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Neurospora crassa suppressors act on *amber*.

The nonsense mutant am^{17}, is suppressible by ssu-1 by tyrosine insertion in residue 313 of NADP-specific glutamate dehydrogenase. It can revert to either Leu^{313} or Tyr^{313}, consistent with the nonsense codon being either amber (UAG) or ochre (UAA) (Seale et al., 1976 Genetics 86: 261-274). DNA sequencing of the wild type gene (Kinnaird and Fincham, 1983 Gene 26 : 253-260) shows codon 313 to be CAG (glutamine). Furthermore, we find that am^{17} is induced to revert with-nitroquinoline oxide (NQO), a mutagen reported to be specific for G-C base pairs (Prakash et al., 1974 J. Mol. Biol. 85: 51-65). We conclude that the nonsense codon,in am^{17} is amber (UAG). Since known Neurospora supersuppressors all suppress the same set of mutants (Seale, 1976 MGG 148: 105-108) they must all suppress *amber*. There is no evidence as yet for ochre- or UGA-suppressing mutations in Neurospora. Given the very selective codon usage found so far in strongly and constitutively transcribed Neurospora genes (reviewed in Kinnaird and Fincham, 1983), UAA and UGA nonsense mutants would in any case be expected to be much less frequent than UAG in such genes. With no condons with A in the 3' position, only tyrosine ($UA\frac{C}{U}$) can mutate by single base-pair substitution to UAA and only tryptophan (UGG) or cysteine ($UG\frac{U}{C}$) to UGA; UAG, on the other hand, can arise from the abundant glutamate (GAG), glutamine (CAG) and lysine (AAG) codons. - - - Department of Genetic, University of Edinburgh, King's Building, Edinburgh EH9 3JN, Scotland. *(Present address: Department of Genetics, University of Cambridge, Cambridge CB2 3EH, England.)