

## Transcriptional regulation of enterohemorrhagic *E.coli* O157 genome

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*Escherichia coli* O157:H7 is a major food-borne infectious pathogen that causes diarrhea, hemorrhagic colitis, and hemolytic uremic syndrome. We had previously reported the complete chromosome sequence of an O157:H7 strain isolated from the Sakai outbreak, and the results of genomic comparison with a benign laboratory strain, K-12 MG1655. The chromosome is 5.5 Mb in size, 859 Kb larger than that of K-12. We identified a 4.1-Mb sequence highly conserved between the two strains, which may represent the fundamental backbone of the *E. coli* chromosome. The remaining 1.4-Mb sequence comprises of O157:H7-specific sequences, most of which are horizontally transferred from foreign DNAs.

By construction of a cloning system, we cloned many promoters that are regulated by several major transcriptional regulators such as CRP, Lrp and PhoB, which are responsive for carbon-, leucine- and phosphate-starvation of the medium, respectively. Molecular understanding of the transcriptional regulation of O157:H7 together with the whole genomic structure sheds new insight into the pathogenicity and the physiology of O157:H7, and will open a way to fully understand the molecular mechanisms underlying the O157:H7 infection.