

<b>Focus</b>	Genome Sequencing of Opportunistic Pathogens
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<b>Period</b>	FY2012
<b>Overview</b>	<p>Among 1200 human pathogenic bacteria, genome sequences of BSL3 and BSL2 pathogens are almost completed. However, genome information of 90% of these human opportunistic pathogens, classified as BSL1, are mostly undetermined. In our project, we focused on these opportunistic pathogens because these pathogens are most frequently appeared in human clinical specimens and acquired drug resistant genes.</p> <p>Classification and detection system of these opportunistic pathogens are still based on phenotypic information. Genome based reclassification of these pathogens is an important issue for medical microbiology. Through this project, we collect many housekeeping genes of opportunistic pathogens to reclassify these pathogens, useful for better genome based classification of human pathogens and epidemiological analysis.</p>
<b>Progress</b>	