

GENETIC ENGINEERING TECHNOLOGIES AND DETECTION OF GENE EDITING

Detecting Genetic Engineering Via Portable Nanopore Sequencing And Reachback Data Analysis Tools

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Recent advances in nanopore sequencing technology have enabled rapid, low-cost, and portable DNA/RNA sequencing analysis in any environment. Untargeted nanopore sequencing allows for the identification of any biological threat, including those that are genetically modified to evade existing detection capabilities. We have developed untargeted nanopore sequencing systems and rapid protocols that can be used by a variety of operators in the field, including those without laboratory training. The goal is to quickly identify if a biological threat is present, then the data can be sent to reachback facilities for further analysis. This reachback analysis will include genome assembly and the utilization of software tools to detect the presence of genetic modifications. The software tools developed under the IARPA Finding Engineering-Linked Indicators (FELIX) program are currently being evaluated against nanopore sequencing datasets. Once downselected, further development of these tools will be needed. These tools utilize artificial intelligence and machine learning (AI/ML) so re-training of the algorithms will be important as code is modified and more data becomes available. Upgrades will also be important as new genetic engineering methods emerge. It is important to note that these software currently require substantial computational infrastructure to run and will for the foreseeable future. Some also require trained bioinformaticians with assistance from subject matter expert biologists in order to make proper assessments. To support the biodefense community, DEVCOM CBC is currently establishing a reachback capability for this type of analysis, which will be critical as genetic engineering becomes more and more prevalent. The ability to quickly identify genetically modified threats will serve to protect the warfighter as well as the general population.

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