

Flexible MiSeq® System Supports a Broad Range of Agrigenomics Applications

The compact and economical MiSeq system delivers next-generation sequencing results in hours rather than weeks, providing a higher throughput alternative to CE for agrigenomics studies.

Introduction

Agrigenomics researchers have made significant advancements in our understanding of plants and animals, increasing crop yield and improving livestock breeding. Whole-genome sequences have been generated for many of the major plants and animals, such as corn, wheat, cotton, bovine (dairy and beef), and chicken, supporting research advances to meet the world's food, feed, fiber, and fuel demands. While whole-genome sequencing is performed with next-generation sequencers, many other agrigenomics sequencing applications such as clone checking, amplicon sequencing, and targeted transcript sequencing are routinely conducted using capillary electrophoresis technology (CE). More than 50-years old, CE technology was first used in the 1980s for DNA analysis and involves lengthy and complex workflows, taking several weeks to generate data. The MiSeq® system (Figure 1), with its faster turnaround time and simplified workflows, offers a cost-effective alternative for performing *de novo* and resequencing applications for small to mid-size genomes, RNA sequencing, and epigenetics studies.

Streamlined Workflow and Faster Data Analysis than CE

The MiSeq system offers the first end-to-end sequencing solution, integrating cluster generation, amplification, sequencing, and data analysis into a single instrument. Its small footprint—approximately two feet square—fits easily into a laboratory environment. The MiSeq system employs Illumina sequencing by synthesis technology, the most widely used, proven next-generation sequencing chemistry with over 2,000 publications to date. As with other Illumina sequencers, the MiSeq system is powered by TruSeq® technology, delivering the highest data integrity, with the highest yield of error-free reads and the most base calls above Q30.

Figure 1: MiSeq System



The compact MiSeq system is the ideal platform for many agrigenomics sequencing applications.

The MiSeq system features enhanced fluidics architecture, enabling a five-fold decrease in chemistry cycle time to provide results in hours, rather than the weeks required by CE. Preparing a sequencing library takes just 90 minutes, with clonal amplification and sequencing completed within as little as 4.5 hours. On the integrated instrument computer, data analysis from quality-scored base calls to variant calling and alignment can be completed in less than 2 hours with no user intervention (Figure 2). This data can be stored, analyzed, and shared with BaseSpace™, an Illumina secure, cloud-based resource, enabling unparalleled collaboration, access, and security. This is in sharp contrast to CE's limited data analysis capability that adds to its cost of operation and strains the personnel resources of most agrigenomics research groups.

Uniquely Suited for a Variety of Agrigenomics Sequencing Applications

Despite its size, MiSeq is a powerful sequencer capable of performing demanding sequencing applications such as small genome *de novo* sequencing, targeted sequencing to analyze a discrete section of the genome, RNA sequencing to elucidate gene and protein function, microRNA sequencing to study the role of these short nucleotide sequences in regulating development, and epigenetics studies to determine the role of DNA methylation in plant and animal development. Continued MiSeq performance enhancements will expand these applications to include resequencing of larger organisms, as well as support small genome sequencing at higher coverage. More importantly, its high accuracy, simpler workflow, and minimal hands-on time will make the MiSeq system a viable CE alternative for performing valuable agrigenomics applications, including:

Library Quality Control

Validating a nucleic acid library before sequencing is an important quality control step that ensures the value of downstream data. A poor quality library can undermine the success of large-scale sequencing, and lead to costly and time-consuming repeat experiments. The MiSeq system can perform a front-end library check using 2 × 25 bp sequencing, enabling researchers to assess the evenness of coverage, insert size, diversity, and GC content of the library.

Clone Checking

MiSeq is capable of performing fast analysis of plasmid constructs used to clone DNA. In less than a day, plasmid constructs can be sequenced, confirming the presence and integrity of the inserted piece of DNA.

De Novo and Resequencing of Small to Mid-Sized Genomes

In a single workday, the MiSeq system can accurately sequence small whole genomes (< 20 Mb), such as those of pathogens and some

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