

Extremely divergent histone H4 sequence from trypanosoma cruzi: Evolutionary implications

Toro, G. Cecilia

Wernstedt, Christer

Medina, Carlos

Jaramillo, Nicolás

Hellman, Ulf

Galanti, Norbel

Trypanosoma cruzi presents six histones electrophoretically resolved in three gel systems. Indirect evidence shows that one of these histones, name, corresponds to H4 in other species. We present evidence that histones is H4 by sequencing its amino terminal end. The amino terminal of T. cruzi histone H4, unlike that of other H4s examined thus far is not blocked. Moreover, this protein presents two variants. This partial amino acid sequence of T. cruzi histone H4 differs greatly from homologous sequences of human, yeast, or Tetrahymena. Since the conservatism of the core histones (H2A, H2B, H3, and H4) is clearly illustrated by comparative sequence analyses, the data shown here demonstrates that T. cruzi histone H4 is the most divergent reported. Quantitative analysis of the data suggests that the rate of substitutions in the histone H4 amino terminal sequence varies among different lineages. We postulate a slow?down in the evolutionary rate of histone H4 amino terminal domain in the me