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Epigenetic stability in Saffron (*Crocus sativus* L.) accessions during four consecutive years of cultivation and vegetative propagation under open field conditions

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Highlights

- Saffron germplasm is characterized by low genetic but high phenotypic variability
- Saffron accessions with different geographic origin show high epigenetic variability
- The cultivation in the same field does not uniform epigenotypes to a common profile
- Saffron epigenotypes are highly stable under open field, natural, conditions
- Only a little variation is present within accessions slightly changing the epigenotypes

Abstract

Saffron (*Crocus sativus* L.) is a sterile species that is vegetatively propagated in the field, year by year, via the production of new corms. While Saffron's genetic variability is extremely low, phenotypic variation is frequently observed in the field and epigenetics could be a possible origin of these alternative phenotypes. Present day knowledge on Saffron epigenetics is very low or absent. In the present paper, to deepen existing knowledge, we focused on the epigenetic differences and stability among 17 Saffron accessions, of different geographic origin, during four consecutive years of vegetative propagation under open field conditions. Before the analysis, the selected accessions have been cultivated in the same field for at least three consecutive years. Despite the low genetic variability and the prolonged co-cultivation in the same environment, Methylation-Sensitive Amplified Fragment Length Polymorphism (MS-AFLP) analysis revealed a very high epigenetic difference among accessions, making it possible to discriminate them based on the epigenetic profiles. During the four years of the study, a little variation has been observed within accessions following different patterns, slightly modifying the accession epigenotypes but not enough to even them to a more uniform profile. These results confirm that, under natural conditions, Saffron epigenotypes are highly stable, supporting a role for epigenetics in phenotypic variability.

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