

Exploring the world of regulation by attenuation in Bacteria

Magali NAVILLE

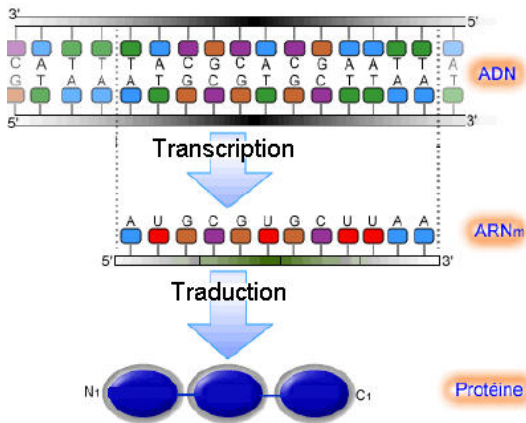
Sequence, structure and function of RNAs – Daniel Gautheret
Institut de Génétique et Microbiologie
Université Paris-Sud

April 14-16, 2009



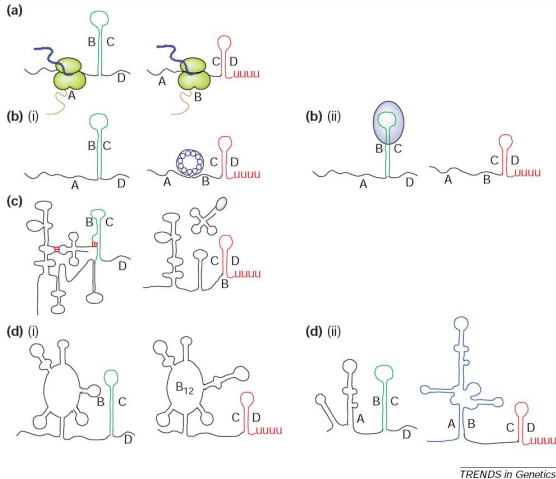
Introduction

Gene regulation



Introduction

Gene regulation and 5'-UTR

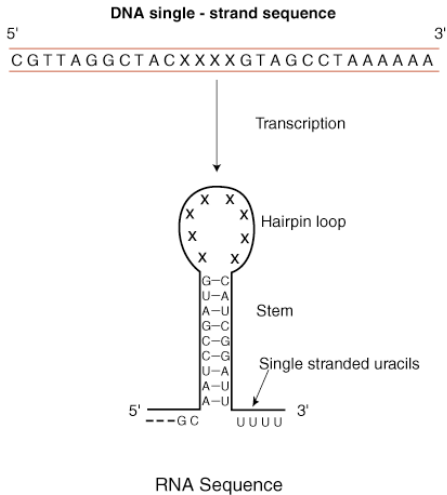


Merino 2005



Problematic

Detecting 5'-RNA elements by their terminator

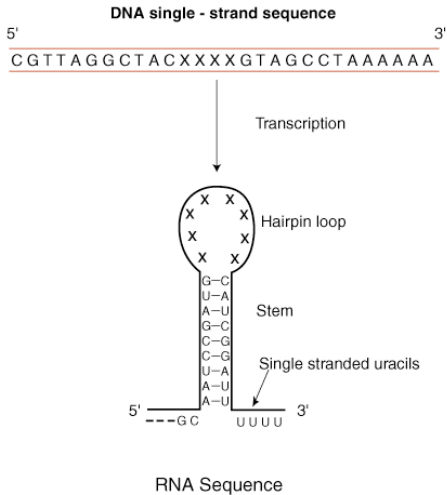


- identification of new regulatory systems
- systems evolution



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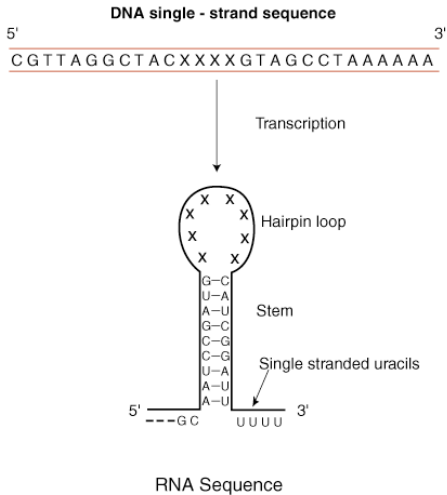


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Problematic

Detecting 5'-RNA elements by their terminator



- identification of new regulatory systems
- systems evolution



Protocole:

- extraction of IGRs in 5' of any gene
 - terminators detection using **erpin** and **RNAmotif**
 - anti-terminators detection using **RNAhybrid**
 - elimination of 3' terminators based on distance criteria
-
- Predictions made in 302 genomes



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Prediction of attenuators : Protocole

Protocole:



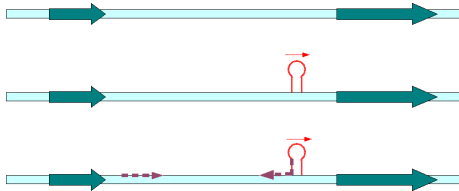
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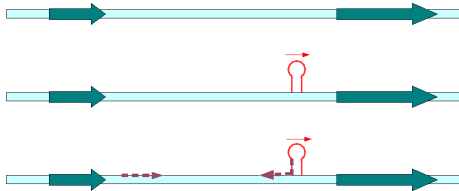
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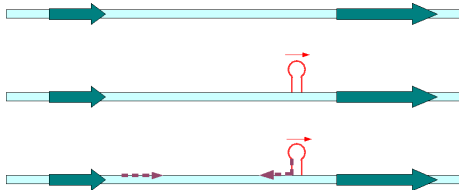
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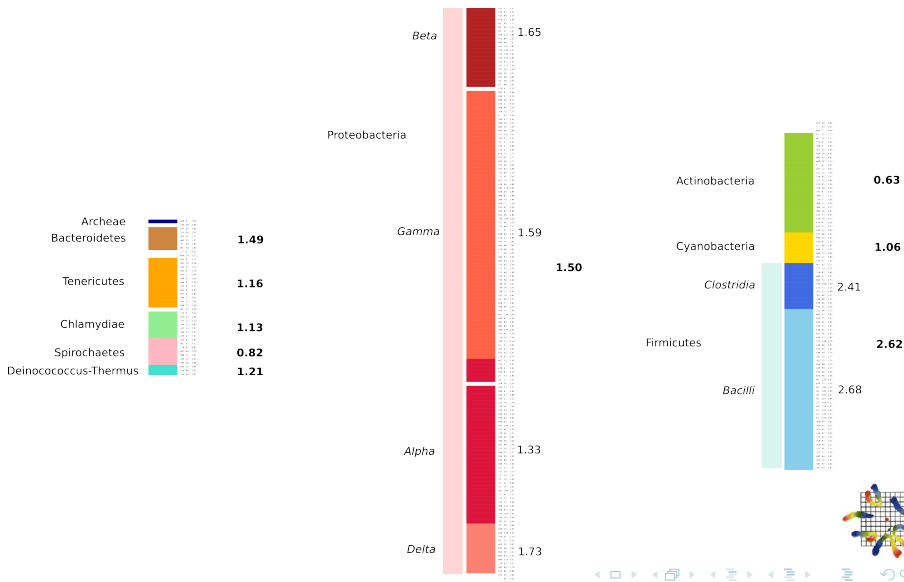
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Results

Numbers of predicted elements



Results

Candidates classification

- Classification by homology of following genes, using the *Hogonom* ontology (HBG#)
- Score by HBG# by Species = ratio of HBG# genes preceded by a candidate
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	<i>Hin</i>	<i>Vch</i>	<i>Sty</i>	<i>Sfl</i>	<i>Eco</i>	<i>Ypr</i>	<i>Xca</i>	<i>Xfa</i>
HBG1	1	1	0.5	0.5	0	0	0	0
HBG2	1	0.5	0	1	0	1	1	1
HBG3	0	0	1	0	1	0	0	1



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HBG1	1	1	0.5	0.5	0	0	0	0	3
HBG2	1	0.5	0	1	0	1	1	1	5.5
HBG3	0	0	1	0	1	0	0	1	3

→ sum of scores by Species



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HBG2	1	0.5	0	1	0	1	1	1	5.5	1
HBG3	0	0	1	0	1	0	0	1	3	3

→ score of 'dispersion'



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HBG1	1	1	0.5	0.5	0	0	0	0	3	0	3+0.1
HBG2	1	0.5	0	1	0	1	1	1	5.5	1	(1.5+0.1)+1+(3+0.1)
HBG3	0	0	1	0	1	0	0	1	3	3	1+1+1

→ score of 'runs'



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HBG1	1	1	0.5	0.5	0	0	0	0	3	0	3.1
HBG2	1	0.5	0	1	0	1	1	1	5.5	1	5.7
HBG3	0	0	1	0	1	0	0	1	3	3	3

→ score of 'runs'



Results

Best candidates

HBG297802	Hypothetical protein yhbC (nusA-infB operon)
HBG369991	50S ribosomal protein L10
HBG000748	Phenylalanyl tRNA synthetase
HBG181500	Threonyl tRNA synthetase
HBG142539	Translation initiation factor IF3
HBG046904	30S ribosomal protein S12
HBG343859	Transcription elongation factor GreA
HBG398889	Histidyl tRNA synthetase
HBG448785	Anthranilate synthase
HBG249606	Tyrosyl tRNA synthetase
HBG444146	S adenosylmethionine synthetase
HBG507301	pyrimidine regulatory protein PyrR
HBG379584	Valyl tRNA synthetase
HBG523338	CTP synthase precursor
HBG114333	30S ribosomal protein S16
HBG001285	DNA directed RNA polymerase beta chain
HBG401792	Serine acetyltransferase
HBG053760	Seryl tRNA synthetase
HBG262099	2 isopropylmalate synthase
HBG258034	Aspartate carbamoyltransferase
HBG380413	Cystathionine beta lyase
HBG507213	Integral membrane protein TerC
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HBG001285	DNA directed RNA polymerase beta chain
HBG401792	Serine acetyltransferase
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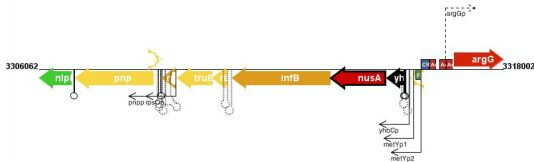
Best candidates

HBG297802	Hypothetical protein yhBC (nusA-infB operon)	nusA attenuator <i>E.coli</i>
HBG369991	50S ribosomal protein L10	Ribosomal protein L10 leader
HBG000748	Phenylalanyl tRNA synthetase	T-box / Peptide leader
HBG181500	Threonyl tRNA synthetase	T-box / Peptide leader
HBG142539	Translation initiation factor IF3	Ribosomal protein L20 leader
HBG046904	30S ribosomal protein S12	"Ribosomal protein S12 leader"
HBG343859	Transcription elongation factor GreA	greA attenuator <i>E.coli</i>
HBG398889	Histidyl tRNA synthetase	T-box
HBG448785	Anthranilate synthase	T-box / Peptide leader
HBG249606	Tyrosyl tRNA synthetase	T-box
HBG444146	S adenosylmethionine synthetase	SAM riboswitch
HBG507301	pyrimidine regulatory protein PyrR	PyrR binding site
HBG379584	Valyl tRNA synthetase	T-box
HBG523338	CTP synthase precursor	PyrR binding site, ...
HBG114333	30S ribosomal protein S16	"Ribosomal protein S16 leader"
HBG001285	DNA directed RNA polymerase beta chain	rpIL attenuator
HBG401792	Serine acetyltransferase	T-box / SAM riboswitch
HBG053760	Seryl tRNA synthetase	T-box
HBG262099	2 isopropylmalate synthase	Peptide leader
HBG258034	Aspartate carbamoyltransferase	PyrR binding site
HBG380413	Cystathionine beta lyase	SAM riboswitch
HBG507213	Integral membrane protein TerC	yybP-ykoY leader
...

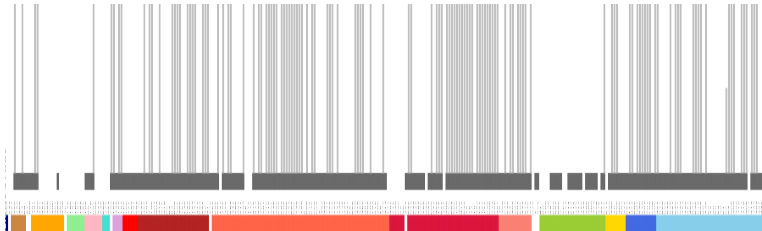


Results

HBG297802 candidates : ylbH-nusA-infB operon

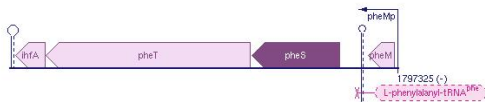


ylbH hypothetical protein
nusA transcription termination/antitermination L factor
infB protein chain initiation factor IF-2

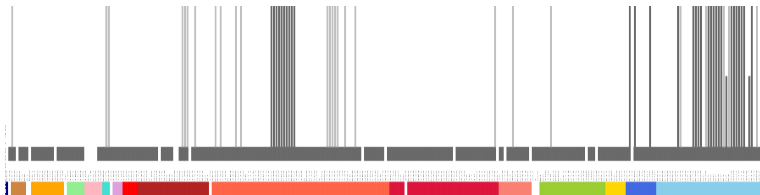


Results

HBG000748 candidates : Phenylalanyl tRNA synthetase



pheS alpha-chain
pheT beta-chain



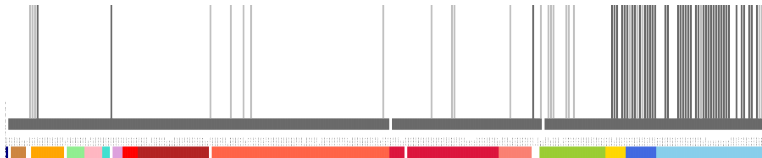
Peptide-leader

T-box

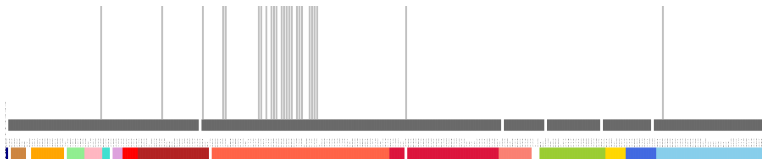


Results

Ribosomal protein leaders



50S ribosomal protein L10 : L10 leader



30S ribosomal protein S16 : ?



Perspectives

Insights into attenuators evolution

- **Finest analysis of best candidates**
- Go through the list to find completely new systems...
- Model of evolution from a T-box to a peptide-leader ?? or independent inventions ?
- Exaptation of terminators to form palindromic TFBS ??



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Perspectives

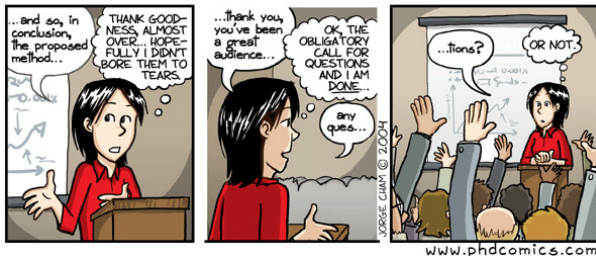
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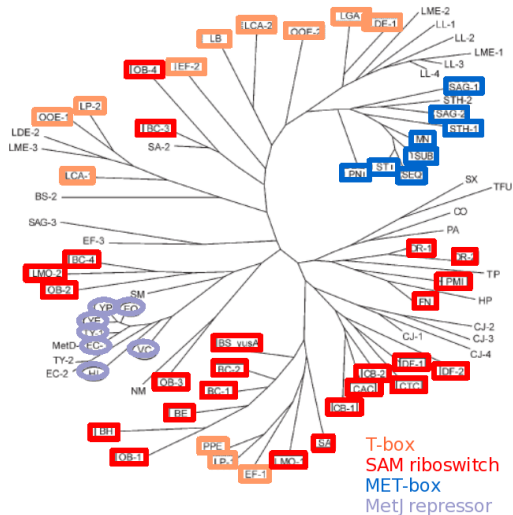


RNA Sequence, Structure & Function

- Daniel GAUTHERET
- Antonin MARCHAIS
- Magali NAVILLE
- Chongjian CHEN
- Claire TOFFANO-NIOCHE



Perspectives: Evolutive behaviour of attenuators



Phylogenetic tree of the substrate-binding components MetQ of bacterial methionine transporters

Adapted from Rodionov 2004

