stoichiometric oxygen- and NADPH-dependent conversion of dimethylamine into methylamine and formaldehyde (Eqn. 1).

The identity of methylamine as product was shown by comparison of the spectrum of its *N*-2,4-dinitrophenyl derivative (Dubin, 1960) with that of authentic methylamine, and by its activity with the purified primary amine dehydrogenase of *Pseudomonas* AM1 (Eady & Large, 1968). The enzyme had K_m 59 μM for dimethylamine and was inhibited by dimethylamine concentrations above 1 mM. NADH could replace NADPH as electron donor and was slightly (1.2-fold) more active. Extracts of succinate-grown cells had no detectable activity. The partially purified enzyme showed no significant activity with primary, tertiary and quaternary amines, nor with sarcosine. Diethylamine was about 28% as active as dimethylamine.

These results suggest that during growth of *P. aminovorans* on dimethylamine, the first step is the reduced nicotinamide nucleotide-dependent oxidative *N*-demethylation of dimethylamine by a mono-oxygenase reaction. We have not yet determined whether the enzyme is a single flavo-protein (cf. imidazoleacetate hydroxylase; Hayaishi, 1966) or a multicomponent system like the fatty acid ω -hydroxylase of *Pseudomonas oleovorans* (Peterson, Basu & Coon, 1966) or the camphor methylene hydroxylase of *Pseudomonas putida* (Katagiri, Ganguli & Gunsalus, 1968).

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Some Problems Associated with the Amino Acid-Sequence Analysis of Proteins by Mass Spectrometry

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In the mass-spectrometric sequence determination of oligopeptides one of the more difficult problems encountered has been the low volatility

of the free peptides. Of the procedures suggested to overcome this difficulty (see Biemann, Cone, Webster & Arsenault, 1966) we have used *N*-acetylation of the peptide methyl ester. In certain cases it has been necessary to enhance further the volatility by using the permethylation technique described by Das, Gero & Lederer (1967).

We have studied derivatives of various synthetic analogues of protein fragments in addition to several readily available small peptides. In every case it has been possible to determine the sequence by using only data obtained at low resolution together with a knowledge of the amino acid composition, though high-resolution techniques have proved valuable for confirmation. The results were sufficiently encouraging for an attempt to be made at the sequence determination of peptides isolated from a protein.

The additional problem was encountered of contamination both from the ion-exchange resin used to fractionate the enzymic digest, and from small amounts of peptide impurity travelling in the main peptide peaks. These small peptide impurities give rise to low-intensity peaks, which do not interfere with the interpretation of the main spectrum. In an extreme case we have been able to show that the sequence of two very similar peptides in an approximately equimolar mixture can be easily identified on the same spectrum. The contamination from the column seems to be a mixture of polymers dissolved out from the resin; these impurities can completely obscure the peptide sequence-determining peaks.

Although further separative procedures might be desirable we have been able to show that a satisfactory spectrum can be obtained without prior removal of the impurities. The sequence of an octapeptide isolated from a chymotryptic digest of silk fibroin by means of ion-exchange chromatography has been unequivocally determined by mass-spectrometric analysis of the permethylated derivative (Geddes *et al.* 1969).

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