



University of Zabol
Faculty of Agriculture
Department of Plant Breeding and Biotechnology

the Thesis Submitted For the Degree of PhD
(In the Field of Agricultural Biotechnology)

Title:

**Rhizosphere soil bacteria community vary and correlate
with saffron quality at four locations**

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Abstract

Saffron is an aromatic plant belonging to the Iridaceae family. It is produced from the dried stigmas of *Crocus sativus*. Microorganisms in the soil are the main factors affecting the production and quality of *Crocus sativus*. In this study, we present a study of the microbial relationship between *Crocus sativus* rhizosphere and quality parameters of *Crocus sativus* (crocin, picrocrocin, and safranal) using a metagenomic approach. This research was conducted in Ghayen city, the center of quality *Crocus sativus* production worldwide. The interesting point in this region is that despite the similar climatic conditions, the quality of *Crocus sativus* in the Shahik region is higher than in the other areas (Zobar, Shahabi, and Jafarabad). This can be attributed to different microbiomes in the root zone or rhizosphere of the soil. The purpose of this study was to investigate and compare the soil microbiome of *Crocus sativus* rhizosphere in the Shahik area of Ghayen city with other areas of this city and, as a result, to identify the microbiome affecting the quality of *Crocus sativus*. In this method, rhizosphere soil of different regions in Ghayen city was first sampled during the *Crocus sativus* harvest time. In the next step, soil DNA was extracted, and the 16srRNA gene sequence of each sample was identified based on the RNA-Seq method; finally, the microbiome of the samples was analyzed. The results showed that beneficial bacteria such as *Kosakonia*, *Enterobacter*, *Salmonella*, *Plesiomonas*, *Pasteurella*, *Lactococcus*, and *Mitsuaria* in Shahik farm are more than in other farms that these bacteria have a significant impact on increasing the quality of *Crocus sativus*.

Keywords: 16srRNA, Bacteria, Metagenomics, *Crocus sativus*, Miseq, Next Generation Sequencing