

University of Zabol

Graduate School

Faculty of Agriculture

Department of Plant Breeding and Biotechnology

Thesis submitted to Uinversity of Zabol for the degree of PhD of Plant Breeding

Association mapping of wheat genotypes resistance to yellow rust disease

Supervisors

Dr. Leila Fahmideh

Dr. Farzad Afshari

Advisors

Dr. Saleheh Ganjali

Dr. Mohammad Reza Bihamta

Dr. Hadi Alipour

By

Amin Afzalifar

June 2021

Abstract

Association study is one of the new methods used to identify quantitative trait loci (QTLs). This study aims to test the genetic diversity of 298 wheat genotypes including Iranian cultivars and landraces and identifying the relationship between some agronomic traits and pathogenicity factors of yellow rust were performed. The experiment in two stages, the first experiment in seedling stage and in order to phenotypic evaluation of experimental genotypes for yellow rust disease in greenhouses of the cereal research department of the cereal farm of Seed and Plant improvement Institute (SPII), Karaj in the year 2018-2019 and in the form of a plan CRD design with three repetitions and the second experiment were performed in order to evaluate the resistance of experimental genotypes in the adult plant stage under the conditions of artificial infection with yellow rust in a SPII field in Karaj region in the form of alpha lattice design with two replications. The greenhouse traits evaluated in this study showed a wide variety of infection type, pustule size and pustule density. According to the results of analysis of variance, the presence of phenotypic variation among the studied traits was identified. The results of correlation analysis, stepwise regression and path analysis showed the importance and effectiveness of number of grains per spike, 100-kernel weight, grain width, grain length, spike length and grain thickness. Based on cluster analysis, the studied genotypes were divided into four groups based on morphological traits. Based on the results, the studied genotypes were grouped into two subpopulations using Structure software and Bayesian statistical method. Based on the general linear model method and the mixed linear model in both greenhouse and field conditions, 500 and 505, a significant relationships between markertrait was found. The highest correlations were observed on chromosomes 2B and 7A and the least significant correlations were observed on chromosomes 4D and 1B.

Keywords: Yellow rust (Stripe rust), Multivariate methods, MLM method, Population structure, Kinship matrix