The constraints between amino acids influence the unequal distribution of codons and protein sequence evolution

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Supplementary Materials Table S1 The characteristics of proteins in 33 species. 33

species were sorted by number of proteins(from 40725 to 517).

Organisms	Median total length (Mb)	Median GC%	Number of proteins	Mean length of proteins(aa)	<100 aa of proteins(%)	>1000 aa of proteins(%)
<i>Zea mays</i>	2067.62	46.82	40725	356.71(8-5101)	12253(30.1)	1006(2.5)
<i>Arabidopsis thaliana</i>	97.38	36.65	27142	398.74(16-5393)	2309(8.5)	1092(3.7)
<i>Danio rerio</i>	1391.74	36.9	25699	542.58(32-29256)	577(2.1)	2784(10.8)
<i>Pan troglodytes</i>	3021.76	41.8745	22251	499.78(24-8827)	878(3.9)	2054(9.2)
<i>Mus musculus</i>	2541.65	42.3	21736	471.47(25-34358)	681(3.1)	1684(7.7)
<i>Homo sapiens</i>	2994.61	41.3255	21560	477.30(24-14507)	777(3.6)	1749(8.1)
<i>Gorilla gorilla</i>	3035.66	41.332	21549	483.05(28-12739)	1078(5.00)	1910(8.86)
<i>Sus scrofa</i>	2508.91	42.226	21338	477.06(31-13288)	626(2.9)	1727(8.1)
<i>Chlorocebus sabaeus</i>	2789.66	40.9303	20771	532.96(23-14184)	630(3.0)	2178(10.5)
<i>Bos taurus</i>	2697.56	41.8776	20745	511.06(30-7569)	594(2.86)	2020(9.74)
<i>Ovis aries</i>	2615.52	42.4	19646	530.53(36-8974)	477(2.4)	2087(10.6)
<i>Gallus gallus</i>	1230.26	42.9197	14683	563.10(32-12010)	357(2.4)	1760(12.0)
<i>Serinus canaria</i>	1152.1	42.6	13632	585.50(28-34416)	336(2.5)	1801(13.2)
<i>Drosophila Melanogaster</i>	148.5	41.9402	13519	478.91(11-22949)	913(6.8)	1140(8.4)
<i>Saccharomyces cerevisiae</i>	12.3018	38.4253	5794	487.37(16-4910)	322(5.6)	481(8.3)
<i>Bacillus anthracis</i>	5.45	35.2	4764	262.84(26-5017)	905(19.0)	68(0.5)
<i>Pseudomonas aeruginosa</i>	6.57	66.2	4665	334.56(23-5627)	308(6.6)	63(1.4)
<i>Pseudomonas putida</i>	6.02	61.9	4366	338.08(23-8682)	387(8.9)	76(1.7)
<i>Escherichia coli</i>	5.17	50.6	4172	306.28(24-5291)	572(13.7)	68(1.6)
<i>Vibrio Parahaemolyticus</i>	5.11	45.3	4131	312.05(216084)	584(14.1)	65(1.6)
<i>Bordetella bronchiseptica</i>	5.2	68.2	3893	328.74(37-4218)	203(5.2)	28(1.1)
<i>Bacillus subtilis</i>	4.1	43.7	3629	292.15(25-5488)	515(14.2)	36(1.0)
<i>Salmonella enterica</i>	4.76	52.1	3384	316.48(13-3624)	302(8.9)	38(1.1)
<i>Vibrio cholerae</i>	4.02	47.5	2974	329.35(26-4555)	261(8.8)	43(1.4)
<i>Bordetella pertussis</i>	3.76	67.7	2868	326.41(37-4196)	163(5.7)	35(1.2)
<i>Pseudomonas syringae</i>	6.04	58.8	2773	350.31(36-13537)	192(6.9)	57(2.1)
<i>Staphylococcus aureus</i>	2.87	32.8	2354	284.58(29-9535)	423(18)	28(1.2)
<i>Staphylococcus epidermidis</i>	2.53	32	2106	286.57(25-9439)	372(17.7)	23(1.1)
<i>Streptococcus pneumoniae</i>	2.1	39.6	1467	315.28(38-2551)	182(12.4)	26(1.8)
<i>Streptococcus pyogenes</i>	1.83	38.5	1398	309.97(27-2045)	159(11.4)	18(1.3)
<i>Helicobacter pylori</i>	1.63	38.9	1142	332.98(30-2893)	104(9.4)	14(1.2)
<i>Chlamydia trachomatis</i>	1.05	41.2643	718	356.34(45-1786)	53(7.4)	21(2.9)
<i>Buchnera aphidicola</i>	0.64	25.6387	517	330.17(38-1407)	40(7.7)	6(1.2)

Supplementary Materials Figure S1 The relationships between the amount of codons and the O:C ratios and between the amount pf codons and the N:C ratios. No correlation was observed unlike the amount pf codons and the C:H ratios.

Supplementary Materials Figure S2 The frequency of the number of Gly and of the length of proteins in human. The number of Gly and of the length of proteins can not fit normal distribution($Z=30.43$ and 27.84 , $p<0.000$) and Poission distribution($Z=65.65$ and 88.25 , $p<0.000$). The number of Gly was 31.98 ± 37.32 (from 0 to 1483) and the length of proteins was 477.30 ± 481.78 (from 24 to 14507).

Figures

Figure 1

The mean of carbon and hydrogen ratios keep a relatively stable value(0.50) in 33 species regardless of the significant change rates of 20 amino acids. a, Relationships between the sum of 20 amino acids of all proteins in 33 species and the number of their corresponding codons($F=(n*61)/(N*c)-1$), N: the sum of 20 amino acid in the genome of a species; n: the number of one amino acid in the genome of a species; c:the number of their corresponding codons. 61 is the sum codons. b, the mean of carbon and hydrogen ratios(0.50), oxygen and carbon ratios(0.50), nitrogen and carbon ratios(0.27) in 33 species.

Figure 2

The reasons of the relatively stable mean of carbon and hydrogen ratios. Relationships between 20 amino acids in 33 species(a), between the amount of codons and C:H ratio in 20 amino acids (b), between O:C and C:H ratio in 20 amino acids(c) and between N:C and C:H ratio in 20 amino acids (d).

Figure 3

The carbon and hydrogen ratios of all proteins in 33 species were tend to 0.50. a, The histogram of C:H ratio of 21560 proteins in homo sapiens(red line: normal curve); b, the kurtosis(red line: $y=1$) of the histogram of C:H ratio of 33 species d; c, the skewness of the histogram of C:H ratio of 33 species.

Figure 4

The interrelations between 20 amino acids in 33 speices. a-d, four kinds of scatter diagrams between in homo sapiens(positive correlation: $r>0.3, p<0.001$; negative correlation: $r<-0.3, p<0.001$; weak correlation: $|r|<0.3, p<0.001$ and indifference correlation: $p>0.001$)e, Pearson correlation analysis between 20 amino acids in 33 species and 12540 correlation coefficient($r, 19\times 20\times 33$) were obtained and shown in the matrix, and a phylogenetic tree was below; f, one of the matrix(e): Pearson correlation analysis between Asp(D) and other 19 amino acids and the matrix of 627 correlation coefficient.

Figure 5

Poisson distribution. a, the model to count the frequency of the figures which is the number of 20 amino acids in a protein; b, the mean frequency of the figure(λ_{mean}) in 33 species, and the highest λ_{mean} was 4, 5 or 6 in 33 species; c, the relationship between λ_{mean} and the theoretical frequency of the figures(λ) when these figures would fit Poisson distribution, red line: $y=x$; d, the histogram of the frequency of 6 and 20 and their fitted curve under the conditions of λ_{mean} and λ .

Supplementary Files

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