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TOPIC INTRODUCTIONS

PROTOCOLS

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Cover Illustration: Genome-wide insertional mutagenesis is a tool to generate loss-of-function mutations for virtually all genes in a genome. In this process, mutations are generated by random integration of mobile DNA elements. In maize, transposons are frequently used as endogenous insertional mutagens, which enables the generation of large mutant populations (libraries) that can be used to characterize gene function. *Mutator* (*Mu*) transposons are commonly used for untargeted insertional mutagenesis in maize, and have been used as mutagens to generate collections such as the *BonnMu* resource, a *Mu*-tagged maize population for functional genomics studies. To identify and map the different mutations in these libraries, a high-throughput approach termed Mutant-Seq (Mu-Seq) can be used, which involves the construction of multiplexed sequencing libraries (known as Mu-Seq libraries) from multiple stocks from a *Mu*-tagged population, followed by high-throughput sequencing and data processing. In this issue, Marcon et al. provide a detailed protocol for Mu-Seq, from the generation of a maize *Mu*-tagged mutant population to data analysis (doi:10.1101/pdb.prot108586). The cover image illustrates *Mutator* (*Mu*) transposon mutagenesis in maize and the use of Mu-Seq to map these mutations. The maize plant on the *left* represents one of the *BonnMu* stocks to be analyzed. The bar *above* the grid represents a *Mu* transposon, with cyan denoting genomic DNA, purple indicating the terminal inverted repeats (TIRs), and white representing the *Mu* internal sequence. The grid depicts the 24 × 24 grid design used in Mu-Seq for pooling 576 stocks to construct a multiplexed sequencing library, with nine randomly colored *BonnMu* stocks. Image provided by the authors.

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