potent antagonist for HP infection to KATO III cells.

[PC2-6] [10/19/2001 (Fri) 09:00 - 12:00 / Hall D]

Sequence Analysis of Regulatory Regions of *ermAM* genes with Unusual Induction Patterns from enterococci

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Target modification is the major mechanism of resistance to macrolide antibiotics in enterococci and is due to the synthesis of a methylase, which modifies the ribosome.
This modification confers cross-resistance to macrolides, lincosamides, and streptogramin B (that is MLS_B phenotype). Genes belonging to erm class commonly mediate MLS resistance. Among MLS antibiotics, 14-membered-ring macrolides such as erythromycin have been considered the most potent inducers in *ermAM* gene.
In the screening of 306 Korean clinical enterococci isolates, we found 58 isolates with two unusual induction specificities. In the phenotype I group, the 16-membered macrolide was the stronger inducer than the 14-membered macrolide. In the phenotype II group, both the 14-membered macrolide and the 16-membered macrolide showed equivalent inducibility.
The regulatory regions of the *ermAM* genes of enterococci isolates were amplified and sequenced. The sequenced regulatory regions of *ermAM*s aligned with the same region of *ermAM* in Tn917. Thirteen *ermAM*s showed two mutations which are identical with those of the *ermAMR* as we previously reported: arginine-to-cysteine change of 7th codon and TAAA duplication in the leader peptide. In the second group of 17 *ermAM*s, one tranversion and insertion of 12 nucleotides were observed: Asn→Tyr of 8th codon and insertion of 4 amino acids. In the third group of 5 *ermAM*s, several substitutions and the duplication of TAAA were found. All the above mutations were identified in the phenotype I group. In the remaining 20 *ermAM*s, only one mutation was identified: the duplication of TAAA in the leader peptide. This variation was observed in the phenotype II group.

[PC2-7] [10/19/2001 (Fri) 09:00 - 12:00 / Hall D]

Isolation and characterization of cytotoxic and immunosuppressant substance 0116p produced by Streptomyces scabies subsp.MO137

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An cytotoxic substance 0116p, which showed cytotoxicity against human macrophage cell line (THP-1), was isolated from mycelial extract of Streptomyces scabies subsp.MO137. The cytotoxic subsatance was purified by solvent extraction, Sephadex LH-20 column chromatography, and silica-gel column chromatography. The molecular formula was determined to be C19H40O2(MW 301.10) by elementary, MS, and IR analysis. 0116p was identified to be a nonadecanoic acid by NMR spectral data, and showed cytotoxic activities to various cancer cell lines including A549, SK-OV-3, SK-MEL-2 and HCT-15. Also, 0116p showed antiinflammatory and immunosuppressant effects and thus showed therapeutic effects on Th1-mediated autoimmune diseases.