Glycines Job Security Revealed by X-ray crystallography

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Analysis of the conserved three dimensional structures of many proteins that are present in all cellular species on earth reveals that in most cases glycine residues play an essential role in controlling and retaining the three dimensional shape required for fold and function of those proteins. These glycines are immutable and have had "job security" for 3 billion years. Analysis of at least 30 ribosomal proteins and dozens of other proteins present in all cellular species reveal the 100% conservation of glycine residues in over 15,000 members of each protein family.

The immutability of these glycines is due to the fact that chiral amino acids in 99% of all proteins produced by the ribosome have the same L- chirality while glycine is achiral. The common L-chirality of all amino acids other than glycine sustains the L-handedness of all helices found in ribosomally produced proteins. L-handed helix would continue indefinitely unless interrupted by a glycine residue. The achirality of glycine makes the formation of globular proteins possible. Glycines present in protein turns between alpha helical or beta strands and other alpha helices or beta strands usually have conformations (psi and phi values in the Ramachandran plot) that are rarely if ever observed for the other 19 amino acids. These glycines resist mutation to any other amino acid because the mutation would drastically alter the protein fold and lead to loss of function. Together with other fully conserved amino acids (most commonly Ala, Pro, and Arg residues) these Gly residues make it possible to align over 15,000 members of each protein family.

When perfectly aligned these families can be analyzed to create rooted evolutionary trees of all cellular species and identify the Last Universal Common Ancestor of each family. These trees can be compared to test the results for consilience. The analysis of several ribosomal proteins will be presented and compared.