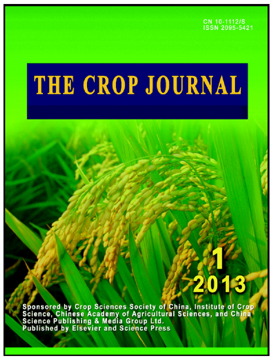

Genomic selection methods for crop improvement: Current status and prospects

Xin Wang, Yang Xu, Zhongli Hu, Chenwu Xu

PII: S2214-5141(18)30040-0
DOI: doi:10.1016/j.cj.2018.03.001
Reference: CJ 286

To appear in:

Received date: 4 February 2018
Revised date: 25 March 2018
Accepted date: 9 April 2018

Please cite this article as: Xin Wang, Yang Xu, Zhongli Hu, Chenwu Xu , Genomic selection methods for crop improvement: Current status and prospects. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Cj(2018), doi:10.1016/j.cj.2018.03.001

Review

Genomic selection methods for crop improvement: current status and prospects

Xin Wang[a, b, c], Yang Xu[a], Zhongli Hu[c], Chenwu Xu[a,*]

[a] Jiangsu Provincial Key Laboratory of Crop Genetics and Physiology/Co-Innovation Center for Modern Production Technology of Grain Crops/Key Laboratory of Plant Functional Genomics of Ministry of Education, Yangzhou University, Yangzhou 225009, Jiangsu, China

[b] College of Information Engineering, Yangzhou University, Yangzhou 225009, Jiangsu, China

[c] State Key Laboratory of Hybrid Rice, College of Life Sciences, Wuhan University, Wuhan 430072, Hubei, China

Abstract: With marker and phenotype information from observed populations, genomic selection (GS) can be used to establish associations between markers and phenotypes. It aims to use genome-wide markers to estimate the effects of all loci and thereby predict the genetic values of untested populations, so as to achieve more comprehensive and reliable selection and to accelerate genetic progress in crop breeding. GS models usually face the problem that the number of markers is much higher than the number of phenotypic observations. To overcome this issue and improve prediction accuracy, many models and algorithms, including GBLUP, Bayes, and machine learning have been employed for GS. As hot issues in GS research, the estimation of non-additive genetic effects and the combined analysis of multiple traits or multiple environments are also important for improving the accuracy of prediction. In recent years, crop breeding has taken advantage of the development of GS. The principles and characteristics of current popular GS methods and research progress in these methods for crop improvement are reviewed in this paper.

Keywords: Genomic selection; Prediction; Accuracy; Crop

1 Introduction

The key step in crop breeding is selection, and conventional breeding is based on phenotypic selection. Breeders choose good offspring using their experience and the observed phenotypes of crops, so as to achieve genetic improvement of target traits. Hazel and Lush [1] first proposed the selection index (SI) method, which uses a total score to select for multiple traits simultaneously. It is more efficient than selection for one trait at a time and can improve aggregate genetic gain. In 1970s, with the development of computer science, Henderson [2] proposed best linear unbiased prediction (BLUP), which became the most widely used genetic evaluation method. Since 1990s, advances in molecular genetic techniques have revealed widespread genetic variation in genomes. Large numbers of molecular markers are available, allowing breeders to use markers to assist in breeding. Marker-assisted selection (MAS) [3] has become a common means of molecular breeding, but it is suitable only for traits controlled by a small number of major genes. Most economic traits of crops are complex and affected by a large number of genes, each with small effect [4], and thus the application of MAS in breeding practice is not as

---

[*] Corresponding author: Chenwu Xu, Email address: cwxu@yzu.edu.cn.

Received: 2018-02-04; Revised: 2018-03-25; Accepted: 2018-04-09.