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Structural comparison of β-CASP nucleases: RNase J and CPSF groups

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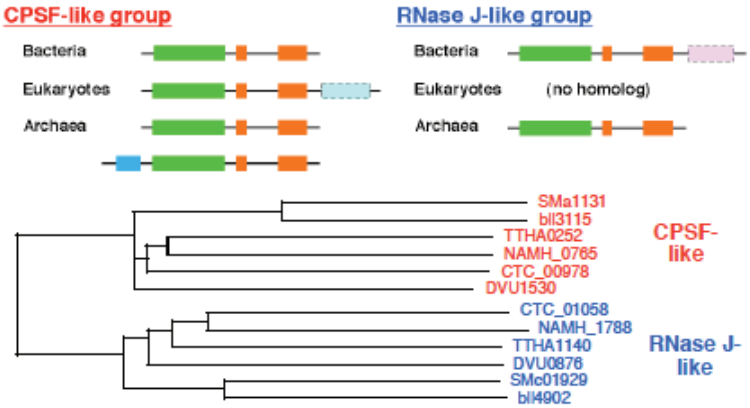
β-CASP family proteins are novel nucleases belonging to metallo-β-lactamase superfamily. These proteins are now very highlighted by its major role in essential biological processes. The members of the β-CASP family proteins are involved in processing of RNA, global mRNA decay, V(D)J recombination, and maintenance of telomere. In eukaryotes, the 73 kDa subunit of cleavage and polyadenylation specific factor (CPSF-73) is a representative member of β-CASP nucleases, which functions in mRNA processing. A bacterial respresentative, RNase J is thought to be a functional homologue of RNase E because many bacteria have no orthologue of RNase E essential for mRNA degradation in *E. coli*. The crystal structures of CPSF-73 and RNase J were also determined. *Thermus thermophilus* HB8 has two β-CASP family proteins, TTHA0252 and TTHA1140 (RNase J). We have determined the crystal structure of TTHA0252 as the first member of β-CASP family proteins [1]. This family proteins commonly have two core domains, the metallo-β-lactamase domain and the β-CASP domain. However, no detailed analysis of the category of the β-CASP family has been performed because this family was recognized recently. In this study, we analyzed the sequence features of β-CASP family proteins, especially in bacteria together with the structural features. We found that β-CASP family proteins can be categorized mainly into two groups. One group is related to RNase J, which is always located adjacent to an exoribonuclease PNPase. Another group was conserved in all three kingdoms, with similarity to CPSF-73 subunit. Phylogenetic distribution of RNase J group members showed clear anticorrelation with that of RNase E. This results supported the notion that RNase J is a functional homologue of RNase E in many bacteria. We also discuss the structural aspects of the β-CASP family proteins.



Two groups of the β-CASP family proteins in bacteria

Reference

[1] Ishikawa *et al.* (2006) *J. Biochem.* 140, 535-542