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Flocatera (Flavonoids as cancer preventive therapy): The usage of flavonoids in Ketepeng Cina (Cassia alata L.) as an anti-cancer through anti-inflammatory mechanism

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The highest flavonoid content is in Ketepeng Cina with 26.86 mg/ mL. Flavonoids can act as an inhibitor of pro-inflammatory enzymes, namely COX-2. Excessive expression of COX-2 inhibits apoptosis of tumor cells and increases the level of invasive; while COX-2 inhibitors, which have been declared, can reduce the risk of tumors in the digestive system, breast and bladder. Inflammatory cells secrete cytokines increase the levels of ROS and RNI in premalignant cells. Chronic inflammatory reaction can cause a variety of pathological changes of cells such as fibrosis, angiogenesis aberan and neoplasia. Experimental studies using a completely randomized design, extract 100% Ketepeng Cina obtained from 95% ethanol maceration method. There are 4 groups of samples of experimental animals Musmuculus females. DMBA cancer inducer (Benzophenanthrene) subcutaneously by injection obtained the value of P <0.05 means that there are an influence on each group and each treatment against the onset of inflammatory cells based preparations histopathology breast tissue of mice, the group that shows the degree of non-inflammation were negative control group and Ketepeng Cina extract dose of 750 mg/kg. Severe inflammation degree (23%) contained in the positive control group. Ketepeng Cina extract dose of 750 mg/kg proved effective in preventing inflammation with no inflammation (23%),the dominance of mild inflammation (60%) and inflammatory cell types show the dominance of PMN cells (acute inflammation) by 63%. While the Ketepeng Cina extract dose of 500 mg/kg dominance mild inflammation (70%) and moderate inflammation (30%), inflammatory cell types show the dominance of mononuclear cells (chronic inflammation) by 67%.

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Glycoproteomics analysis of breast cancer using *in vivo* model

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Glycosylation is a post-translational modification processes that play a crucial role in many biological processes such as protein-protein interactions and cell adhesion. Aberrant glycosylation of proteins was found to be associated with cancer progression. Characterization of protein glycosylation profiles may identify potential biomarkers for the diagnosis and prognosis of cancer. This study aimed to elucidate the serum protein profile and protein glycosylation profile (N- and O-linked glycosylation) in the breast cancer progression using mouse 4T1 breast tumour model. The female BALB/c mice were injected with 4T1 tumour cells in the mammary fat pad. The mice sera samples were collected weekly (up to four weeks) and subjected to two-dimensional electrophoresis (2D-E) coupling with glycan-binding lectins and further analysed through mass spectrometry. Analysis of protein profiles identified eight differentially expressed proteins (A2M, AAT, AHS, APOA4, CON, HP, KNG and PRO), of which AAT, CON, HP and KNG were significantly up-regulated in mice sera from week 1 to week 4 after 4T1 cells injection. Aberrantly N-glycosylated PRO was detected in all the mice sera from week 1 to week 4 after the injection. As for the O-glycosylated protein detection, A2M, AHS, CON and HP were aberrantly expressed in mice sera after injection, of which A2M, CON and HP were detected on week 1 and week 2, while AHS and CON were detected on week 3 and week 4. Combination of 2D-E with lectin-based analysis were effective to identify various biomarkers that could serve as potential diagnostic and prognostic markers for breast cancer.

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