A RE-EXAMINATION OF THE AMINO ACID SEQUENCE DATA OF CYTOCHROMES *c* FROM *SOLANUM TUBEROSUM* (POTATO) AND *LYCOPERSICON ESCULENTUM* (TOMATO)

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1. Introduction

The amino acid sequence of potato cytochrome *c* has been presented recently by Martinez et al. [1] and compared with the sequence of tomato cytochrome *c*, determined by Scogin et al. [2]. The two plants belong to the same family (Solanaceae). Because of a typographical error in the original report [2], the number of differences between the two sequences should be reduced from the five reported by Martinez et al. [1] to a probable four.

2. Discussion

The main interest of Martinez' paper [1] is their estimate of the number of differences between the sequences relating to the two members of the same plant family. For comparison, Thompson et al. [3] found three differences in the cytochromes of two members of the *Malvaceae.* It is surprising, therefore, that Martinez et al. rely so heavily on homology with the tomato sequence in their determination. The assumption that peptides of the same electrophoretic mobility and the same amino acid composition are identical is not necessarily valid, even for closely related species, particularly if the peptides contain a number of 'variable' residues. Thus, in peptides T14 and C16 [1] the sequence Glu–Ala–Thr–Ala is assumed for residues 108–111. However, both residues 108 and 109 vary considerably from cytochrome to cytochrome. Moreover, residue 108 is Ala in the sunflower sequence [4] and residue 109 is Glu in buckwheat [5].

The assignment of both Asp and Glu to residue 98, supposed polymorphic, is also doubtful. There is no indication of polymorphism in the values for Asp or Glu in the total hydrolysate of potato cytochrome [1]. The assignment of Asp in this position from data of peptide C14 could easily have arisen from Asp-101 and in any case, the yield of peptide C14 is very low (2%). The assignment therefore rests entirely on the hydrolysis data of peptide T11, which is very long and might well be expected to contain traces of aspartic acid. It is therefore quite likely that this residue is actually Glu. If so, then in this position the sequence is identical to that of tomato, although in the original manuscript [2] the residue is presented as Gln. The paper by Boulter et al. [6] gives the correct sequence (table 2).

It should also be noted that the number of 'characteristic' residues of higher plant cytochromes *c* is much less than suggested by Martinez et al. [1]. Thus, *Ginkgo* [7] and *Acer* [8] cytochromes *c* have more than 111 residues. Several cytochromes have Ala–Thr–Ala instead of Ala–Ser–Ala as N-terminus [6]. Spinach [6], *Nigella* [9], and leek [10] do not have the Thr–Thr sequence in positions 50 and 51.

It therefore seems unwise to regard any given residue as 'characteristic' on very limited data sets, still less totally invariant in all cytochrome *c* sequences.

References

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