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Pathway analysis of genes affected in Mcf-7 breast cancer cells treated with recombinant bromelain (Article)

Fouz, N.^a, Amid, A.^b, Hashim, Y.Z.H.-Y.^c 

^aDepartment of Biotechnology Engineering, Faculty of Engineering, International Islamic University Malaysia, P.O. Box 10, 50728 Kuala Lumpur, Malaysia

^bBioprocess and Molecular Engineering Research Unit, Department of Biotechnology Engineering, International Islamic University Malaysia, P.O. Box 10, 50728 Kuala Lumpur, Malaysia

^cInternational Institute for Halal Research and Training, Faculty of Engineering, International Islamic University Malaysia, Block E0, 50728 Kuala Lumpur, Malaysia

Abstract

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The contributing molecular pathways underlying the pathogenesis of breast cancer need to be better characterized. The goal of the present study is to understand the probable molecular mechanism and the associated pathway related to recombinant bromelain treatment on MCF-7 breast cancer cells. Within 1102 known genes differentially expressed to a significant degree ($p < 0.001$) set, 34 genes were significantly changed between treated cells and the control cells with cutoff fold change more than 2. These genes are LYRM2, TUBB2C, LRRFIP1, HMGN2, HMGN2, GLTSCR2, RN28S1, HIST2H4B, HIST2H4A, PA2G4, ACTB, C1orf152, RPS3A, C12orf51, RAP1B, FLJ16171, CCDC59, MGEA5, KIFAP3, GPBP1, KLHDC2, TBPL1, STK38L, RIOK3, CLK4 SNORD46, C7orf60, BTG1, TMEM59, ARID4A, C6orf62, FRG1, DEFB109P1B and RBMS1. With this exploratory study using Ingenuity Pathway Analysis IPA, we aim to identify the overlapping pathways associated with recombinant bromelain treatment and its anti-cancer mechanisms in MCF-7 breast cancer cells. The pathways identification has been shown to be associated with recombinant bromelain function on cell cycle, cancer, cell death & survival, cellular development, tumor morphology, cellular growth and proliferation. This finding will enhance the power of In-vitro breast cancer study and lead to better understanding on mechanisms of action of recombinant bromelain in fighting cancer.

Author keywords

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Amid, A.; Bioprocess and Molecular Engineering Research Unit, Department of Biotechnology Engineering, International Islamic University Malaysia, P.O. Box 10, Malaysia; email:azuraamid@iiu.edu.my
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