

What Might be the Difference in Viral Proteins?

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Abstract— The contrast among ordinary and viral proteins is the manner in which the amino acids sorted out in some structure. Despite the fact that the two proteins utilize same 20 normally happening amino acids, it contrasts in courses of action. This distinction can't be felt by only looking at the amino corrosive arrangement yet at iota level. This is breaking down and analyzed as far as carbon appropriation as carbon is the main component that contributes towards the predominant power, hydrophobic association. For this reason, the arenaviruses have been chosen here for study. The protein groupings of 7 arenaviruses are examined. Our outcomes demonstrate that the carbon dispersion in viral proteins is not the same as the ordinary proteins. Either the carbon substance is unique or the conveyance isn't uniform. This carbon appropriation investigation utilizes our prior report of 31.44% of carbon for its structure and action.

Keywords— Carbon dissemination, arenaviruses, hypothetical examination, succession investigation.

1. Introduction

Carbon is the main component contributes towards the predominant power, hydrophobic connection in proteins. Protein's carbon substance develops in light of carbon accessibility and may impact the essence of copied qualities [1]. This carbon substance and dispersion in viral proteins is expectedly unique in relation to ordinary one in light of the fact that the association of amino acids in viral proteins is diverse however both utilize same 20 normally happening amino acids. It is accounted for that proteins likes to have 31.44% carbon for its steadiness [2]. This portion of carbon substance can be utilized as standard of carbon estimation and correlation [3]. The distinction in carbon circulation in viral proteins is the focal point of this work by accepting arenavirus as contextual investigation.

The family arenaviridae comprises of two antigenic gatherings, the New World arenaviruses found in the Americas and Old-World arenaviruses local to Europe and Africa. The arenaviruses tend to cause quiet diseases in their regular hosts, rodents and people. The genome of length 5000-7400 nucleotides comprises of two single-stranded RNAs, the little (S) and the huge (L), sections. Each fragment encodes two distinct proteins. The S RNA encodes the nucleocapsid protein (NP) and the glycoprotein antecedent (GPC) which experiences present translational preparing on yield two develop proteins (GP1 and GP2). The L RNA encodes the viral RNA-subordinate RNA polymerase (L) and a zinc-restricting network protein (Z). Nucleotide successions of 3'- end to a great extent integral to comparative districts on the 5' end; saved nucleotide arrangements; the equivalent in types of same variety; S on RNA; 19-30 nucleotides in length. Epitomized nucleic corrosive both genomic and non-viral; including three atoms of host ribosomal RNA. Just seven of the twenty-three arenaviruses are related with human ailment which are recorded here.

2. Method

The four distinctive protein groupings of seven arenaviruses are gathered from the NCBI. The amino corrosive syntheses are determined utilizing AACOMP program. The outcomes are talked about and not appeared in here. The carbon dispersion in these proteins is figured utilizing CARANA program which

uses the standard of 31.44% of carbon [2]. The CARANA program can be gotten to online [6]. The outcomes on carbon conveyance as a component of nuclear position are plotted as appeared in figures.

3. RESULTS AND DISCUSSION

We have contemplated the carbon conveyance in protein successions of 7 arenaviruses containing 4 distinct proteins. The name of the infections contemplated and length of each arrangement are given in table 2. As can be seen from the Fig.1, the carbon content in GPC protein is more prominent than the normal estimation of 31.44 in whole grouping with the exception of in few spots. This protein could communicate with a few different biomolecules that start or smother biochemical responses. The underlying bit of this protein contains higher carbon content that could hold other cooperating atoms for sliding or for further response. On the opposite end the carbon substance is not exactly the normal worth that may not partake in biochemical responses. This end may either be quiet in water or can have electrostatic interaction with different atoms. Additionally, at position around 5250 iota number (or 333 amino corrosive number) there is a dunk in carbon content. The plots for different proteins, for example, NP-protein, L-protein and Z-protein are not appeared but rather examined. The Z-protein is a little protein demonstrates a higher measure of carbon content up and down the grouping aside from toward the finish of the succession. There is no single practical site found in this protein. The Z-protein of LCMV apparently lesser measure of carbon contrasted with different infections. This present protein's carbon circulation in LCMV and Sabia infections are very not the same as different infections. This shows this protein might not have a particular capacity in all infections. NP-protein then again having comparable conveyance in all infections. The carbon dispersion seems like ordinary proteins with couple of dynamic destinations and sufficient carbon content. There is hydrophilic district for length of 99 amino acids between amino corrosive position 30 and 129. The L-protein is an enormous protein indicating again rich measure of carbon. Generally speaking, these viral proteins appear higher measure of carbon. The Large hydrophobic buildups (LHR, for example, F, I, L, M and V are the significant patrons towards this carbon content [4]. These LHRs are coded by codon XTX (where X = A, T, G or C) [5]. We have additionally explored the job of thymine in mRNA successions of these proteins. The outcomes demonstrate that there is more prominent measure of thymine in all cases. Adenine is lesser contrasted with thymine in all cases however in L-genome of LCMV. This distinction is additionally seen in carbon dispersion of Z-protein of LCMV. The measure of AT together is constantly more prominent than GC in both genome and in all infections. This isn't the situation in human mRNA successions.

4. Conclusion

To finish up, carbon substance and circulation are distinctive in viral proteins. The carbon dissemination thinks about on viral proteins uncover that the viral proteins appear with higher measure of carbon. The nuclear structure assumes a job in advancement of proteins. The distinction in carbon dissemination in proteins causes ailment. The carbon dispersion think about along the protein chain is the most critical advance towards understanding the natural responses. The mRNA groupings of these proteins appear with more prominent measure of thymine all cases. The measure of AT together is constantly more prominent than GC in both L and S genome of all infections. This isn't the situation in human mRNA groupings. In other words, nature is adding increasingly hydrophobic proteins to the host cell through infections.

5. References

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Table 1: The Arenavirus Disease and its geographic distribution

Virus	Disease	Geographic Distribution
Lymphocytic Choriomeningitis virus	Meningitis	Europe, Americas
Lassa virus	Hemorrhagic fever	West Africa
Junin Virus	Argentine hemorrhagic fever	Argentina
Machupo Virus	Bolivian hemorrhagic fever	Bolivia
Guanarito	Hemorrhagic fever	Venezuela
Sabia virus	Brazilian hemorrhagic fever	Brazil
White water arroyo virus	Hemorrhagic Fever	North America

Table 2: Number of amino acids in all 4 types of proteins and 7 arenaviruses

Name of the Virus	GPC-protein	NP- Protein	L-Protein	Z-Protein
Guanarito virus (GV)	479	560	2198	95
Junin virus (JV)	485	564	2210	94
Mopeia Lassa reassortant 29 (LV)	491	569	2220	99
Lymphocytic choriomeningitis virus (LCMV)	498	558	2209	90
Machupo virus (MV)	496	564	2209	94
Whitewater Arroyo virus (WWAV)	480	562	2219	95
Sabia virus (SV)	488	562	2212	100

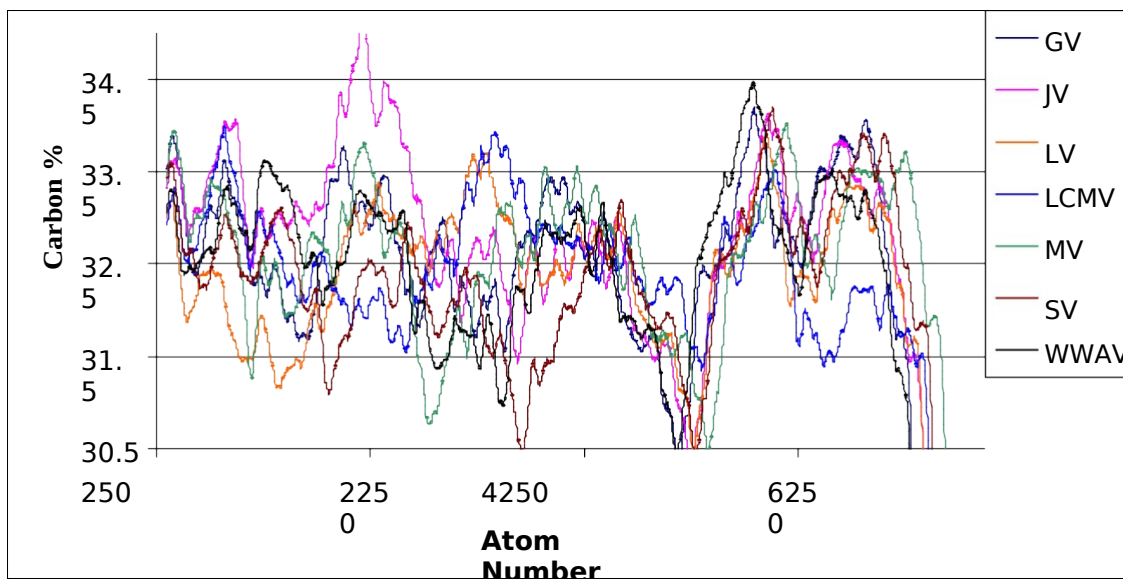


Fig 1: Carbon distribution in the GPC protein in all 7 viruses



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