DISSIMILAR RATES IN MOLECULAR EVOLUTION

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ABSTRACT

In this work we present an evolutionary tree based on the differences in the physico-chemical properties involved in amino acid substitutions, instead of considering, for its construction, only the number of changes between species. Phylogenetic trees were constructed from the differences in bulkiness, refractivity index, hydrophobicity, polarity and optical rotation of 9 vertebrate calcitonins. A correlation of the form $y = a\ x^b$ was found between the number of changes (x) and the differences in any given physico-chemical property (y). This correlation implies that the evolutionary time can not be evaluated directly from the number of changes between species.

INTRODUCTION

The evaluation of the time elapsed in the evolution of the species has always been measured counting the number of substitutions occurring between the species. Nevertheless, not all these changes involve the same degree of feasibleness, being, probably, the more difficult changes produced in a larger span of time.

In this communication, we propose to evaluate the rate of evolution from the qualitative difference between exchanged amino acids. These are accounted for according to their physico-chemical differences. Actually, a high degree of conservation of some physico-chemical properties

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(refractivity index, bulkiness, hydrophobicity, polarity and optical rotation) was found for the most frequent exchanges of amino acids, described in a previous work for families of modern proteins.(1). Therefore, we have investigated the relevance of the physico-chemical changes involved in amino acid substitutions in the construction of evolutionary dendograms. These evolutionary trees are constructed taking into account not only the number of changes between aligned sequences, but also the differences in the physico-chemical properties inherent to these changes. Phylogenetic trees, derived from any one of these property differences, are compared with that generated by the number of changes. In this comparison, attention was paid to the general pattern and to species distances within the trees.

METHODS

For the construction of all the evolutionary trees analyzed in this work, we have used an algorithm described in a previous paper (2). This algorithm allows the correction of the original matrix of differences between aligned sequences and the proper selection of the nearest neighbours, giving a unique dendrogram.

The matrix of differences between amino acid sequences of 9 calcitonins of vertebrates was used in this analysis. (3). The reliability of the resulting trees was evaluated in each case by comparing the reconstructed and original matrices.

Finally, a correlation was found between the number of changes separating two species and the physico-chemical property differences involved in these changes.

RESULTS

Phylogenetic trees constructed from matrices of the number of changes between species (Fig. 1) and those constructed from differences in bulkiness, refractivity index and optical rotation show a topology similar to that displayed in figure 2. On the other hand, trees constructed from polarity and hydrophobicity differences conserve the above mentioned general pattern, excluding the salmon distribution. The degree of confidence in these dendrograms is supported by the small percentage of divergence found between the original and the reconstructed matrices. (For bulkiness

Calcitonin phylogenetic tree based on aminoacid changes

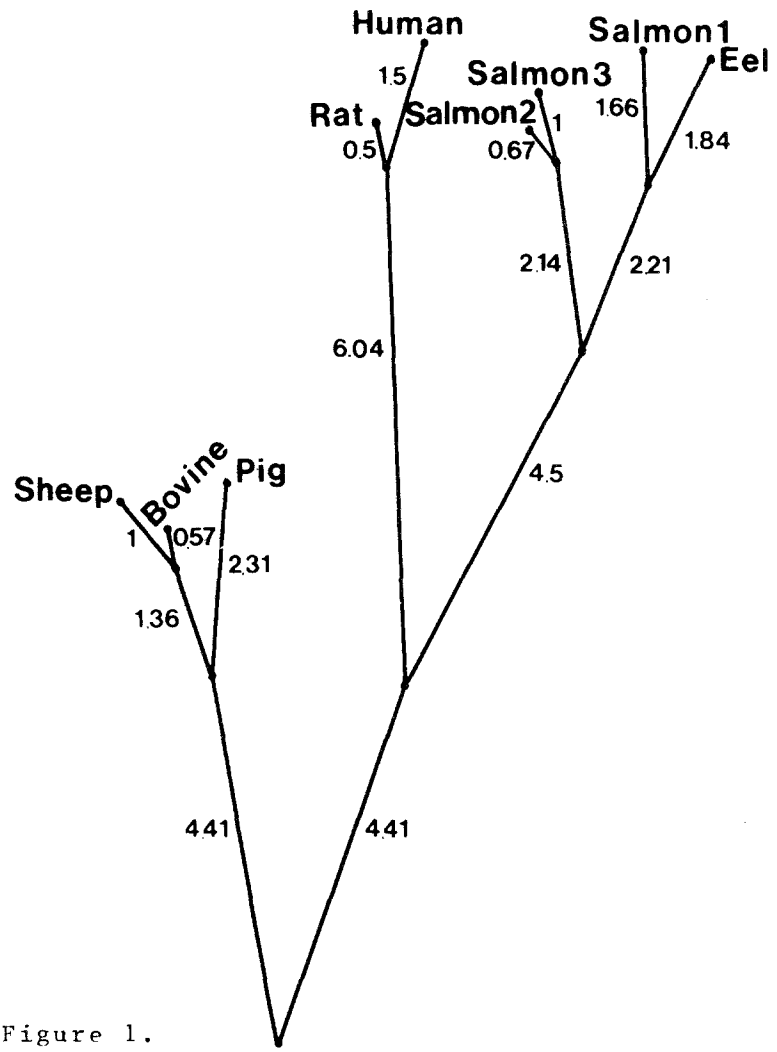

Figure 1.

tree: 5%, for refractivity index: 6,6%, for optical rotation: 6%, for polarity: 1% and for hydrophobicity 5%.).

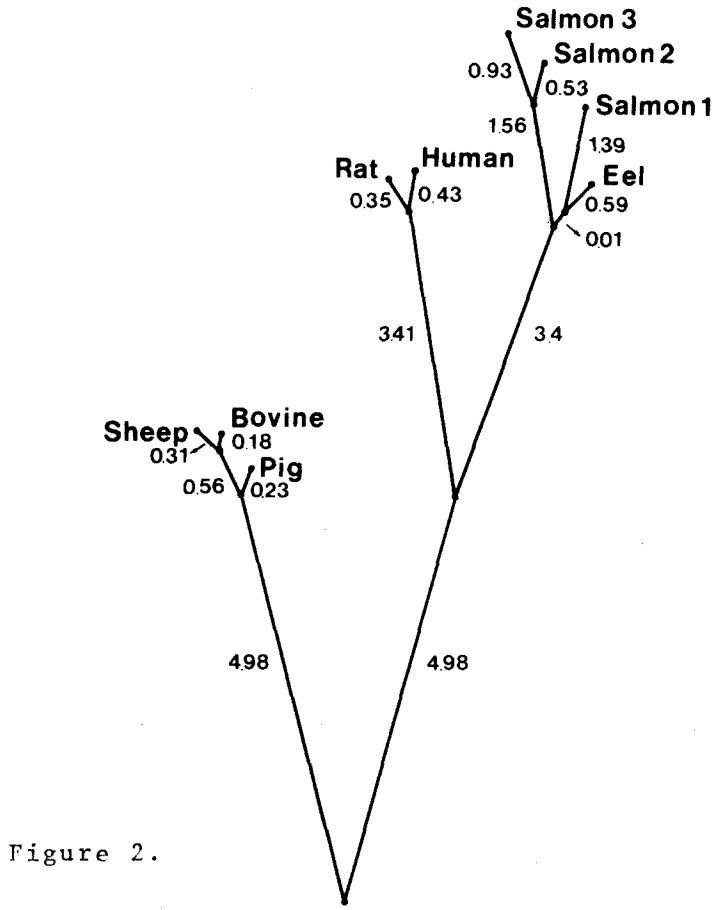

Figure 2.

The correlation between the number of changes between species and the differences of physico-chemical properties involved in these changes was found to satisfy the power function:

$$Y = a\ X^b$$

where Y= physico-chemical property differences between the proteins of the different species.
X= number of changes between the species.
a,b= constants.

Figure 3 illustrates this correlation for bulkiness, where $\underline{a}$ = 0.29; $\underline{b}$ = 1.31; r^2= 0.93.

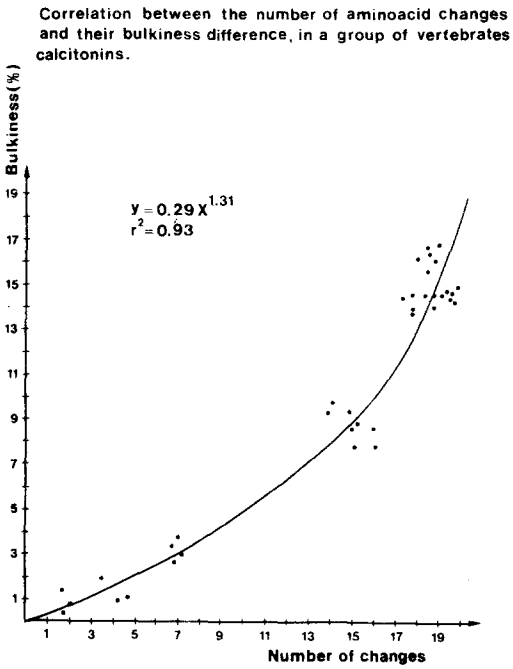

Figure 3.

For the other physico-chemical properties also studied, the following values were obtained:

	a	b	r^2
Refractivity index	0.23	1.36	0.89
Optical Rotation	0.17	1.5	0.88
Polarity	0.06	1.98	0.86
Hydrophobicity	0.22	1.45	0.91

DISCUSSION

The algorithm used to construct the evolutionary trees generates a self consistent table of distances. This corrected table permits without ambiguity the restoration of the predetermined tree.

The remarkable power function displayed in Fig. 3 shows a significantly lesser slope for the nearest species than for the unrelated ones. Consequently, the degree of difficulty for the changes to take place could be a better measure of the time spent in the evolution of the species than only the number of changes. Thus for a more realistic estimation of the time spent in the evolution of species, we suggest the determination of the parameters a and b from more recent archeological data which could allow to extrapolate the function $Y = a X^b$ to distant species.

Furthermore, the equation $Y = a X^b$ implies the existence of a singular tree in which the length of the branches increases progressively from the terminal vertices towards the first ancestor.

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