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6-shogaol, 6-gingerol and curcumin's effects on GSK3β/β-catenin pathway in Lung Cancer Cell Line

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Lung cancer is the *deadliest* type of cancer for both men and women.Non small cell lung cancer (NSCLC) is the most common type of it. β-catenin overexpression disrupts the cell differentiation and make the cells proliferate so fast. It is believed that mPGES-1/cyclooxygenase- 2 contributes to this. So as a new aspect, it is supposed that anticancer effect might be seen after decreasing the β-catenin levels in the cell. We investigated the anticancer effects of 6-gingerol and 6-shogaol from *Zingiber officinale*. Also we aimed to see the anticancer effect is dependent on whether mPGES-1 (microsomal prostaglandine E_2 synthase 1), β-catenin and GSK3β (glycogen synthase kinase 3 β) pathway or not. NSCLCcell line named A549wasused in our study. Cells were incubated with IL-1β (interleukin 1 β) for 24 hours in order to get their mPGES-1 enzyme induced. Experiments are performed both on IL-1β treated and non treated groups. Curcumin from *Curcuma longa,* a natural compound that is known for its mPGES-1 inhibitory and anticancer effect, is used as a positive control.

Cytotoxicity of molecules were determined using MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay. Data obtained from MTT was used to perform western blottingassay. After 24 hrs of incubation with molecules, mPGES-1, GSK3β, p-GSK3β and β-catenin protein levels were measured. As a result of 24 hrs MTT assay, 6-shogaol's IC_{50} was 62μM. In western blot analysis mPGES-1, p-GSK3β, β-catenin were higher and GSK3β was lower in IL-1β treated group, while the effects of curcumin and 6-shogaol on these parameters were completely against it. As a result of the assays, we saw that 6-shogaol showed as much anticancer effect as curcumin and it is thought that 6-shogaol might be a potential candidate in NSCLC treatment because it is cytotoxic and decreases the protein levels of mPGES-1 and β-catenin.

Biography

Eren Demirpolat works as a research assistant in deparment of pharmacology and he has a two years experience in good clinical practice. He participated in nearly 150 bioequivalance trials as a clinical research pharmacist in Turkey. His phD thesis is focused on potential mPGES-1 inhibitors and can perform cell culture, western blotting and PCR methods.

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Identification and validation of novel genes that underpin the transition to the invasive phenotype of breast tumour

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Breast cancer (BC), a heterogeneous disease, can invade locally or metastasize to lymph nodes or other organs. Despite advances in technology and research in BC, the complexity of the molecular basis of BC development and progression is still nascent. In the multistep process of BC metastasis, invasion is the recurring and the defining event and elucidation of its molecular mechanisms is critical for understanding BC progression. Previous studies have suggested that different breast tumour grades are associated with distinct gene expression signatures. This study aims to test the following dual hypothesis: i) that a subset of specific genes is associated with the transition from pre-invasive to invasive growth of breast tumor; and ii) the process of cell invasion involves specific anti-invasive and pro-invasive genes that interact to coordinate breast tumour cell migration/invasion. To test this hypothesis, RNA was extracted from breast tumour tissues and microarray analysis was performed. Our results showed that the analysis of the microarray data revealed a set of genes that could potentially interplay into signalling pathways that regulates the switch from pre-invasive to invasive phenotype; these genes will undergo further screening tests to identify and validate the candidate genes that will pave the way towards the design of targeted anti-invasive therapeutic strategies.