

Effect of *Nigella sativa* L. extract and thymoquinone on the genes responsible for cell proliferation, migration and NK cell cytotoxicity in breast cancer

¹Tuğcan Korak, Zeliha Emrence², Sema Sirma Ekmekci², Neslihan Abaci² & Emel Ergül^{1*}

¹Department of Medical Biology, Faculty of Medicine, Kocaeli University, Kocaeli 41001, Türkiye

²Department of Genetics, Aziz Sancar Institute of Experimental Medicine, Istanbul University, Istanbul 34093, Türkiye

Received 11 July 2023; revised 23 October 2023

The black cumin, *Nigella sativa* L. is known to be effective against various diseases including cancer. Thymoquinone (TQ), active ingredient of *N. sativa* extracts, can inhibit proliferation metastasis and regulating immune system in different cancers as with breast cancer (BC). The mechanisms of action behind TQ are not clearly understood yet. The purpose of the current study is to investigate the effects of TQ, water (WE) and alcohol extracts (AE) of *N. sativa* on BC cells by focusing attention on the following genes; *CDK4*, *MYC*, *NF-κB1*, *VEGFA*, *FGF1*, *N-cadherin*, *ULBP1*, *ULBP2* and *CD155*. Conventional protocols were performed in order to obtain extracts. Cell viability was measured by RTCA and MTT assay, and gene expressions were analyzed by qRT-PCR. Association was significant for *CDK4* ($P = 0.07$), *MYC* ($P < 0.001$), *NF-κB1* ($P = 0.011$), *VEGFA* ($P = 0.013$), *FGF1* ($P < 0.001$), and *ULBP1* ($P = 0.021$) genes. *CDK4* and *MYC* genes may be candidate genes for mechanisms involved in reduced cell proliferation induced by AE and TQ. Increased ULBP1 expression through AE and TQ indicates that *N. sativa* may trigger ULBP1-mediated NK cell cytotoxicity. Our results support the idea that active ingredients in *N. sativa* promise an encouraging therapeutic approach in the future.

Keywords: Anticancer, Black cumin, Kalonji