Whole Cell Project of *T. thermophilus* HB8

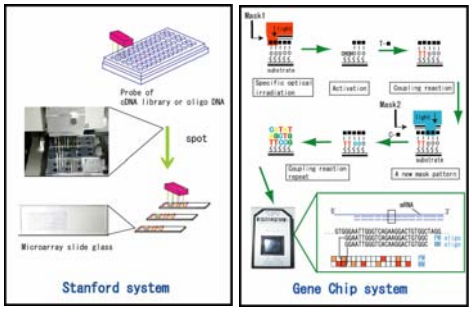
Structural Genomics
(1) genome analysis (2) overproduction of protein (3) 3D structural analysis

Functional Genomics
(1) 3D structure
(2) gene disruptants
(3) mRNA expression DNA chip
(4) protein expression : proteome analysis, protein chip
(5) protein-protein interaction : protein chip, two-hybrid analysis
(6) identifying all molecules in the cell : time dependence of location and amount

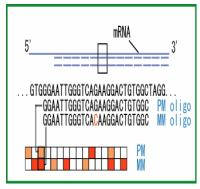
Molecular Functional Analyses on Each Protein
(1) development of new methods for functional analyses
(2) detailed functional analyses on each protein

Simulation of All Biological Phenomena in the Cell

Two technologies

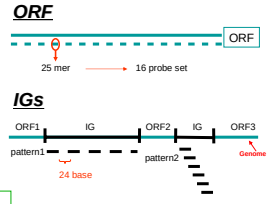


Probe array design - Gene Chip system -



Perfect match (PM)
Mismatch (MM) - Only the base of the middle of PM probe was replaced by the mismatch.

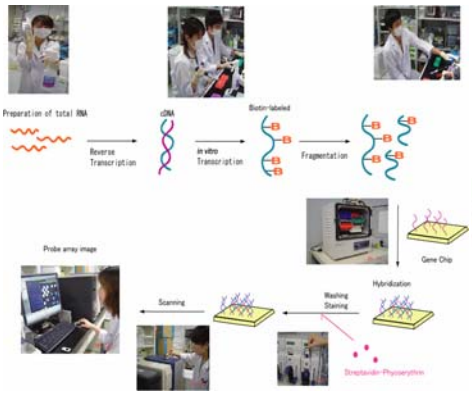
A nonspecific crossing hybridization signal is quantified from the signal intensity of MM. The value is deducted from the signal intensity of PM, and the true signal used as the index of the amount of expressions of a specific target can be detected.



Expression Probe Array information:
Array Name: TTHB8401
Feature Size: Other 11 micron
Array Format: CustomExpress Advantage: 49-5241

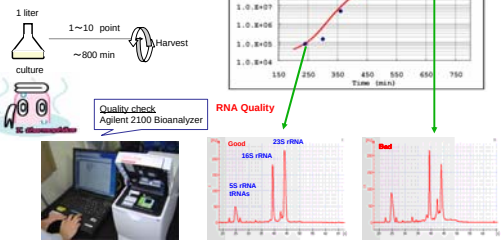
ORF: 2829 probe set
IG: 1157 probe set

Method - Gene Chip system -

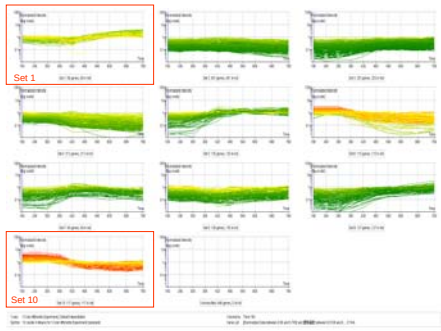


Trial experiment - Contents -

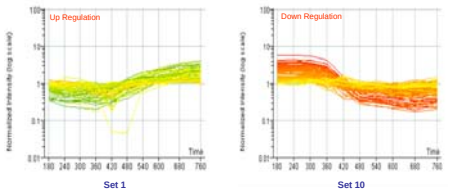
The wild type of *T. thermophilus* HB8 was cultivated and RNA for each time was extracted.
Changes in the expression pattern during cell growth was studied.



Clustering - *K*-means (10 cluster) -



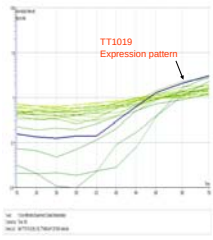
Trial analysis - Set 1 and Set 10 -



Set 1		Set 10	
hypothetical protein	38%	ribosomal protein	50%
ABC transporter	10%	ATP synthase	20%
regulator	7%	hypothetical protein	15%
degradation protein	5%	elongation factor	7%
Other		Other	

Analysis - example TT1019 -

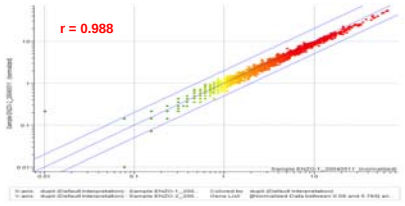
TT1019
probable transcriptional regulator (FNR/CRP family)



The similar expression

No.	Correlation Coefficient to TT1019	Description
TTx	0.99082	conserved hypothetical protein
TTx	0.99073	glycerol-3-phosphate ABC transporter, periplasmic glycerol-3-phosphate-bindingprotein
TTx	0.98895	probable isochorismatase
TTx	0.98516	conserved hypothetical protein
TTx	0.98010	pterin-4-alpha-carbinolamine dehydratase
TTx	0.97757	S-layer-like protein
TTx	0.97733	GTP cyclohydrolase I
TTx	0.97719	conserved hypothetical protein
TTx	0.97688	glutaredoxin-like protein
TTx	0.97518	cytochrome c-552 precursor (C552)
TTx	0.97328	conserved hypothetical protein
TTx	0.97052	methylmalonyl-CoA mutase, N-terminal domain/subunit
TTx	0.96496	probable NADPH quinone oxidoreductase
TTx	0.96371	acetyltransferase, putative
TTx	0.96022	conserved hypothetical protein
TTx	0.95377	'metallo-beta-lactamase superfamily protein
TTx	0.95245	hypothetical protein
TTx	0.95195	conserved hypothetical protein

Comparison - duplicate -

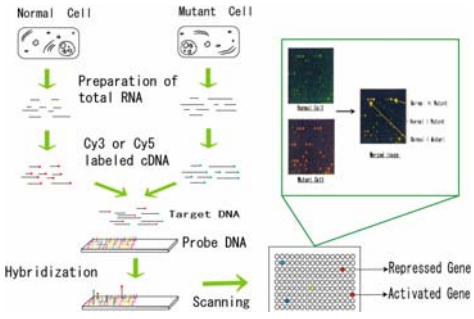


T. thermophilus HB8

Culture 360 min (Wild Type) VS Culture 360 min (Wild Type)

Good reproducibility

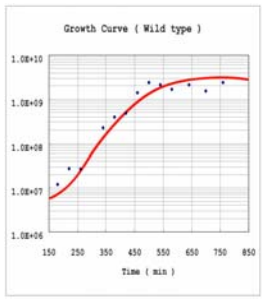
Method - Stanford system -



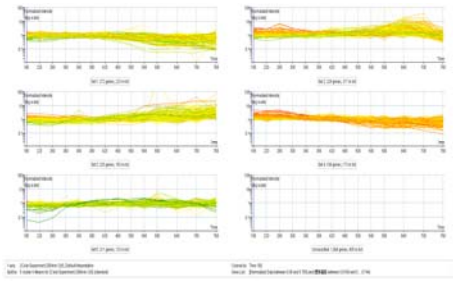
Trial experiment - Contents -

The wild type of *T. thermophilus* HB8 was cultivated and RNA for each time was extracted.
Changes in the expression pattern during cell growth was studied.

The DNA Microarray chip which arranged the gene of about 1200 *T. thermophilus* HB8 was produced in collaboration with KUHARA Lab. (Kyushu Univ.)

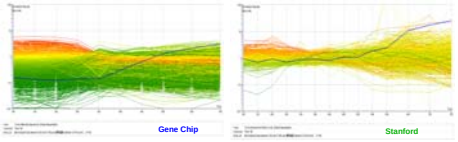


Clustering - *K*-means (5 cluster) -

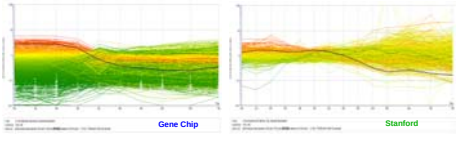


Comparison - Gene Chip VS Stanford -

TT1019 - probable transcriptional regulator (FNR/CRP family)



TTxxxx – 50S ribosomal protein



Future

The Gene Chip system (above) and the stanford system (below) gave similar results.

If you want to use this Gene Chip system, please contact me.

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Member