It is worth noting that these figures were sginificantly lower than those of conventional grain crops of our region, but potentially low production expenses and high selling price may prove its yield as quite competitive.

Parcel No.	Plant yield (kg/ha)	Seed yield (kg/ha)	Seed kernel weight, *1,000 (g)
1	5216	1410	0.297
2	4420	1205	0.277
3	4996	1350	0.307
4	4678	1405	0.323
Average:	4827.5	1342.5	0.301

The weight of a thousand seeds was 0.301 g, which was higher than the figures shown in available literary sources.

Molecular targets and drug-likeness analysis of chrysin against Alzheimer's disease: bioinformatics approach

Sevgi GEZICI[1,3], Nazim SEKEROGLU[2,3]

1- Gaziantep University, Faculty of Medicine, Department of Medical Biology and Genetics, Turkey; e-mail: drsevgigezici@gmail.com; sevgigezici@gantep.edu.tr
2- Gaziantep University, Faculty of Science and Literature, Department of Biology, Turkey; e-mail: nsekeroglu@gmail.com; nazimsekeroglu@gantep.edu.tr
3- Gaziantep University, Phytotherapy and Medicinal-Aromatic Plants Application and Research Center (GAUN-FITOTABAUM), Turkey

Chrysin is a natural compound with numerous pharmacological properties, especially antioxidant, anti-inflammatory, antiviral, antitumor, anticancer, and hepatoprotective activities. Although the biological activities of chrysin have been described and its possible pharmacological properties have been previously determined, its pharmacokinetic properties against Alzheimer's disease (AD) have not been fully elucidated based on gene targets, drug-likeness, molecular signaling pathways, and network-based pharmacology analyses. In this study, we aimed to reveal the molecular targets and potential interactions of chrysin against AD by gene-set enrichment and bioinformatics approach. The chrysin was entered into the PubChem and ChEBI database, and the targets of chrysin were estimated using DIGEP-Pred. Then, GeneCards, DisGeNET, PharmGKB, and SwissTargetPrediction were used to identify possible interacting genes and proteins. The drug-likeness properties and toxicity characteristics of chrysin were determined using SwissADME and ProToxII databases. In addition, STRING and KEGG enrichment database were used to elucidate the role of probable interacting proteins to construct a protein-protein interaction (PPI) network and a network of molecular targeting pathways, respectively. Based on the results of pharmacokinetic properties and drug-likeness analysis, chrysin predicted to have a good drug-likeness activity (score = -0.21), as well as good brain barrier permeability (BBB score = 3.71) with no observable toxicity. A total of 38 genes were identified as the top genes that interact with chrysin against Alzheimer's disease. ILB, IL6, TNF, MAPK1, CASP3, PSEN1, PSEN2, PTGS2, NFKB1, AKT1, GSK3B, and APP were selected as top core targets that may play a significant role in AD treatment. Furthermore, a total of 158 different pathways were identified as the probably modulated pathways, corresponding to 38 protein targets. Besides neurodegeneration and AD, pathways in cancer, lipid and atherosclerosis, EGFR tyrosine kinase inhibitor resistance, AGE-RAGE signaling in diabetic complications, HIF-1 signaling, PI3K-Akt signaling, MAPK signaling, IL-17 signaling, neurotrophin and sphingolipid signaling were defined as the top pathways associated with chrysin-regulated proteins. Overall, the results indicated that the network-based approach could provide a novel approach to uncover the therapeutic mechanisms of chrysin against AD.