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부산지역 유흥업소 종사여성으로부터 분리된 HPV16형의 발암유전자(E6/E7) 돌연변이 유형분석

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Intratypic Variants of HPV-16 E6/E7 Oncogene Isolated from Sexually High-Risk Women in Busan

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Abstract

Recent studies have reported that the distribution of HPV-16 sequence variations differs geographically and specific HPV-16 E6 and E7 intratypic variants might carry a high risk for development of ICC (invasive cervical cancer) and CIN (cervical intraepithelial neoplasia) in a given population. To investigate the genetic diversities of HPV-16 E6 and E7 oncogene, we analyzed the genetic variation of HPV-16 E6 and E7 genes isolated from sexually high-risk women in Busan. We amplified the E6 and E7 coding region (nt 34 to 880) with HPV-16 E6/E7 specific PCR and analyzed nucleotide and amino acid sequences of these regions by using the DNASTAR software. At the nucleotide level, eleven variants of the E6 genes and nine variants of the E7 genes were identified as followed: E6 T178G (n=11), E6 T178A (n=1), E6 T350G (n=3), E6 A442C (n=2), E6 A104T, E6 A111G, E6 C116T, E6 G145T, E6 T183G, E6 C335T, E6 G522C and E7 A647G (n=12), E7 A645C, E7 A777C, E7 G663A, E7 T732C, E7 T760C, E7 A775T, E7 T789C and E7 T795G, respectively. At the amino acid level, the isolated HPV-16 E6 and E7 genes showed eleven E6 variants: E6 D25E (n=12), E6 L83V (n=4), E6 E113D (n=2), E6 M1L, E6 Q3R, E6 P5S, E6 Q14H, E6 D25N, E6 I27R, E6 H78Y, E6 C140S and three E7 variants : N29S (n=12), L28F, T72S. HPV16 E6 L83V, the dominant variant in Caucasian population, showed relatively low frequencies in our study population. We elucidated that the dominant HPV-16 E6 and E7 variants were HPV-16 E6 D25E (63.2%) and HPV-16 E7 N29S (63.2%), which were included in Asian lineage phylogenetically. Further study is needed to evaluate the risk as a cervical cancer of HPV-16 E6/E7 intratypic variants in Korean population.

Key words : Sexually high-risk women, HPV-16 E6 and E7 variants, E6 D25E, E7 N29S

한국생명과학회 학술심포지움 및 국제학술대회
2009.10.15~16, 부산BEXCO

Variation of the N1 Influenza Virus Hemagglutinin in Busan 2009

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Influenza viruses were isolated from several hospitals in Busan from January to August. Reverse transcription and PCR amplification were carried out under standard conditions by using influenza-specific primers. The nucleotide sequences of influenza virus Neuraminidase (NA) genes of the N1 serotype from human hosts were analysed and their evolutionary relationships with natural reservoir species were evaluated. The aligned data sets for N1 serotype from human hosts are 1413 nucleotides (bp) and the contents of A, C, G, and T for them in Korea were generally similar to those for New York 2009 and California 2009. However, they were different from those of California 2009. Many substitution mutations in the N1 serotype, i.e. Phe to Leu at position 6 and Pro to Leu at position 57, were also observed in Busan 2009 and USA. A/N1 types in this study does not evolve anomalously very fast. The phylogenetic tree indicates that the human virus of the H1N1 serotype originated from a lineage closely related to a series of California in USA.

Key words: Influenza Virus, A/N1, Busan, substitutions

한국생명과학회 학술심포지움 및 국제학술대회
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Evolution of the H1 Influenza Virus Hemagglutinin from 2007 to 2009 in Busan

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The nucleotide sequences of Influenza virus hemagglutinin genes of the H1 serotype from human hosts in Busan were analysed and their evolutionary relationships with natural reservoir species were evaluated. Overall rates of evolutionary change(nucleotide substitution per site, per year) and the age of the most recent common ancestor were estimated using the BEAST program. We found high nucleotide variation in A/ Busan/23/2009 among the Busan 2009 H1N1 sequences in HA genes which was isolated from 2year old female. The most notable aspect of these results was that the substitution rates estimated for A/H1N1 were very slow, ranging from 2.1×10^{-4} substitutions per site, per year (subs/site/year) to 5.2×10^{-3} substitutions. A/H1N1 types in this study does not evolve anomalously slow or very fast. The phylogenetic tree indicates that the human virus of the H1N1 serotpe originated from a lineage closely related to a series of Hawaii and pennsylvania.

Key word : Influenza viruses, A/H1, Busan, hemagglutinin genes

한국가축위생학회지 제32권 제1호(2009)
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소와 돼지유래 *Salmonella*속 균의 혈청형 및 약제감수성

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Serotype and antimicrobial susceptibility of *Salmonella* spp. isolated from pigs and cattle

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Abstract

At the present study, it was aimed to explore the states of antimicrobial resistant *Salmonella* spp. isolates from 3,850 pigs (2,732 ileocecolic lymphnodes and 1,118 cecal contents) and 1,764 cattle (965 cecal lymphnodes and 799 cecal contents) slaughtered in Busan province from December 2000 to November 2001. Among 5,614 samples, 457 of *Salmonella* spp. were isolated from pig lymphnodes (13.5%), pig cecal contents (4.4%), cattle lymphnodes (3.5%) and cattle cecal contents (0.5%). *Salmonella* spp. were showed different isolation ratio, that was 10.8% in summer, 9.0% in autumn, 8.4% in spring and 5.0% in winter. As a result of serotyping, B group (65.4%) were identified as the most common in pigs and cattle, in order of C₁ (14.0%), D₁ (5.5%), C₂ (4.2%), E₁ (4.2%) and L (3.5%). 34 serotypes were found, among them, *Salmonella* Typhimurium (*S.* Typhimurium) (21.0%) was the most common serotype from pigs and cattle. The major serotypes were in order of *S.* Derby (15.3%), *S.* Schwarzengrund (14.7%), *S.* Typhimurium var Copenhagen (9.2%), *S.* Mbandaka (5.7%), *S.* Enteritidis (5.5%) and *S.* Ruiru (3.5%). The most common serotype was *S.* Typhimurium in pigs, and *S.* Ruiru in cattle. *S.* Ruiru was firstly isolated from pigs and cattle in Korea. In antimicrobial susceptibility test, all the isolates were demonstrated susceptibility to norfloxacin and ofloxacin. But the isolates were showed resistance other antibiotics in order of doxycycline (68.3%), tetracycline (67.8%), penicillin (54.5%) and streptomycin (52.5%). *S.* Typhimurium were exhibited resistance to ampicillin (34.8%), chloramphenicol (36.2%), streptomycin (94.9%), sulfamethoxazole/trimethoprim (34.8%) and tetracycline (97.8%). There were 53 strains (38.4%) which had multidrug resistant (MDR) isolates, resistant to more than 6 antimicrobial agents. The most common resistance patterns of MDR isolates were ampicillin, chloramphenicol, carbenicillin, doxycycline, nalidixic acid, penicillin, streptomycin, sulfamethoxazole/trimethoprim and tetracycline (ACCbDNaPSSuT).

Key words : *Salmonella*, Ileocecolic lymphnodes, Serotypes, Multidrug resistant

한국가축위생학회지 제32권 제2호(2009)
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Multiplex PCR 기법을 이용한 *Salmonella* Enteritidis와 *S. Typhimurium*의 특이적 검출에 관한 연구

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Identification of *Salmonella* Enteritidis and *S. Typhimurium* by multiplex polymerase chain reaction

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Abstract

Salmonella species are the most important etiologic agents of food-borne acute gastroenteritis. The most common serotypes isolated from humans are *Salmonella enterica* serotype Typhimurium (*S. Typhimurium*) and *S. Enteritidis*. Traditional detection methods for *Salmonella* are based on cultures using selective media and characterization of suspicious colonies by biochemical and serological tests. These methods are generally time-consuming and not so highly sensitive. Recently, the polymerase chain reaction (PCR) has been used as a highly sensitive, specific, and rapid test for the presence of pathogenic bacteria. In this study, a multiplex PCR (m-PCR) was used to detect *S. Typhimurium* and *S. Enteritidis*. We selected m-PCR target genes, which were the *spv* (virulence plasmid specific for *S. Enteritidis*) and *sefA* (*S. Enteritidis* fimbrial antigen) genes, *fliC* (H1-i antigen specific for *S. Typhimurium*) and a randomly cloned sequence specific for the genus *Salmonella*. With m-PCR, random sequence was detected from all strains of *Salmonella* spp, *spv* and *sefA* were detected from all strains of *S. Enteritidis* (100%), and *fliC* was detected from all strains of *S. Typhimurium* (100%). This assay indicate that the specificity of the m-PCR make them potentially valuable tools for detection of *S. Typhimurium* and *S. Enteritidis*.

Key words : Multiplex polymerase chain reaction, Virulence plasmid, Fimbrial antigen

한국가축위생학회지 제32권 제1호(2009)
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소와 돼지유래 다제내성 *Salmonella*속 균의 분자유전학적 특성

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Molecular genetic characterization of multiple antimicrobial resistant *Salmonella* spp. isolated from pigs and cattle

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Abstract

At the present study, it was aimed to explore the molecular genetic characterization of multiple antimicrobial resistant *Salmonella* spp. isolated from pigs and cattle. A total of 138 *Salmonella* Typhimurium (*S. Typhimurium*) isolates were typed with phage, among them, 83.3% of *S. Typhimurium* tested could divide into a 10 phage types. Definitive type 193 (DT193) (25.4%) and DT195 (24.6%) were exhibited as the dominant types. DT104 and U302 were found from pigs and cattle. On the other hand, *S. Enteritidis* had 6 phage types, of them, phage type 21 (PT21) and PT1 lb were the popular types. In the plasmid profiles, 135 of *S. Typhimurium* isolates were exhibited 1 to 6 plasmid bands which molecular weight ranged from 90 to 2kb. 35 isolates (25.4%) harbored a 90kb plasmid which is thought to be the serotype specific virulence plasmid. Two of twenty five *S. Enteritidis* had common plasmids at 2 and 1.5kb. With multiplex polymerase chain reaction, virulence genes (*invA* and *spvC*) were detected from all *Salmonella* spp. from 167 of *S. Typhimurium*, *S. Enteritidis* and chloramphenicol resistant *S. Schwarzengrund*, but some drug resistant genes, such as PSE-1, *cml/teR* and *flo* were not determined but other drug resistant genes, for example TEM and *int* were found. The detection rates of *spvC*, TEM and *int* gene was 35.3%, 29.3% and 72.5%, respectively. The TEM gene was highly popular in *S. typhimurium*, which was detected from ampicillin and amoxicillin resistant strains as 95.9%, *int* gene was able to detect from all the isolates identified as multidrug resistant (MDR), particularly DT193 was thought as the most prevalent virulence and multidrug resistance isolate. The major plasmid profile and drug resistance pattern of DT193 were 90, 40, 10.5, 6.3, 3.0kb and ACCbDNaPSSuT, respectively. MDR was commonly found in other phage types, particularly DT104, U302 and DT203.

Key words : Definitive type, Phage type, Plasmid, MDR, Virulence gene

한국가축위생학회지 제32권 제3호(2009)
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소와 돼지유래 살모넬라속 균의 약제내성유전자의 특성에 관한 연구

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Investigation on antimicrobial resistance genes of *Salmonella* spp. isolated from pigs and cattle

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Abstract

At the present study, it was aimed to detect virulence genes and antimicrobial resistance genes among 102 strains of 12 *Salmonella* serotypes isolated from pigs and cattle. In polymerase chain reaction (PCR), *invA* was detected from all strains of *Salmonella* spp.. *spvC* was detected from *Salmonella enterica* serotype Enteritidis (*S. Enteritidis*) (100%), *S. Bradenburg* (75%), and *S. Typhimurium* (20.4%). Drug resistance related genes of 12 types were detected from all strains. TEM (*bla*_{TEM}) genes was detected from 51 (92.7%) of 55 β -lactams (54 ampicillin or 1 amoxicillin) resistance strains. 55 (100%) of 55 chloramphenicol resistance strains, 3 (100%) of 3 gentamicin resistance strains and 5 (100%) of 5 kanamycin resistance strains did contain *cml*, *aadB*, and *aphA1-Iab*, respectively. *strB* (89.9%), *strA* (88.4%), *aadA2* (84.1%) and *aadA1* (72.5%) were detected from 69 streptomycin resistance strains. *sullI* and *dhfrXII* were detected from 49 (100%) of 49 sulfamethoxazole/ trimethoprim resistance strains, but *sullI* was not detected. *tetA* (97.9%) and *tetB* (21.6%) were detected from 97 tetracycline resistance strains. *int* gene was detected from 58 (56.9%) of 102 strains.

54 *S. Typhimurium* of 102 *Salmonella* spp. were attempted to detect drug resistance genes. TEM was detected from 44 (95.7%) of 46 β -lactams (45 ampicillin or 1 amoxicillin) resistance strains. *cmlA* was detected from 51 (100%) of 51 chloramphenicol resistance strains. *aadA2* (100%), *strA* (100%), *strB* (100%) and *aadA1* (79.6%) were detected from 54 streptomycin resistance strains. *sullI* (100%) and *dhfrXII* (100%) were detected from 49 sulfamethoxazole/trimethoprim resistance strains. *tetA* was detected from 54 (100%) of 54 tetracycline resistance strains. *int* gene was detected from 54 (100%) of 54 strains. The major drug resistance pattern and resistance gene profile were ampicillin, chloramphenicol, streptomycin, sulfamethoxazole/trimethoprim and tetracycline (ACSSuT) and TEM, *cmlA*, *aadA1*, *aadA2*, *strA*, *strB*, *sullI*, *dhfrXII*, *tetA* and *int*, respectively.

Key words : Polymerase chain reaction, Virulence gene, Antimicrobial resistance gene

한국가축위생학회 제32차
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유통되는 쇠고기에서 분리한 대장균의 항생제 내성 조사 · 연구

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서 론

항생제는 동물과 사람에서 질병의 치료, 예방 목적 및 동물의 생산성을 증가시키기 위한 목적의 성장 촉진제로 사료첨가용의 형태로 오랫동안 많이 사용되어오고 있어 최근 들어 오, 남용에 의한 부작용으로 잔류 문제나 약제 내성균의 출현, 전파 등에 따른 항생제 내성과 같은 축산물 안전성에 대한 중요한 문제를 야기시키고 있고 전 세계적으로 커다란 공중보건학적 문제로 대두되고 있어 여러 국가별로 항생제 내성균 모니터링 시스템을 구축하여 운영하고 있는 실정이다. 따라서 본 연구에서는 축산과 수의 분야에서 항생제의 효율적인 사용 및 안전관리를 위한 대책을 수립하고 우리가 생활하면서 꾸준한 증가 추세로 섭취하는 축산식품 중 대표적인 식육에 대한 안전성 확인의 한 과정으로 유통 중인 쇠고기에서 분리한 대장균을 대상으로 항생제 내성 실태를 조사하고자 2007년~2008년까지 2년간 본 조사, 연구를 실시하게 되었다.

키워드 : 쇠고기, 대장균, 항생제 내성

한국가축위생학회지 제32권 제1호(2009)
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유통되는 쇠고기에서 분리한 대장균의 항생제 내성 조사·연구 (2)

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Study on antimicrobial resistance of *Escherichia coli* isolated from domestic beef on sale (2)

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Abstract : In this study, antimicrobial resistance of *E. coli* isolated from domestic beef on sale in Busan and Gyeongnam province was investigated from March to October 2008. A total of 400 beef samples were collected for the monitoring of antimicrobial resistance, and 39 (9.8%) strains of *E. coli* were isolated. Antimicrobial resistance test was carried out by agar disc diffusion method with 17 antimicrobials. In general, *E. coli* isolates showed the highest antimicrobial resistance to tetracycline (85.3%), followed by doxycycline (76.5%), streptomycin (61.8%) and sulfamethoxazole/trimethoprim (61.8%). Then they showed higher resistance to several antimicrobials like kanamycin and neomycin (55.9%). However, They had low antimicrobial resistance to amikacin (8.8%), amoxicillin/clavulanic acid (2.9%). Of 39 isolates, 31 (79.5%) were resistant to more than 2 antimicrobials. Among 17 antimicrobials examined, tetracyclines were the most resistant, followed by aminoglycosides, sulfonamides. The resistance was seemed to be correlated to amounts of antimicrobial use. In the result of this study, we suggest that there be need to regulate the abuse of antimicrobial on food-producing animals in Korea because the concern on antimicrobial resistant is gradually increased worldwide.

Key words : *Antimicrobial resistance, Antimicrobials, E. coli, Beef.*

부산지역 지하수의 방사성물질 특성

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Radionuclides of Ground waters in Busan

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Abstract

This study was performed to research the characteristic of radionuclides of 80 groundwater monitoring networks in Busan. According to the research, average concentration of Uranium was $4.33\mu\text{g/L}$, maximum concentration of Uranium was $171.55\mu\text{g/L}$ among the 80 sampling sites. One sample exceeded the Proposal standard of drinking water in USA in Uranium ($30\mu\text{g/L}$) and four samples exceeded the recommendatory value of WHO about Uranium ($15\mu\text{g/L}$). Radon and gross- α concentration of all samples were far less than the Proposal standard of drinking water in USA. In this study average concentration of radionuclides in underground water wasn't too high, but needed to control the concentration of them to prevent exposure to the people. And it needs to be taken measures in some sites with high concentration of Uranium by closing the pipe line or etc through more studies.

Key words : Radionnelides, Groundwater. Uranium, Radon, gross- α

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A study on the formation of photochemical air pollution and the allocation of a monitoring network in Busan

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Abstract

The characteristics of concentration variations for dust, O₃, and its precursors in Busan, South Korea were analyzed on the basis of pollution data from 19 stations during 2005. The objectives of these analyses were (i) to observe the ozone precursor concentrations under various conditions, (ii) to examine the mechanism of high [O₃] episode development, (iii) to examine the formation of photochemical aerosols, (iv) to observe the spatial distribution of high [O₃] occurrence over time, and (v) to observe the spatial distributions of temperature and wind speed over the whole area of Busan on high [O₃] episode days. The ratio of initial [NO₂] to initial [NO], O₃ dosage, and O₃ formation/hazard potential were established as relevant parameters on which to base allocation of monitoring stations according to each regional type, and criteria based on these parameters were determined for reallocating stations over the Busan area according to various regional types based on monitoring purposes. It was found that the current allocations of stations for investigating photochemical pollution do not reflect the areas where high O₃ occurs and areas where it is desirable to measure O₃ and its precursors flowing out of the target area. Therefore, based on these criteria, reallocated monitoring stations according to each regional type were suggested.

Key words : Ozone, Precursor, VOCs, Nitrogen Oxides, Photochemical Air Pollution, Monitoring Network, Allocation of Photochemical Monitoring Station

벗짚재 및 솔잎재를 이용한 폐주물사내 중금속 제거에 관한 연구

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Study on Reduction of Heavy Metals in Waste Foundry Sand Using Rice Straw Ash and Pine Needles Ash

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Abstract

In order to recycle the waste foundry sand for covering and filling materials, it must obey the heavy metal standards of Soil Environment Conservation Act and waste control Act. But most of waste foundry sand have not been satisfied the heavy metal standards of Soil Environment Conservation Act. The purpose of this study is to utilize rice straw ash and pine needles ash as natural washing agents and to remove the heavy metals (Cu, Pb, Cd, Zn, Ni) in waste foundry sand. From the results of Zn leaching test by the Soil Environment Conservation Act, Zn concentration was decreased to 52% removal rate of initial concentration by the rice straw ash, to 54% removal rate by the pine needles ash. Hence the rice straw ash and pine needles ash as natural washing agents will be possible to field application.

Key Words : Waste foundry sand, Recycle, Rice straw ash, Pine needles ash, Washing agent, Waste control act, Soil environment conservation act

Multivariant Statistical Analysis Of Dioxin Congeners in Soil Sample from Different Sites in Busan, South Korea

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Abstract

In this study, soil samples in Busan have been sampled and analysed to determine the level of dioxins, summarize the systematic information and provide the major trends of the data. Soil samples collected in 2008 showed concentration ranging from 0.157 to 28.772 pg-TEQ/g dry weight with a mean values of 11.929 pg-TEQ/g dry weight. In the case of real values, OCDD is the major contributor with 53.3%. In contrast to real values, dioxin congeners profiles in TEQ values were dominated by 2,3,4,7,8-PeCDF, which contributed about 36.7% to the total dioxin concentrations. The ratio of PCDFs/PCDDs in real values was about 0.45, but that in TEQ values was the opposite with approximately 2.4 of the ratio of PCDF/PCDDs. Multivariate data analysis method was adopted in this research to combine a large amount of variables into several underlying compounds, which summarize the systematic information and provide the major trends of the data. PCA provides a two dimensional model, which would explain the data variance. The first principal component(PCI) explains 82.4% of the total variance. The second principal component(PC2) explains 9.0% of the total variance.