

Abstract

Combinatoric Properties of Restriction Sites [†]

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Endonucleases from the restriction–modification complex are known to recognise specific sites with tremendous precision. The symmetry of the site is said to allow an enzyme to recognise the pattern despite the strand. However, there are many exceptions towards non-symmetrical restriction sites, and even enzymes that are not strictly specific to only one site.

We study four- and six-nucleotide palindromes that also happened to function as restriction sites. The study revealed that not all positions in the palindrome are equally important for the enzyme while recognition—symmetry of a palindrome—is strict only in the middle of the site, whereas at the periphery it may end in a non-palindromic sequence.

Based on the duplets ‘strength’ method and editing distance algorithms, these restriction sites were compared pairwise and clusters of resembling sites were found. Due to different costs for reverse substitutions, it was possible to assume which sequence out of two was more likely the original since its conversion in another sequence costed less. The idea is to track down evolutionary modified restriction sites to those original sequences. Therefore, a phylogenetic tree was constructed using respective restrictases and their clusters obtained from the tree were used for primary pairwise comparison.



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