The Thirteenth International Symposium on Artificial Life and Robotics 2008(AROB 13th '08),
B-Con Plaza, Beppu, Oita, Japan, January 31-February 2, 2008

Asymmetry underling Protein

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Abstract: Density ratio of hydrophilic and hydrophobic amino-acids averaged for a lot of proteins in bacteria and archaebacteria is asymmetric. The density ratio is calculated for the proteins over 1,000 types. The reason why the asymmetric ratio can be observed is related to the density ratio of purine and pyrimidine in codon. The density ratio of purine and pyrimidine at the center locus of codon is close to that of hydrophilic and hydrophobic amino-acids in proteins.

Keywords: hydrophobic, hydrophilic, amino-acid, asymmetry, protein.

I. INTRODUCTION

We can classify five bases of adenine (A), guanine (G), cytosine (C), thymine (T), and uracil (U) into two groups, purine and pyrimidine. Purines, i.e., A and G, have relatively larger size, while pyrimidines, i.e., C, T, and U, are smaller. [1]

Specifically, this refers to the asymmetric size ratio of purine and pyrimidine of around 1.50 in their hydrogen bonds within DNA and RNA, although a symmetric size ratio of 1.00 is often observed in RNA.

This size asymmetry of around 1:1.5 of the main rings in purines and pyrimidines naturally leads us to the asymmetric number of types, i.e., "two" types of purines (adenine and guanine) and "three" types of pyrimidines (cytosine, thymine, and uracil). This asymmetry of 2:3 can be understood from the mass conservation law with respect to molecular weight, that is, from the fact that the main rings of purines have "nine" molecules of carbon and nitrogen, while "six" molecules of carbon and nitrogen form the main rings of pyrimidines. [2-7]

II. EIGHT HYDROPHOBIC AND TWELVE HYDROPHILIC AMINO-ACIDS

Curious to say, the numbers of hydrophobic and hydrophilic amino-acids are 8:12, which is also 2:3. (See Table 1.) In the later sentences, we will show that the asymmetric frequency ratio of 2:3 for nitrogenous bases and amino-acids is not accidental coincidence.

First, it is stressed that the nitrogenous base, which is at the center locus of codon coding most of hydrophobic amino-acids in Table 1, is pyrimidine, while hydrophilic amino-acid correspond to purine at the codon center. As is well-known [1,8], this is because the center locus is closest to amino-acid in tRNA. (See Fig. 1.)

Transfer RNA (tRNA) showing two-dimensional structure in Fig. 1 bends in three-dimensional space in-vivo and then anti-codon is close to amino-acid. The present access of anti-codon and amino-acid leads to the fact that the asymmetric frequency ratio of hydrophobic and hydrophilic amino-acids in protein is close to that of purine and pyrimidine in anti-codon (and also codon). Size-difference between purine and pyrimidine will bring that of hydrophobicity, i.e., exclusion of water molecules.

III. AMINO-ACIDS IN PROTEINS

In this section, we will examine the accurate value of the frequency ratio of purine and pyrimidine. Let's see the frequency ratio of hydrophobic and hydrophilic amino-acids in a lot of proteins of some bacteria and archaebacteria. (Table 2)

Actual frequency ratio of hydrophobic and hydrophilic amino-acids in proteins shows the asymmetric values less than 1.5. Why will the ratio be reduced a little less than 1.5?

Figure 2 demonstrates that, in nucleic acids, nitrogenous bases are connected by covalent bonds with sugar and phosphoric acids. The molecular weight ratio of purine connected with sugar and phosphoric acid and pyrimidine with sugar and phosphoric acid is around 1.20. This consideration clarifies the values between 1.0 and 1.4 in Table 2. Then, the frequency ratio of purine and pyrimidine in codon is mostly between 1.0 and 1.5.
For example, let' s see Aeropyrum pernix. Density ratio of purine and pyrimidine in codon of Aeropyrum pernix is about 1.10. The frequency ratio of hydrophobic and hydrophilic amino-acids in proteins of Aeropyrum Pernix is about 1.15.

IV. THREE - DIMENSIONAL STRUCTURE OF PROTEIN

In our previous reports [2,4,5,6,7], we clarify that asymmetric frequency ratio of purine and pyrimidine in tRNA and rRNA promotes the clover-structure, because redundant loci, which can not make stems of base-pairs, become leaves. Asymmetric frequency ratio of hydrophilic and hydrophobic amino-acids in proteins also leads to complex shape of concavoconvex in these proteins, because identical amino-acids such as hydrophilic-hydrophilic ones face each other in many cases, which correspond to purine-pyrimidine pair.

Table 1: Twenty types of amino-acids and hydrophobicity (Classification of amino acids: S. Okayama, Seimei kagaku Nyuumon, Baifukan [8])

	Base at the center of codon	Hydrophilic or hydrophobic
Ala	pyrimidine	hydrophobic
Val	pyrimidine	hydrophobic
Leu	pyrimidine	hydrophobic
Ile	pyrimidine	hydrophobic
Pro	pyrimidine	hydrophobic
Phe	pyrimidine	hydrophobic
Trp	purine	hydrophobic
Met	pyrimidine	hydrophobic
Asp	purine	hydorphilic
Glu	purine	hydorphilic
Lys	purine	hydorphilic
Arg	purine	hydorphilic
His	purine	hydorphilic
Gly	purine	hydorphilic
Ser	purine	hydorphilic
Thr	pyrimidine	hydorphilic
Cys	purine	hydorphilic
Tyr	purine	hydorphilic
Asn	purine	hydorphilic
Gln	purine	hydorphilic

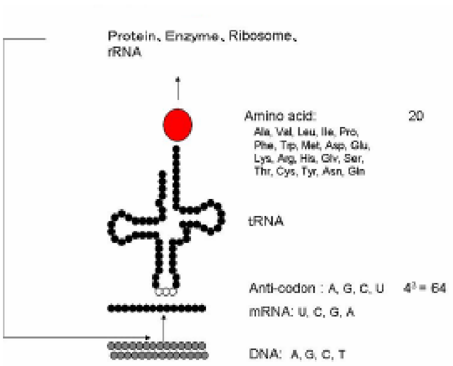

Fig. 1. Anti-codon and amino-acid

V. CONCLUSION

Asymmetric frequency ratio of purine and pyrimidine correspond to that of hydrophilic and hydrophobic amino-acids in proteins. The asymmetric frequency ratio of hydrophilic and hydrophobic amino-acids brings us complex structures of proteins.

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Table 2: Hydrophobic amino-acids / Hydrophilic amino-acids in Proteins of some species (Calculated by using Data bases [9, 10, 11, 12,13])

Species	The number of proteins	Ratio
Sulfolobus solfataricus P2	2993	1.31
Aeropyrum pernix K1	2620	1.15
Pyrobaculum aerophilum IM2	2605	1.12
Methanopyrus kandleri AV19	1687	1.25
Pyrococcus horikoshii OT3	2061	1.19
Escherichia coli K-12 MG1655	4188	1.21
Pseudomonas aeruginosa PAO1	5566	1.13

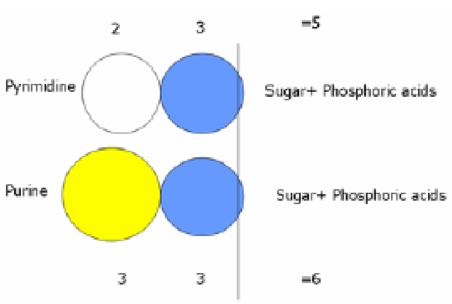

Fig. 2. Molecular weight ratio of purine and pyrimidine with sugar and phosphoric acids.