Seminar
Graduate Institute of Food Science and Technology
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Topic: Genomic Analysis of the Effects of Selected Antidepressants on the Brain Using Microarray
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Abstract:
Major depressive disorder is a serious illness, and yet no molecular and/or cellular mechanism has been identified that satisfactorily explains its cause. DNA microarray is a powerful tool that is useful in measuring changes in gene expression levels induced by depression. Studies often include the mechanisms of the antidepressants, the target brain areas, and the change in gene expression level upon the use of the antidepressants. The three examples of antidepressants with genomic analysis of the brain done by DNA microarray are nicotine, fluoxetine, and escitalopram. The animal model involves either a depression-inductive regime, or simply a comparison between the consumption and no consumption of antidepressants, without a depression-inductive regime. Nicotine inhibits the reuptake of dopamine and noradrenaline, and fluoxetine and escitalopram function by increasing the level of serotonin available to bind to the postsynaptic receptor. Research has shown that nicotine down-regulates phosphodiesterase (Pde) 4b1 and 4b2 in the hippocampus, Pde4b1 in the nucleus accumbens, and Pde4b2 in the prefrontal cortex. Phosphodiesterases are enzymes that breakdown cyclic AMP, causing depression. In addition, fluoxetine evokes transcriptional changes in various parts of the brain, mainly in the hypothalamus, dorsal raphe, and amygdale. Finally, escitalopram decreases the mRNA levels that relate to apoptotic pathways. All in all, DNA microarray technology enables us to study the changes in gene expression levels induced by depression, so that we can devise a reasonable mechanism for the function of a particular antidepressant.

Key Words: antidepressants, rats, gene expression, microarray

References:


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