

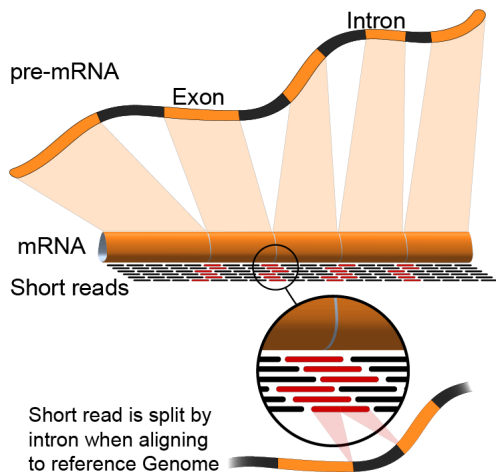
Determination of sRNA Expressions by RNA-seq in *Yersinia pestis* Grown *In Vitro* and during Infection

Yanfeng Yan *et al*, 2013

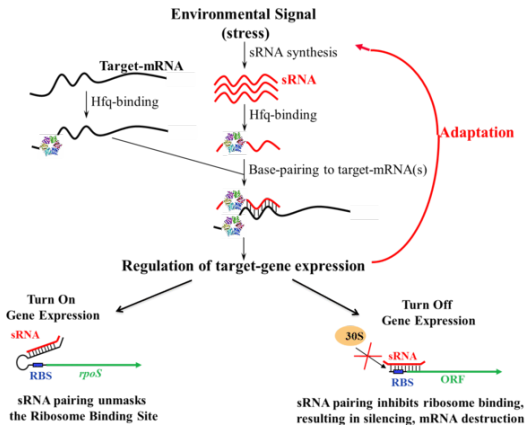
JC in Bioinformatics

February 28th, 2014

RNA-seq



Bacterial sRNA



<http://www.horizons.uni-goettingen.de/horizont3/index.php?id=990>

Motivation

Use RNA-seq to:

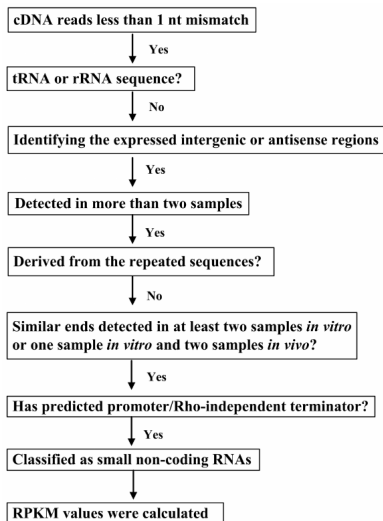
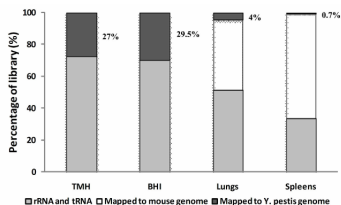
- discover the novel sRNAs
- monitor sRNA expression in *Y. pestis* infected lungs of mice

sRNA Classification Pipeline

- Samples from four growth conditions (BHI, TMH, lung, spleen)
- RNA isolation
- Size-selection
- cDNA library construction
- RNA-seq

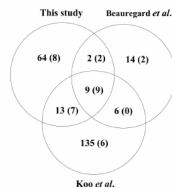
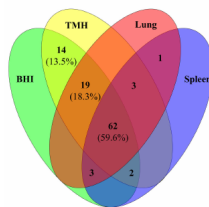
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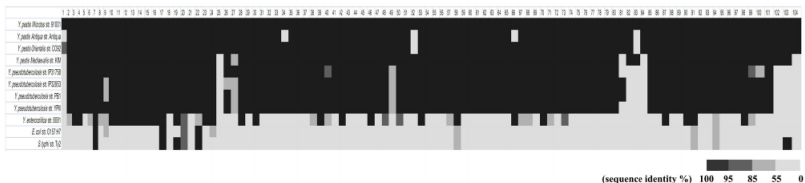
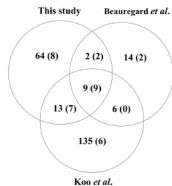
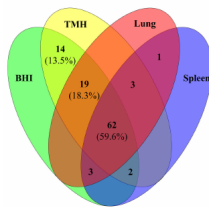
Detected sRNAs

- A total of 104 sRNAs
- 26 annotated (intergenic),
78 novel sRNAs
- 62 intergenic,
16 antisense sRNAs

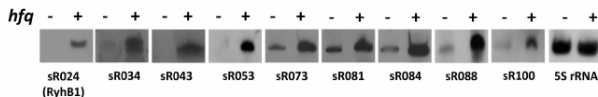


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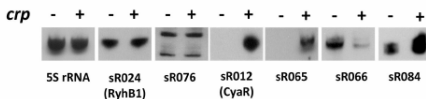
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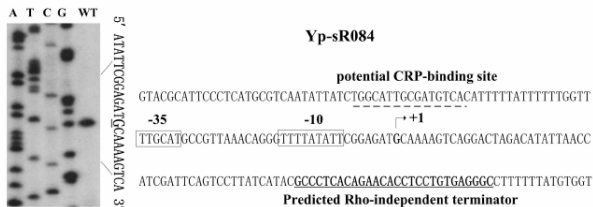
Validation and Characterization



(A)



(B)

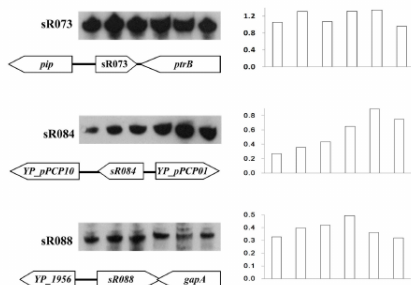
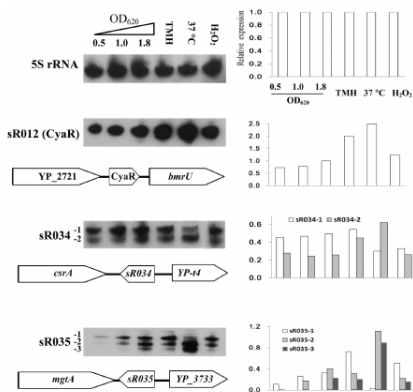


(C)

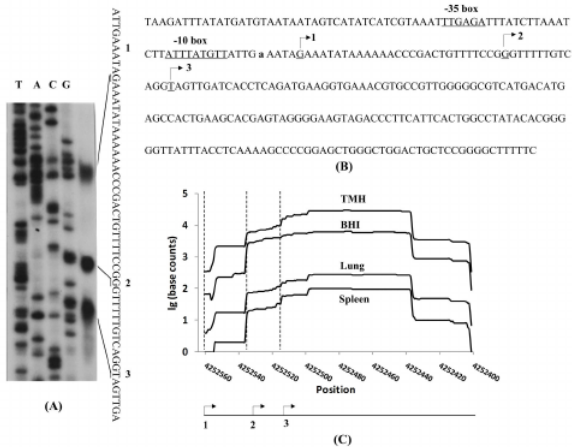
Differentially Expressed sRNA candidates

ID	Annotated ^a	Length (nt)	Samples detectable by using RNA-seq	Fold changes (Lung/ BHI) ^b	
				RNA-seq	qPCR
sR009	RyhB2	108	BHI, TMH, Lung, Spleen	112.9	15.2
sR012	CyaR/RyeE	93	BHI, TMH, Lung, Spleen	31.9	-
sR017	6S RNA/SsrS	184	BHI, TMH, Lung, Spleen	7.1	2.0
sR023	RybB	86	BHI, TMH, Lung, Spleen	13.5	1.9
sR024	RyhB1	110	Lung, Spleen	>100	8.1
sR039	-	232	BHI, TMH, Lung, Spleen	16.5	0.5
sR003	CsrB	323	BHI, TMH, Lung, Spleen	-7.6	-3.2
sR026	CsrC	386	BHI, TMH, Lung, Spleen	-40.6	-7.2
sR027	-	284	BHI, TMH, Lung, Spleen	-10.7	-2.5
sR020	4.5S RNA	135	BHI, TMH, Lung, Spleen	-10.7	-

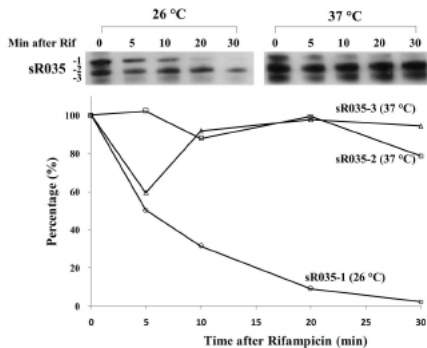
Northern Blot Analysis



sR035



sR035



(D)

Finding Peaks from Coverage Data

- 1D signal processing
- Two basic methods:
 - Wavelet transform
 - Derivative based approach (+ smoothing the signal)
- User can set cut-offs for peak length, height, steepness, . . .

Thank you for your attention!

