

Illuminating the Role of Next-Generation Sequencing Approaches in Transgenesis

Vijaya R. Dirisala*

Ohio State University Medical Center, USA

Next-generation sequencing approaches are believed to play a vital role in transgenesis, which is evident from the recent literature. They serve as a trusted source for the molecular characterization of transgene sequence. This technology enables researchers to know the integration sites and also determine copy number in transgene species. This is significantly important as the integration of transgene site and copy numbers are instrumental in determining the relationship between integration site and specific phenotype, which can thus be applied to the growing number of transgenics to yield commercial benefit.

In one of the recent studies, the authors successfully demonstrated the utilization of next-generation sequencing technology to characterize cattle harboring a 150 kb Bacterial artificial chromosome (BAC) that expresses human lactoferrin [1]. The author's initial attempt to characterize it with the conventional chromosome walking was met with no success [1].

In another recent study, the researcher's objective was to characterize mice that were homozygous for the transgene with the Hutchinson-Gilford progeria syndrome (HGPS) causing variant [2]. They tried a number of conventional tools such as real-time PCR (RT-PCR), fluorescence in situ hybridization (FISH) and Southern blots for characterization without success. They came up with a coupled approach of microarray hybrid capture and next-generation sequencing and were successful in identifying the anatomy of the transgene.

In another interesting study, a group of researchers working on transgenic plants utilized next-generation sequencing and junction sequence analysis bioinformatics for achieving molecular characterization of genetically modified soybean (*Glycine max* (L.) Merr) line [3] and the authors proved that this method is on par with the currently employed Southern-blot based method. They also demonstrated that the new method employed by is also effective in dissecting complex cases of transgenics.

Given above are some of the examples, where next-generation sequencing played a significant role in dissecting complex problems related to transgenics. The advancement of this technology coupled with other methods will have a great impact in the field of cloning & transgenesis.

References

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*Corresponding author: Vijaya R. Dirisala, Ohio State University Medical Center, USA, E-mail: drdirisala@gmail.com

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