Research in Pharmaceutical Sciences, 2012;7(5)
School of Pharmacy and Pharmaceutical Sciences
Isfahan University of Medical Sciences

Affinity based target deconvolution of safranal

H. Hosseinzade[1], S. Mehri[1], M. Abolhassani[2], M. Ramezani[3], K. Abnous[2], M. Nabavinia[3,*]

[1]Pharmaceutical Research Center, Pharmacodynamics and Toxicology Department, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, I.R. Iran
[2]Pharmaceutical Research Center, Department of Medicinal Chemistry , School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, I.R. Iran.
[3]Nanotechnology Research Center, Department of Biotechnology, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, I.R. Iran

Background and Aims: Affinity based target deconvolution of natural products and/or drug candidates is recently becoming more popular. In this study, we hypothesized that a part of safranal pharmacological effects, one of the major constituent of Crocus sativus L., relies on its physical interaction with target proteins.
Methods: Affinity chromatography beads were prepared by covalently attachment of safranal to agarose beads. Proteins that bind to safranal were isolated and separated on SDS-PAGE and/or 2D gel.
Results: Proteins were identified using MALDI-TOF/TOF and Mascot software. Our data show that safranal physically binds to beta actin, cytochrome b-c1 complex subunit 1, trifunctional enzyme subunit beta and ATP synthase subunit alpha and beta.
Conclusions: We concluded that affinity chromatography can be used to reveal physical interaction of safranal with some cellular proteins. These interactions may explain a part of safranal pharmacological effects.

Keywords: Safranal; *Crocus sativus*; Saffron; Target deconvolution and affinity chromatography