

the mycorrhizal fungus and the rhizobium by the same mechanism. The control of the degree of infection of the root under high nutrient supply has been found to differ in these two types of symbioses<sup>17</sup>.

A particularly intriguing aspect of the biotrophic interactions of soybean roots with microorganisms is the fact that biotrophic pathogens and nodule-forming bacteria generally display a very limited host range, often extending only to a few genotypes of a single plant species<sup>6, 18</sup>, whereas VAM fungi generally have an extremely wide host range<sup>1</sup>. Further investigations will have to examine whether the lack of phytoalexin elicitation has a similar basis in the interactions of plants with biotrophic pathogens, nodule-forming bacteria and VAM fungi or whether the plants have the capability of specifically recognizing mutualistic symbionts. It may be speculated that the VAM symbiosis represents a basically compatible plant-microorganism interaction, while both nodule symbiosis and the interaction with biotrophic pathogens exemplify specialized adaptations of the partners to originally incompatible plant-microorganism interactions.

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## Correction

**T. H. Jukes:** Genetic Code 1990. Outlook; *Experientia* 46 (1990) 1149–1157.

Data in Table 3 should read as follows:

Caption: COX III should be **COX II**

Site 129: *UUG* should be **UGG**

First column: RNA ONE should be **RNA OBE**

Furthermore, lines 38–43, left column, p. 1153, should read:

Leinfelder et al.<sup>26</sup> have suggested that 'UGA was originally a **sense** codon' (presumably for SeCys) and 'after introduction of oxygen into the biosphere this highly oxidizable amino acid could be maintained only in anaerobic organisms or in aerobic systems which evolved special protective mechanisms' . . .