Journal of Applied Pharmacy

Mani and Narayanasamy, J App Pharm 2016, 8:2
http://dx.doi.org/10.4172/1920-4159.1000216

Commentary Open Access

Conformational Angles and Properties of Ω-Amino Acids in Protein Folding

VS Saravana Mani[1,2*] **and R Narayanasamy**[3]

[1]*Research and Development Centre, Bharathiar University, Coimbatore, India*

[2]*Department of Chemistry, Annapoorana Engineering College, Salem, India*

[3]*Department of Chemistry, Coimbatore Institute of Technology, Coimbatore, India*

[*]**Corresponding author:** VS Saravana Mani, Research and Development Centre, Bharathiar University, Coimbatore, India, Tel: 9842766788; E-mail: saravanamani@gmail.com

Received date: March 16, 2016; **Accepted date:** March 30, 2016; **Published date:** April 06, 2016

Introduction

The conformational properties of α-amino acids are defined by three sets of torsion angles φ, ψ and ω, while in omega (ω) amino acids, due to the insertion of one or more methylene groups between the N- and Cα-atoms into the peptide backbone, the accessible conformational space is greater than α-amino acids. β-, γ-, δ-…. amino acid residues belong to the family of ω-amino acids.

While significant work has been done using the alpha, and beta amino acids for the conformational transitions and their importance in the field of nanomaterials and peptide based vaccine adjuvant developments [1-7]. The angles of amino acids and their three dimensional structure play a crucial role in enhancing immune response and vaccine development [5-7].

The conformational properties of β-amino acid residues are based on three degrees of freedom: φ (N - Cβ), θ (Cβ - Cα), ψ (Cα - CO). Similarly, the conformational variabilities of γ- and δ- amino acid residues are defined as four [φ (N - Cγ), θ1 (Cγ - Cβ), θ2 (Cβ - Cα), ψ (Cα - CO)] and five [[φ (N - Cδ), θ1 (Cδ - Cγ), θ2 (Cγ - Cβ), θ3 (Cβ - Cα), ψ (Cα - CO)] degrees of freedom, respectively [8]. Figure 1a illustrates the comparison of backbone torsion angles in α-, β-, γ- and δ-amino acid residues.

These torsion angles about the polymethylene chains are denoted as θ1, θ2,……θn, with increasing subscript numbers begin from N-terminus to C-terminus. The θ torsion angles lie close to gauche (θ ≈ ± 60°) or trans (θ ≈ 180°) conformations. Conventionally for β and higher ω-amino acids the Cβ / Cω atom precedes the Cα-atom, when the chain is read from N-terminus. βGly (β-homoglycine) is the simplest member of the β-amino acid family. For example, in β-residues, when substutituent takes at the Cα-carbon atom it is defined as β^2 while at the Cβ-carbon atom, it is defined as β^3. Figure 1b illustrates the nomenclature of acyclic substituted β-amino acid residues.

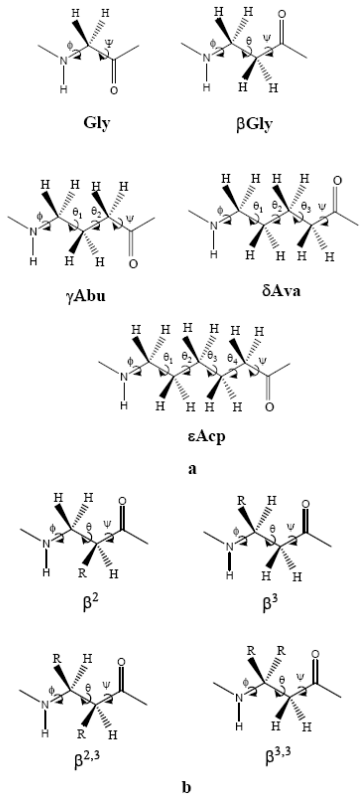

Figure 1: (a) Definition of backbone torsion angles in α, β, γ, δ and ε-amino acid residues: Gly → glycine, βGly → beta glycine, γAbu → gamma amino butyric acid, δAva → delta aminovaleric acid and εAcp → epsilon amino caproic acid. (b) Acyclic β-amino acid residues.

Figure 2 shows the definition of β^3-HAla, β^3-HVal, β^3-HPhe, β^3-HLeu and β^3-HPro residues. β^3-HAla, β^3-HVal, β^3-HPhe, β^3-HLeu and β^3-HPro residues are referred in this thesis as βAla, βVal, βPhe, βLeu and βPro, respectively. γAbu (gamma aminobutyric acid) and δAva (delta aminovaleric acid) are the simplest members of the γ- and δ-families, respectively.

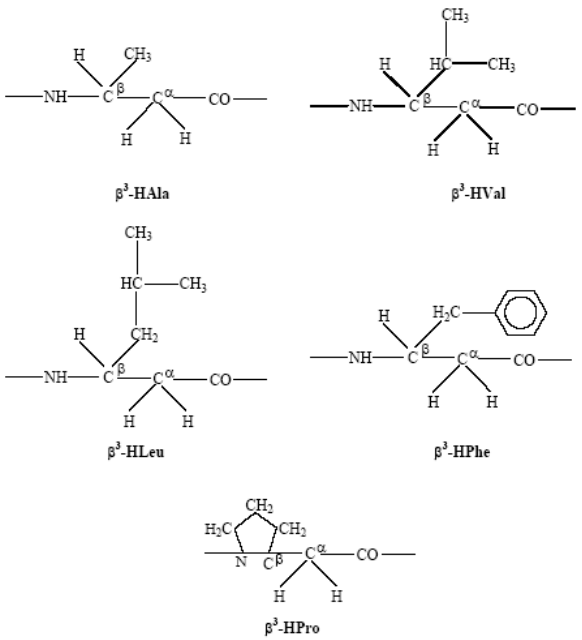

Figure 2: Chemical structure of some β^3-amino acid residues: β^3-HAla → β^3-homoalanine; β^3-HVal → β^3-homovaline; β^3-HLeu → β^3-homoleucine; β^3-HPhe → β^3-homophenylalanine; β^3-HPro → β^3-homoproline.

Currently, small molecule based drug increasingly interest in development of anti-cancer therapy molecules like Bortezomib, gold nanoparticles platinum based inorganic molecules for anti-tumor therapy [9]. The homologation alpha amino acids to beta amino acids or gamma amino acids would enhance the penetration of drug molecules inside the cellular lever to develop the anticancer drugs. The incorporation of inorganic drug molecules co-ordination with protein secondary structures would help for development for vaccines for cancer treatment [10,11].

References

1. Rajagopal A, Aravinda S, Raghothama S, Shamala N, Balaram P (2011) Chain length effects on helix-hairpin distribution in short peptides with Aid-^{D}Ala and Aib-Aib Segments. Biopolymers - Peptide Sciences 96: 744-756.
2. Raghavender US, Bhaswati B, Indranil S, Rajagopal A, Shamala N, et al. (2011) Entrapement of a Water Wire in a Hydrophobic Peptide Channel with an Aromatic Lining. Journal of Physical Chemistry 115: 9236-9243.
3. Rajagopal A, Aravinda S, Raghothama S, Shamala N, Balaram P (2012) Aromatic interactions in model peptide β-hairpins: Ring current effects on proton chemical shifts Biopolymers - Peptide Sciences 98: 185-194.
4. Krishnayan B, Rajagopal A, Raghothama S, Shamala N, Balaram P (2012) β-Turn Analogues in Model αβ-Hybrid Peptides: Structural Characterization of Peptides containing $\beta^{2,2}$Ac6c and $\beta^{3,3}$Ac6c Residues. Chemistry an Asian Journal 7: 1671.
5. Rajagoapl A, Charles BC, Alexey YK, Joshua DS, Frederick JK, et al. (2015) Enhancing the Magnitude of Antibody Responses through Biomaterial Stereochemistry. ACS Biomaterials Science and Engineering 1: 601-609.
6. Koyfman AY, Rajagopal A, Samantha S, Rudra JS (2015) Self-Assembly of Heterochiral Peptides with Varied Sequence Patterns.
7. Rudra JS, Ding Y, Neelakantan H, Ding C, Rajagopal A, et al. (2016) Suppression of Cocaine-evoked Hyperactivity by Self adjuvanting and Multivalent Peptide Nanofiber Vaccines. ACS Chemical Neuroscience.
8. Banerjee A, Balaram P (1997) Stereochemistry of Peptides and Polypeptides Containing Omega Amino Acids. Current Science 73: 1067-1077.
9. Appavu R, Mohan D (2016) Bortezomib in Anti-Cancer Activity: A Potential Drug. Global Journal of Cancer Therapy 2: 005-008.
10. Appavu R (2016) Expanding the Loop Segments in β-hairpin Nonapeptides in Protein Folding and Biological Functions. Transcriptomics 4: e116.
11. Appavu R, Mohan D, Kakumanu R, Munisamy G (2016) Fundamental of Secondary Structures in Peptide Based Synthetic Nanovaccine Development. Transcriptomics 4: 131.