## Chain Termination Technique

Robert<sup>1</sup>

<sup>1</sup>New York Genome Center, New York, USA

## INTRODUCTION

The process of crucial the order of the ester bases on a polymer strand is named sequencing. In 1977, 24 years once the invention of the structure of polymer, 2 separate strategies for sequencing polymer were developed: the chain termination technique and therefore the chemical degradation technique. each strategies were equally standard to start with, but, for several reasons, the chain termination technique is that the technique a lot of usually used these days. This technique relies on the principle that fiber polymer molecules that dissent long by simply one ester will be separated from each other victimization polyacrylamide gel catachresis delineate earlier. The polymer to be sequenced, known as the guide polymer, is initial ready as a fiber polymer. Next, a brief oligonucleotide is hardened, or joined, to constant position on every guide strand. The oligonucleotide acts as a primer for the synthesis of a brand new polymer strand which will be complimentary to the guide polymer. this system needs that four nucleotide-specific reactions-one every for G, A, C, and T-be performed on four identical samples of polymer. The four sequencing reactions need the addition of all the elements necessary to synthesize and label new polymer, including.

Variations of this technique are developed for automatic sequencing machines. In one technique, known as cycle sequencing, the dideoxynucleotides-not the primers-are labeled with totally different colored fluorescent dyes, therefore all four reactions occur within the same tube and area unit separated within the same lane on the gel. As every tagged polymer fragment passes a detector at rock bottom of the gel, the color is recorded and therefore the sequence is reconstructed from the pattern of colors representing every ester within the sequence.

Finally, so as to scan the bases, a method known as sequencing by synthesis is employed. Through a spread of cycles, the complement nucleotide is another to the strands of polymer, and therefore the signal from that complement nucleotide is recorded. Then, the method is perennial to sequence ensuing nucleotide, and is perennial till the complete strand has been sequenced. Overall, the scan error is a smaller amount than simple fraction with this technology. Whereas this approach is that the commonplace because of its cheap value purpose, the technology incorporates a form of disadvantages. First, this technology is restricted to reads of roughly one hundred fifty bp. in addition, this technology incorporates a giant sequence bias, therefore despite the coverage, and some regions of the order can perpetually be poorly sequenced.

Craig Ventura believed Weber and Myers were correct, and beside Jim Myers, he based the corporate Celera firms. The goal of Celera was to sequence the human order victimization the small-arm sequencing approach. This spurred the Human order Project, because the government was troubled that the human order would become property of Celera, rather than associate degree open scientific resource. Eventually, each comes finished at constant time, and a draft of the primary human order was completed in early 2000. Therefore, it's laptop scientists, not geneticists, that we have a tendency to should give thanks for the fast advancements of genetics.

\*Correspondence to: Robert, New York Genome Center, New York, USA

Received: May 03, 2021; Accepted: May 17, 2021; Published: May 24, 2021

Citation: Robert (2021) Chain Termination Technique. Next Generation Sequencing & Applic 7: e113

**Copyright:** © 2021 Robert. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.