Code CGN-PSxxx

Efficient viability testing of genebank seed samples

Question Can a more efficient alternative for germination testing be implemented by genebanks?

Level HBO / MSc

Keywords Genebank management, Protocol improvement, Seed ageing, Viability testing

Description The Centre for Genetic Resources, the Netherlands (CGN) maintains a collection of genetic resources of agricultural and horticultural crops, mainly in the form of seeds. To ensure maintenance of sufficient viability during conservation, seed samples are periodically monitored through germination testing. However, such tests are cumbersome, laborious, and error-prone, while it also reduces available seed quantities. Introduction of a high-throughput, reliable and non-destructive alternative for germination testing would highly increase the efficiency in monitoring seed viability by genebanks. Recently, several technological advances in predicting seed viability have emerged, but how applicable are these techniques for genebanks and can they be used for a wide variety of crops? Furthermore, options for the development of new methods can be explored. For instance, considering the physiological processes that are involved in seed ageing, could an analytical method be devised that is indicative for seed viability?

Approach The project will start with a literature study to review existing techniques for predicting seed viability. All relevant features of the techniques will be examined, including reliability, workload, throughput, required infrastructure, general applicability and costs. Based on these findings it will be evaluated which techniques could be considered efficient alternatives for germination testing by genebanks. Secondly, based on existing knowledge about seed ageing processes, it will be investigated if novel analytical methods could be applied for measuring seed viability in a genebank setting. This project will be carried out in a cooperation between CGN and the Wageningen Seed Science Centre.

Result Report on viability testing methods, recommendations for implementation at genebanks and suggestions for research directions for the development of new techniques.

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