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Strategic application of genome information and germplasm collections will accelerate plant breeding

ゲノム情報と遺伝資源の戦略的活用により植物育種を加速する

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A cutting-edge plant breeding method, "genomic selection", is expected to be a key technology to accelerate the rate of genetic improvement of crop productivity. Genomic selection uses genome-wide DNA markers to predict the genetic potential of untested breeding lines to identify the most valuable parents to initiate the next breeding cycle without actually testing them in a field. This rapid identification at the seedling or even seed stage can shorten the breeding cycle by placing the slowest breeding task, field testing, outside of the cycle. Although the success of genomic selection in dairy cattle breeding is encouraging, many questions remain on how best to take advantage of the predictions enabled by genomic selection in plant breeding. Since the accuracy of genomic selection depends on several factors (e.g., the density of genome-wide markers, genetic relationships among breeding lines), it is important to perform empirical evaluations and simulations based on real data. In this lecture, the basic idea of genomic selection will be presented. Then, statistical methods for genomic selection, ranging from simple ridge regression to Bayesian and machine learning methods, and their performance in empirical and simulation studies will be presented. Finally, latest updates and future perspectives will be discussed.

Keywords: genomic selection, next-generation sequencing, Bayesian model, machine learning, simulation