

Evidence for symmetric chromosomal inversions around the replication origin in bacteria

ABSTRACT

The most likely mechanism of generation of X-alignments involves large chromosomal inversions that reverse the genomic sequence symmetrically around the origin of replication. The finding of these X-alignments between many pairs of species suggests that chromosomal inversions around the origin are a common feature of bacterial genome evolution.

INTRODUCTION

Background Large-scale genomic rearrangements and duplications are important in the evolution of species. Previously, these large-scale genome-changing events were studied through genetic or cytological studies. With the availability of many complete genome sequences it is now possible to study such events through comparative genomics. The publication of the yeast genome has led to much better insight into the duplication events that have occurred in fungal and eukaryotic evolution (for example, see). Large chromosomal duplications have also been found from analysis of completed chromosomes of *Arabidopsis thaliana*. The ability to detect large-scale genomic changes is dependent in large part on which genomes are available. Such studies in bacteria, for example, have been limited by the availability of genomes only from distantly related sets of species. Recently, however, the genomes of sets of closely related bacterial species have become available. We have compared these closely related bacterial genomes and have discovered an unusual phenomenon - alignments of whole genomes that show an X-shaped pattern (which we refer to as X-alignments). Here we present the evidence for these X-alignments and discuss mechanisms that might have produced them.

CONCLUSION

Conclusions We present here a novel observation regarding the conservation between bacterial species of the distance of particular genes from the replication origin or terminus. The initial observation was only possible due to the availability of complete genome sequences from pairs of moderately closely related species (for example, *V. cholerae* and *E. coli*). This shows the importance of having genome pairs from many levels of evolutionary relatedness. Comparisons of distantly related species enable the determination of universal features of life as well as of events that occur very rarely. Comparison of very closely related species allows the identification of frequent events such as transitional changes at third codon positions or tandem duplications. To elucidate all other events in the history of life, genome pairs covering all the intermediate levels of evolutionary relatedness will be needed.