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# Genome Physical Characterization Using BAC End Sequencing

**Shuai Fan***

*Department of Genetic Medicine, University of Chinese Academy of Sciences, Beijing, China*

## Introduction

Physical characterization of genomes plays a crucial role in understanding the structure, organization, and function of genetic material. One approach that has revolutionized genome analysis is BAC end sequencing. Bacterial Artificial Chromosomes (BACs) are powerful tools for the isolation and manipulation of large DNA fragments, making them ideal candidates for physical mapping and sequencing of genomes. This article provides an in-depth exploration of BAC end sequencing as a method for physical characterization of genomes, highlighting its principles, applications, advantages, and limitations. Advances in DNA sequencing technologies have propelled genomics research to unprecedented levels. However, the assembly and interpretation of whole genomes remain challenging due to the presence of repetitive and complex sequences. Physical characterization of genomes offers valuable insights into their structural features, including repetitive regions, gene clusters, and chromosomal rearrangements. BAC end sequencing provides an effective strategy for capturing this physical information by analyzing the ends of large DNA fragments cloned into BAC vectors.

## Description

BAC end sequencing involves isolating BAC clones from a genomic library, extracting DNA, and sequencing the ends of the cloned DNA fragments. The BAC clones serve as physical landmarks that span various regions of the genome. By sequencing both ends of each BAC clone, researchers can gather information on the adjacent genomic regions, including gene content, repetitive elements, and potential rearrangements. BAC end sequencing can be performed using Sanger sequencing or high-throughput sequencing platforms. BAC end sequencing aids in constructing high-resolution physical maps of genomes by identifying neighbouring BAC clones and their relative order. This information helps in understanding the large-scale organization of genomic regions, such as the identification of gene clusters, centromeres, and telomeres. BAC end sequences provide valuable scaffolding information for genome assembly. By linking BAC clones with overlapping end sequences, researchers can bridge gaps in assembly and resolve ambiguities, leading to improved genome contiguity and accuracy, BAC end sequencing is particularly useful for studying complex genomic regions, such as those rich in repetitive elements, segmental duplications, or structural variations. It helps in delineating the architecture and organization of these regions, contributing to a better understanding of their role in genome evolution and disease [1,2].

BAC end sequencing facilitates comparative analyses between closely related genomes. By comparing the sequences of BAC end pairs from different species, researchers can identify conserved regions, gene order rearrangements, and evolutionary breakpoints, shedding light on genome evolution and species divergence. BAC end sequencing provides information about genomic regions that span tens to hundreds of kilobases, enabling the analysis of large-scale structural features and long-range interactions. BAC end sequencing allows researchers to focus on specific genomic regions of interest, minimizing the complexity and cost associated with whole-genome sequencing. Combining BAC end sequencing with emerging technologies such as long-read sequencing and chromosome conformation capture techniques can enhance the accuracy and resolution of physical genome characterization [3-5].

## Conclusion

BAC end sequencing can be applied to non-model organisms to facilitate the generation of reference genomes and comparative analyses, aiding in evolutionary and ecological studies. BAC end sequencing is a powerful method for physical characterization of genomes, allowing the investigation of large-scale structural features, gene content, and chromosomal rearrangements. Despite its limitations, BAC end sequencing has proven instrumental in genome assembly, comparative genomics, and studying complex genomic regions. Continued advancements in sequencing technologies and computational tools will further enhance the accuracy and resolution of BAC end sequencing, opening new avenues for understanding genome structure and function.

## References

1. Gálvez, Juan Manuel, Daniel Castillo, Luis Javier Herrera and Belén San Román, et al. "Multiclass classification for skin cancer profiling based on the integration of heterogeneous gene expression series." *PloS one* 13 (2018): e0196836.
2. Van Manen, Labrinus, Jouke Dijkstra, Claude Boccara and Emilie Benoit, et al. "The clinical usefulness of optical coherence tomography during cancer interventions." *J Cancer Res Clin Oncol* 144 (2018): 1967-1990.
3. Hoover, Brian G., and J. Scott Tyo. "Polarization components analysis for invariant discrimination." *Applied optics* 46 (2007): 8364-8373.
4. Youn, Su Hyun, Taeyong Sim, Ahnryul Choi and Jinsung Song, et al. "Multi-class biological tissue classification based on a multi-classifier: Preliminary study of an automatic output power control for ultrasonic surgical units." *Comput Bio Med COM* 61 (2015): 92-100.
5. Nagendran, Monica and Daniel Riordan."Automated cell-type classification in intact tissues by single-cell molecular profiling." *Elife* 7 (2018).

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***Address of Correspondence:** Shuai Fan, Department of Genetic Medicine, University of Chinese Academy of Sciences, Beijing, China, E-mail: Shuaifan@ipb.ac.rs*



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