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Biochemical characterization of bacteriocin produced by Lactobacillus isolated from kimchi

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Bacteriocins have been defined as proteinaceous, bactericidal substances synthesized by bacteria, which usually have a narrow spectrum of activity, only inhibiting strains of the same or closely related species. Bacteriocin screening of 18 strains of lactobacillus was performed against 8 indicators. Three strains of Lactobacillus are selected by this screening. Three strains of Lactobacillus, isolated from kimchi, produce a bacteriocin which is active against various crop pathogens Burkholderia glumae, Clacibacter michiganensis subsp. michiganensis, Erwina carotovora, Xanthomonas campestris pv. glycines, Xanthomonas translucens pv. translucens ktx2, Xanthomonas oryzae pv. oryzae and Xanthomonas campestris pv. vesicatoria sdi 833. Three strains of Lactobacillus grew well at 30°C and in the stationary phase after 10h incubation. pH values of Lactobacillus culture decrease about 4.0. The bacteriocin production started in the early exponential phase after 7 hour incubation and activity of bacteriocin retained after 72 hour incubation. The bacteriocin were active at pH value between 3.0 and 10.0 and active at temperature between 0°C and 60°C. A part of proteolytic enzymes inactivated this bacteriocin.

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Biogenesis of a small noncoding RNA, RygC, and its possible function in Escherichia coli

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Small noncoding RNAs (sRNAs) with a variety of regulatory functions have been found in numerous organisms over the past years. In Escherichia coli, about 100 sRNA molecules have been identified and expression of some sRNAs is involved in the responses to a certain stress condition. Although studies have attempted to characterize the role of sRNAs in E. coli, biological functions of most sRNAs are still unknown. In this study, first, we studied biogenesis of a small noncoding RNA, RygC. RygC was previously identified as about 140-nt RNA, which is encoded by rygC gene located in the downstream region of srS-ygFA gene. Interestingly, RygC has a significant sequence homology with other three ncRNAs, RygD, RygE and RygD, which reside in different intergenic regions. We found the presence of two RygC molecules of 141 nt and 109 nt in the cell, respectively. The 109-nt RNA is derived from the 141-nt RNA by processing of 3' end. We did not find any mutant phenotype in an rygC-knockout strain, but we observed that a strain overexpressing RygC entered the stationary phase earlier than the control strain. We performed a comparative proteomic analysis between the RygC-overexpressing strain and the control strain. We found that some proteins were differentially expressed between two strains.

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BiP IRES activity is controlled by heat-induced Interaction with NSAP1

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The BiP protein plays an important role in proper folding and assembly of nascent protein and in scavenging the misfolded proteins in the ER lumen. Translation of BiP is directed by an internal ribosomal entry site (IRES) in the 5' nontranslated region (5' NTR) of the mRNA. Here, we report that NSAP1 specifically enhances the IRES activity of BiP mRNA through an interaction with the IRES element. We found that overexpression of NSAP1 in 293T cells augmented the IRES activity of BiP mRNA, whereas knockdown of NSAP1 by introduction of NSAP1-specific siRNAs diminished the IRES activity of BiP mRNA. NSAP1-binding to BiP IRES increased at heat stress condition, and concomitantly IRES activity of BiP mRNA was elevated. Moreover, the increase of BiP IRES activity by heat treatment was abrogated in cells lacking NSAP1 by an siRNA. Together, these data suggest that NSAP1 modulates IRES-dependent translation of BiP mRNA through an RNA-protein interaction at heat stress condition.

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Chromatin homeostasis during transcription elongation is maintained by histone chaperones

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When RNA polymerase II participates actively in RNA synthesis in the euchromatic region, how does it overcome nucleosome barrier? Since nucleosomes normally block the progression of polymerase, it is easily conceivable that there are many chromatin remodeling and elongation factors that assist it to proceed through the chromatin structure. The extent of chromatin change or the characteristics is not well understood. To elucidate the transcription coupled chromatin change, we first examined whether yeast HIR and CAF1 complex can be directly recruited to the transcribed genes. Our data shows that both CAF1 and HIR complexes are recruited to the actively transcribed region in yeast. The steady state level of GAL1 mRNA was greatly increased in the absence of hir1, suggesting that Hir1 down-regulates GAL1 transcription in vivo. Hir1 is targeted to the transcribed region in two distinctive ways. The Hir1 protein physically interacts with itself and with the Hir2 protein in vivo. The individual deletion of Hir1, Hir2, CAC1, or CAC2 resulted in a significant resistance to the 6AU. These data suggest that histone chaperones are recruited to the transcription complex and play a direct role in transcription elongation.