	4.2±0.3	5.7±0.7	35.7	3.6±0.5	5.0±0.4	38.8
TKM 9	5.4±1.0	6.9±1.3	27.7	4.4±0.7	5.4±0.9	22.7
CD ($P=0.05$)		1.1			0.9	
Wet-season						
ADT 38	4.8±0.2	5.7±0.7	18.8	4.2±0.1	5.0±0.3	19.0
Co 43	5.3±0.3	6.8±0.4	28.3	5.1±0.3	6.1±0.1	19.6
IR 20	6.2±0.8	7.3±0.4	17.7	5.5±0.3	6.6±0.3	20.0
White Ponni	6.5±0.4	8.4±1.0	29.2	4.9±0.7	5.8±0.8	18.4
CD ($P=0.05$)		0.9			0.8	

All values are mean ± SD.

one hectare, 60 l of water were used for soaking the seeds. The soaked seeds were allowed to sprout for 24 h and sown in the nursery. At the time of transplantation, the roots of 25-day-old seedlings were dipped in 400 l of water containing 2 kg of inoculum for 20 min. Another 2 kg of inoculum was mixed with 15 kg sand and broadcast in the main field just before transplanting[8].

The trials were conducted in both dry and wet seasons of 1987–88. During the dry season, short-duration (105–110 days) varieties, viz. ADT 36, ADT 37, IR 50 and TKM 9, were tested. During the wet season, medium-duration (130–135 days) varieties, viz. ADT 38, Co 43, IR 20 and White Ponni, were tested. The soil was fertilized with 75 kg nitrogen, 37.5 kg phosphorus and 37.5 kg potassium for dry-season crops and 75 kg nitrogen, 50 kg phosphorus and 50 kg potassium for wet-season crops. While both phosphorus and potassium were applied basally, nitrogen in the form of urea was applied in three split doses (50% at planting, 25% at 15 days after transplanting and 25% at panicle initiation) for dry-season crops and in four splits (28% at planting, 24% at 15 days after transplanting, 24% at maximum tillering and 24% at panicle initiation) for wet-season crops. Plant height and number of productive tillers/hill were measured on day 100 after sowing. Twenty-five plants selected at random were assessed for plant height and for number of productive tillers. Straw (dry) weight of the plants and grain yield at 12% moisture were also recorded. Three replicates were employed and the data were statistically analysed.

Azospirillum application increased plant height in all the varieties tested. There was also an increase in the number of productive tillers due to bacterial inoculation in all the cultivars. Increased growth rate of rice plants due to *Azospirillum* has been reported[5,9]. This increase may not be due to nitrogen fixation by the bacterium alone, as clearly demonstrated by Watanabe and Lin[5], using ^{15}N. *Azospirillum brasilense*, another nitrogen-fixing bacterium, has been shown to produce plant growth substances[2,4]. Similarly *Azospirillum lipoferum* would have also produced auxins[6]. The increase in straw and grain yields due to the treatment was much more pronounced and all the eight cultivars responded almost equally well (table 1).

Variations in nitrogen-fixing ability of *Azospirillum* in different maize cultivars have been reported[10]. Varietal differences in nitrogen fixation in the rhizosphere of rice planted in pots have also been reported. However, Indu Bala and Kundu[11] observed that the wheat varieties tested by them uniformly responded to *Azospirillum* inoculation. The present results show that the yield response due to *Azospirillum* inoculation does not vary among the different rice varieties tested.

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ALTERATIONS IN AMINO ACID BALANCE IN RICE MUTANTS

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SINCE induction of mutation is the easiest and quickest method of rectification of genetic defects and improvement of a few traits in an otherwise well-adapted desirable variety, it was tried in rice using γ-rays, ethylmethane sulphonate (EMS) and diethyl sulphate (DES), singly and in combinations. Of the 396 mutants isolated from an M_2 population of 22,64,300 plants, the seeds of 14 mutants exhibited specifically patterned aminogram variability in M_4–M_7 generations. In the remaining 382 mutants, the variability was random and non-directional. Of the 14 mutants, five (Jm_1, Jm_4, IRm_1, IRm_6 and Bm_1) exhibited certain desirable phenotypic traits like shorter stature, earlier maturity, higher grain number or better grain-fineness than their corresponding initial lines (Kaul and Neelangini, unpublished). In addition, in all these mutants seed protein production was slightly increased. But the alterations in their essential amino acids are specific. These changes, termed amino acid balance alterations by Kaul[1], are described here.

For seed protein and amino acid analyses, four samples of 5 g of seeds of each mutant in each of the four generations were used. For amino acid analysis, 100 mg each of the four samples from each genotype were defatted with refluxing petroleum ether, hydrolysed under N_2 in 0.6 N HCl in a sealed tube at 40°C for 24 h, and subjected to amino acid analysis in a Spinco Model 120°C analyser with Spinco PA–35 and AA–5 resins[2]. Tryptophan was determined by PA–35 chromatography following the method of Knox *et al*[3]. The methionine content was determined similarly in AA–15 resin column as methionine sulphone after performing acid oxidation and hydrolysis with 0.6 N HCl[4]. The amino acid data were subjected to Duncan's multiple range test by the method outlined by Gomez and Gomez[5]. The seed protein content was estimated by the conventional micro-Kjeldahl's method using the established conversion factor 5.95. Estimates and significance of variability were computed following methods outlined by Steel and Torrie[6].

The mutants showed significant alterations in the levels of the essential amino acids arginine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine and valine (tables 1 and 2). Whereas isoleucine was significantly decreased in all the mutants, there was no significant alteration in tryptophan (table 2). Leucine, methionine and threonine were increased in Bm_1, IRm_1 and IRm_6, but both leucine and methionine were decreased in Jm_1 and Jm_4. The two mutants of Jhona and the two mutants of IR_8 showed similar amino acid alterations. One IR_8 mutant, IRm_1, and the Basmati mutant Bm_1 showed increase in seed protein content over their parents (table 2), but this enhancement was not proportional to increase or decrease of any individual amino acid (table 1). On the other hand, though there was no significant alteration in the seed protein content of the two Jhona mutants, Jm_1 and Jm_4, both of these showed significant decrease in isoleucine, leucine, methionine, phenylalanine, and increase in arginine and valine contents (table 2).

These findings indicate that amino acid alterations are independent of protein alterations in rice. This has also been found by many other workers[3,7–9], but the presently reported directional alterations in specific amino acids were unknown in rice. Mutants exhibiting such alterations are termed amino acid