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A simple method to screen ligands of peroxisome proliferator-activated receptorδ as therapeutic target for improvement of metabolic disorders

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Peroxisome proliferator-activated receptors (PPARs) are transcription factors belong to the nuclear receptor superfamily that directly modulates gene expression by binding to specific ligands. Recently, it has been reported that PPARδ ligands play an essential role in improvement of metabolic disorders and skin disorders. We introduce enzyme-linked immunosorbent assay (ELISA) as a simple method in order to screen new PPARδ ligands. This method is based on the activation mechanism of PPARδ that the ligand binding to PPARδ induces interactions of the receptor with transcriptional co-activators. We optimized a simple ELISA method for screening PPARδ ligands. Among co-activators, PPARδ had more strong binding with SRC-1 in an ELISA system. The well-known ligands of PPARδ such as GW501516 and linoleic acid increased the binding between PPARδ and co-activators in a ligand dose-dependent manner. The recruitment of co-activator SRC-1 into ligand-bounded PPARδ is also more effective than those of other coactivators such as TIF-2 and p300. We optimized and developed a novel and useful ELISA system for the mass screening of PPARδ ligands. This screening system may be a promising system in the development of drugs for metabolic disorders and skin disorders.

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Anthocyaninsinhibit lipogenesis and adipogenesis of 3T3-L1 preadipocytes

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Anthocyanins suppressed the development of obesity through down-regulation of the genes involved in the fatty acid synthesis and adipogenesis. When induced to differentiate in the presence of anthocyanins (1.0-40 ug/ml), 3T3-L1 preadipocytes reduced to accumulate cytoplasmic triglycerides. This phenomenon was rapidly reversible. When applied to mature 3T3-L1 adipocytes, anthocyanins induced a moderate reduction in cellular triglyceride content. mRNA expression levels of both CCAAT/enhancer-binding protein α (C/EBPα), peroxisome proliferators-activated receptor γ (PPARγ), and sterol regulatory element-binding protein-1c (SREBP-1c), which act as key transcription factors at an early stage of adipogenesis and lipogenesis, were decreased by anthocyanin treatment. Anthocyanins decreased mRNA and protein expression of lipogenic genes such as fatty acid synthase (FAS) and steroyl-CoA desaturase-1 (SCD-1). These results suggest that the inhibitory effect of anthocyanins on adipocyte differentiation might be mediated through down-regulation of adipogenic transcription factors and the inhibition of the SREBP-1c-dependent lipogenic pathway.

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Anti-inflammatory effects of the cultured fruitbody of cordyceps bassiana butanol fraction

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Cordyceps bassiana has been used in traditional folk medicine to treat numerous diseases. The pharmacological and biochemical actions of C. bassiana in inflammation has not been clearly elucidated. We investigated if C. bassiana show any differences in inhibition of NO production. Also, we tested the inhibition of iNOS and COX-2 protein expression by the addition of C. bassiana butanol fraction(CBBF). We examined the signal pathway how the butanol fraction of C. sacarabaecola regulates production of COX-2, iNOS, Akt, Erk, p38, and IkB in LPS-induced macrophage. The CBBF inhibits these inflammatory mediators in LPS-stimulated murine macrophage cell line(RAW264.7). But CBBF was not effective on the inhibition of extracellular signal-regulated kinase (ERK)1/2 activation. The results suggest that the CSBF suppress inflammation through suppression of NF-kappa B-dependent inflammatory gene expression, suggesting that the C. bassiana butanol fraction (CSBF) may be beneficial for treatment of endotoxin shock or inflammation [Supported by grants from (ARPC)]

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Antibiotic resistance and virulence markers in enterococci isolated from non-tertiary hospitals

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Increasing the resistant rates of antibiotics and being more diverse of virulence factors in Enterococci in recently, we researched relation of the resistant rates and virulence factors in enterococci isolated from non-tertiary hospitals. 587 enterococci were isolated from non-tertiary hospitals in 2005, identified by using PCR, and tested antimicrobial susceptibility by agar dilution method. Analysis of virulence factors, cytolysin, enterococcal surface protein (esp), hyaluronidase (hyl), aggregation substance, and gelatinase were determined by multiplex PCR method. Of 587 enterococci, the antibiotic resistant rates were ranged from 10.4% to 81.8% in Enterococcus faecium (138, 23.5%) and from 29.4% to 86.9% in E. faecalis (424, 72.2%). The rates of vancomycin-resistant E. faecium was 1.4%. The frequency of virulence factors but hyl were 28.8%-74.1% in E. faecalis, and, hyl and esp were 69.6% and 73.9% in E. faecium, respectively. Especially, hyl and esp gene were detected in 87 strains (84.5%) and 90 (87.4%) of 103 gentamicin-resistant E. faecium, in 8 (23.5%) and 11 (32.4%) of 34 gentamicin-susceptible E. faecium, 89 (79.5%) and 94 (83.9%) of 112 erythromycin-resistant E. faecium, and 6 (24%) and 7 (28%) of 25 erythromycin-susceptible E. faecium, respectively. In E. faecium, the frequency of VRE was 1.4% and the rates of esp and hyl determinants were relatively high.