Mutated Protein's Stability Accordance To Carbon Force Of Interaction

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***Abstract*—Analysis leading to carbon value appreciation in biological phenomena are focus of our work in the last decades. Accordingly the elsewhere appreciation in mutation study is the focus of this work that can be extended to disease solving in human. Analysis of anthrax protective antigen on stability of native and mutated form are the main focus. Otherwise our CARd of all analysis in protein one is derived to extend here in mutational stability values. Available and availability of carbon value is the main theme here to derive stability. Understandably, analysis prove to be in accordance with the reported experimental value. That is comparison of anthrax protective antigen mutations such as Q277A and F554A are confirmed to be stabilized by the carbon value of available and availability. We have appreciated the role of carbon in mutation that leads to stability and all. Over and above it phenomenal to note that carbon alone is going to be the factor of appreciation in dealing such mutational study which is evident from this study appreciation. All and all it is the only force coming from carbon for the disease solving and applications to new development in living things.**

Keywords— CARd; mutational study; anthrax protective antigen; carbon value; availability of carbon; COD; carbon profile;

I. INTRODUCTION

In order to explain the phenomena of binding of proteins, we have conducted a series of research analysis to put forth the carbon value distribution [1-4]. Accordingly the results are in agreement with several phenomena of unexplained values [4]. Otherwise carbon value was appreciated in many problematic activities in biology. Notable activities are appreciated in binding of macro one to another in the vicinity of water persistent [3]. Whole of the matter restricted to carbon profile obtainable from value of 0.3144 of carbon elsewhere in the system [5]. Restrictions are to the profile value which eventually govern the protein binding and all. Needless to say that carbon factor of appreciation is in the core of issue. When in need to improve binding there are unprecedented carbon for favoring binding. Nonetheless carbon favors binding and leading to stability as in DNA-probe one [6]. During the analysis and our thoughts are to be in the verifiable parameter of protein mutation in the vicinity of water one and all. Accordingly we have tested several phenomena of activities in series with the available data from database of biological work [7-10]. Very interesting observations are appreciated in detail and also in the process of solving several diseases in human sufferings [10]. According to the interaction of carbon value in proteins, it is worth doing mutational study that can be evaluated for salvation of human one. We are in thought of doing such imitative in the years to come. In this juncture it is essential to study and validate the mutational study leading to stability of proteins. Accordingly we have selected a known case study involved in the previous work [11]. That is anthrax protective antigen was stabilized by two mutations namely Q277A and F554A with experimental study. It is worth supporting this phenomena of stability which comes from carbon value and all. We have studied this mutational one leading to stability of anthrax one. Similar to this work very many examples are studied which are to be considered appropriately. Here in reported that the mutations are to be due to the carbon profile of interaction in accordance to the neighboring aminoacids. This can be extended further with amino acid mutation in improving protein stability and all.

II. METHODOLOGY

The protein sequence is taken from protein data bank (1ACC). Although one can analyze the structure of it, the sequence alone is taken for study as carbon value can be derived from sequence information that meets the requirement of mutation followed by stability and all. Otherwise analyses were carried out with PERL program written specifically for mutational study and stability factor of comparison. Method of analysis is given in the reference (Pubmed ID: 22829720) paper. Complete carbon value at each amino acid positions were computed with the help of CARd program [5] and also the available carbon and standard deviations at mutational sites are computed using the PERL one. Otherwise these are named as CarValue and Mute respectively for carbon value and mutational comparison. All and all using code previously shown in the CARd program as in reference. Obtained values are plotted for comparison appropriately as in figures 1 to 3. Available are the method of calculation and management of output values. Calculations using the parameters of inner length 35, step value 1 and variable outer length from 3 to 45. Otherwise available outer lengths are limited by position of the mute site in the sequence. Maximum consideration have up to 45 aminoacids length. One can stop at 15 for moderate comparison. Otherwise we have computed up to 60 here as the sites are at middle of the sequence with adequate length in both sides.

III. RESULTS AND DISCUSSION

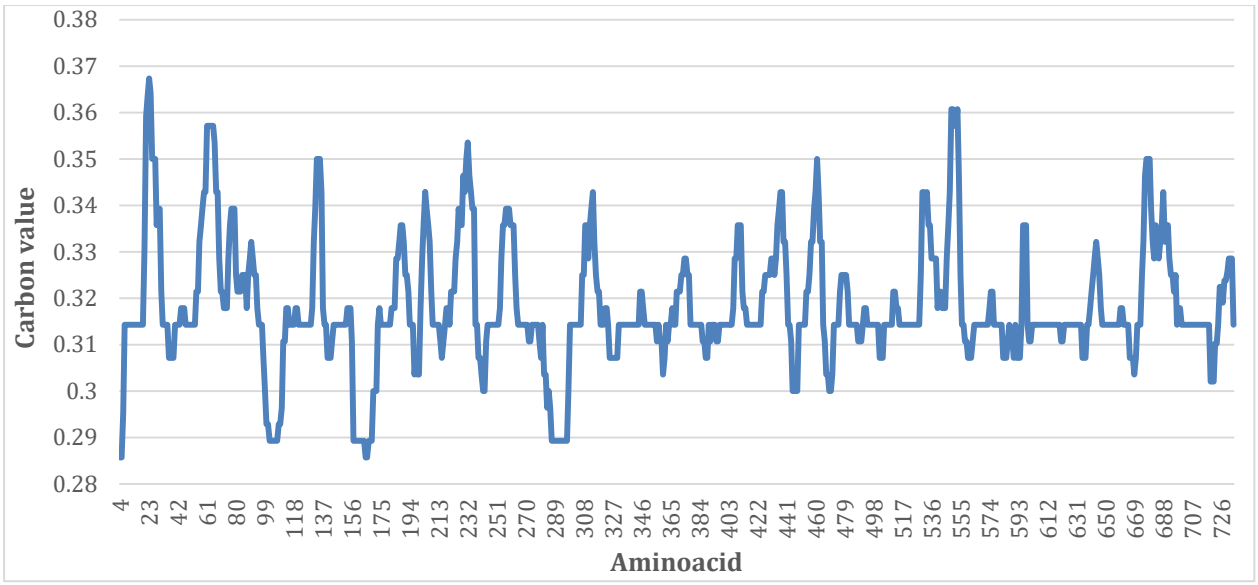

Figure 1: Carbon value along the sequence of anthrax protective antigen.

Mutational sites (277 and 554) are given with carbon values as shown in figure 1. Otherwise it is carbon-less portion at site 277 and carbon rich portion at site 554. It will be confirmed later in the figures 2 and 3. According to our earlier work [11], the mutations (Q277A and F554A) at these two sites stabilize the thermo labile anthrax protective antigen protein significantly. Whereas it is unstable in terms of carbon profile point of view here in this map of carbon value. Overall the protein is highly unstable in terms of carbon profile where the magnitude of carbon value goes up to very high value of 0.36 and significant number of carbon-less portions along the sequence as can be referred in the figure. Accordingly the protein show up with very high temperature factor and in fact several aminoacids are missing in the crystal analysis. Our work on stability of proteins reveal that correlation between thermostability and temperature factor [12]. Over and above the profile may not match with carbon value very well which supposedly around 0.3144 all along the sequence, but significant deviation all along. Overall the protein is destabilized from carbon point of view which in support of missing residues in crystal structure of it.

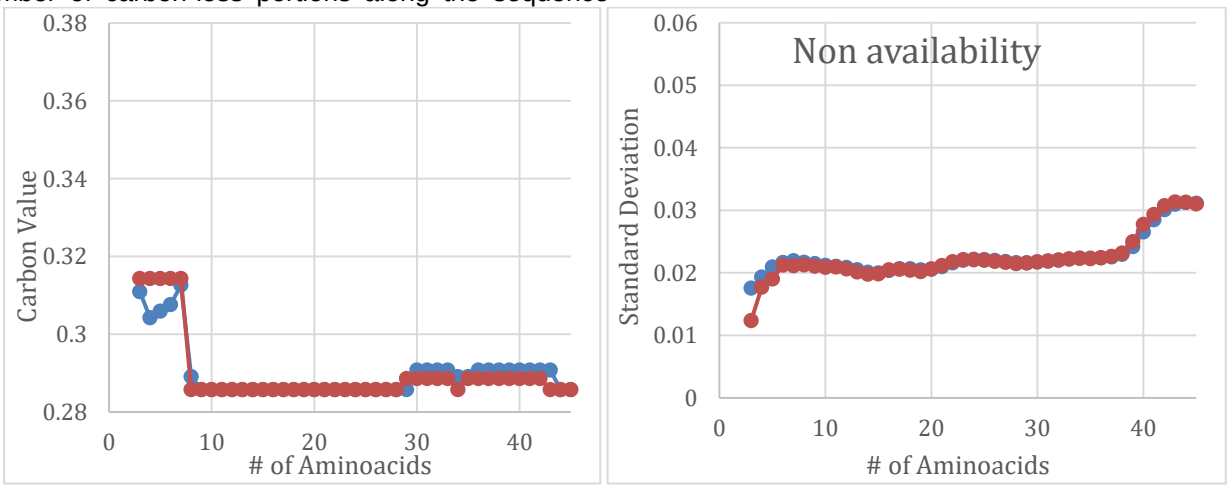

Figure 2: Carbon value at different length of aminoacids at site 277 for native (blue) and mutated (Q277A) (dark brown) form. Also the standard deviation at each lengths are given in the nonavailability plot.

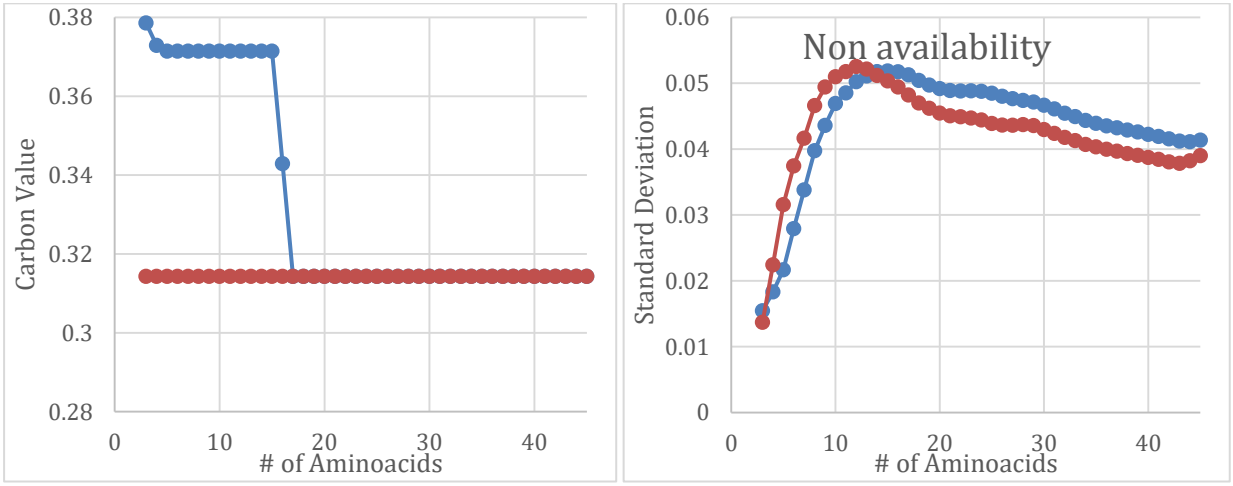

Figure 3: Carbon value at different length of aminoacids at site 554 for native (blue) and mutated (F554A) (dark brown) form. The standard deviation at each lengths are given in the nonavailability plot.

Carbon and standard deviations of available mode are expressed in terms of aminoacids group in figures 2 and 3. It is observed that available carbon at site 227 is less relative to 554 which are in agreement with carbon value observed in figure 1 of this anthrax protective antigen. Otherwise there are changes in carbon value according to group averages. That is to say that available carbon varies with length of the sequence from the site of interest. How long does it matter and all needed to be studied here. Otherwise up to 15 it is certainly affecting the carbon profile one to another in terms of mutation or so. It is going to be the deciding factor all mutations to be stable or not. Accordingly the available carbon are better in both the mutations considered here which are in agreement with experimental data produced earlier in reference [11]. Available carbon supposedly the value of 0.3144 which are said to be selection in every proteins and also in other biomolecules. Needless to say that any deviation from this value considered to be invalid in terms of stability and all [13]. In either of this case it is improving the value nearer to the carbon of available source. Improvement in this number get stabilized accordingly. Variations may attract other molecules to bind to alter carbon profile accordingly. Interestingly this raises question on how we can go about stabilization of protein appropriately leading to effective function avoiding diseases and all. Mutation of carbon profile are the critical here in stability point of view. Over and above it will improve the performance of the involved one. Originally in its core, available carbon value may be changing according to the closeness from the neighboring aminoacids. Otherwise all carbon profile high or less leading to instability in the system of operation which needs to be taken care here in the form of mutational study on available carbon profile. One would go about available carbon value with existing one which are natural selection according to the carbon of available source in the vicinity of entitled amino acid in consideration. Either of the database value of natural selection or the carbon value can lead to stability and all. Otherwise all of us have to be considered in terms of nano force coming from carbon value here in mutational one that and all allowed according to near carbon available source. Availability are according to neighboring aminoacids adjacent to the one where and all interested in mutation is considered. Accordingly one may choose from sequence of available sources and alter the carbon profile of interest. Adjusting this phenomena of carbon availability may also be done through program here used for alteration. Otherwise other program which statistically arrange all 20 aminoacids at the site of interest. Meaningfully one would choose to coordinate carbon profile and other possibility of interactions coming from internal one in every system of interest. In this context meaningful selection could be arrived at available sequence which are known earlier in the literature of available databases.

Standard deviation of statistical values in terms of carbon profile are given in the plot nonavailability of figure 2 and 3. Carbon profile may also assessed from this standard deviation value coming from carbon value calculations where and all any deviation of carbon value at point to 0.3144 are measured in terms of carbon distribution at outer window rolling the inner window inside it. This change in carbon profile of inner window is considered to be availability measure. Variations in this value is measure of standard deviation which indirectly involved in carbon value distribution. Verifying this value could be of interest in terms of validation to fit or not in the site of interest. Verification leads to validation and all in the vicinity of adjacent aminoacids for carbon profile fit. Accordingly this phenomena of fit is verified in both mutations considered here in anthrax protective antigen at sites 277 and 554. While both mutations are stabilized from carbon available value. Here in standard deviations it is stabilized at 277 always and the other site 554 show deviation up to 15 aminoacids long or so. Otherwise it is completely stabilized after length 15 in mutation F554A. In this context it is important to consider both available carbon value and availability value coming from standard deviation. Mostly the improvement in carbon available value clearly explain than that of

availability value. Weightage of this deviation of standard is to be prioritized very soon at least for selected cases where mutation may be stabilized but nonaligned in terms of carbon availability. Overall it is satisfying this phenomena of carbon value and all. Verification all this parameter of interest is essential for mutational one that and all going to be studied here in our lab while on the other analyses are on. Mutation leading to stability is undoubtedly part of carbon value as shown and demonstrated here with known cases. Accordingly one would choose to work with mutational study for improvement in the protein of interest. Ever since discovery of this carbon value 0.3144, variety of applications leading to human health care are tested and validated where as it is time to mutate unknown one to test the reality of it. Over and above it is going to be the salvation of all diseases so far available in the literature. Also needless to say that all that happen in the biology is based on this force of attraction which is coming from carbon one [14, 15]. Parallel cases are demonstrated to be involved in this profile of interest and according to nature of interaction [16-20] it will be implemented in the upcoming studies.

IV. Conclusion

Carbon value of available and availability are computed for native and mutated form. According to the value of report the prescribed mutations are stabilized by carbon value of available and availability. It is important to note that carbon alone is going to be the ruler of mutational study in the future to come and all. Available carbon seems to be the best predictor of adjustment in mutational study. Otherwise all studies leading to stability of protein are to be borne by carbon value here in reported. Based this value alone be predicted further with stability and all.

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