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Analysis of conformational preferences of the dehydro residues have become very important mainly in designing of the folded peptides which have biological functions. Conformational maps obtained during the course of this dissertation has suggested a few things that could be useful in understanding the dehydro residues. The $\phi, \psi$ map has the allowed regions in almost all the four quadrants. This shows that incorporation of a dehydro residue does not impose stringent constraint on the backbone folding. However the nature of the residue preceeding and succeeding the dehydro residue may be important before drawing any conclusion. Analysis done on a limited system is suggestive of higher preference for $\beta$-turns. This is in agreement with the conclusion drawn from the X-ray structural analysis and also from solution studies such as NMR. Extended conformations are not preferred and this again is due to the position of the dehydro residue constrained by the $C^\alpha-C^\delta$ atoms. Incorporation of the dehydro leucine also shows a similar conformational preference as that of the dehydro phenyl alanine. The central region in this map is completely forbidden for the reasons stated above i.e. the dehydro nature of phenyl alanine residue. Variation in the bond
angle at Cα, varying the dielectric constants etc., has not produced significant changes in the conformational maps.

The results therefore, in general, suggest that the dehydro residue can be used to produce chain folds and reversal, as could be useful for designing of the folded peptides. For a complete understanding, one has to carry out further studies by considering (1) one dehydro residue linked to another dehydro residue and (2) normal residue preceding or succeeding a dehydro residue and also the variation in the amino acid sequences. Further calculations for a pair of peptides and a tripeptide having dehydro residue, are underway, in our laboratory.