Module I: Introduction

20.109 Lecture 14 February, 2010

Module Overview

Introduction to:

- Fundamental concepts and techniques in molecular biology
- A powerful and accessible strategy (SELEX) for identifying nucleic acids (aptamers) having desirable binding properties for a defined target

Module Overview

Lectures:

- Conceptual and practical considerations for successful SELEX
- Become comfortable with the concept of a nucleic acid library
- Broadly consider the practical applications of aptamers
 - Biology
 - Technology

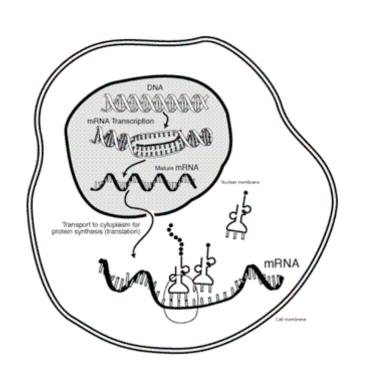
Module Overview

Day	Lecture	Lab
1	Introduction	DNA library synthesis (PCR)
2	SELEX I: Building a Library	DNA library purification (agarose gel electrophoresis)
3	SELEX II: Selecting RNA with target functionality	RNA library synthesis
		(<i>In vitro</i> transcription = IVT)
4	SELEX III: Technical advances	RNA purification and heme
	& problem-solving	affinity selection
5	Characterizing aptamers	RNA to DNA by RT-PCR
6	Introduction to porphyrins: chemistry & biology	Post-selection IVT
		Journal Club 1
7	Aptamer applications in biology & technology	Aptamer binding assay
8	Aptamers as therapeutics	Journal Club 2

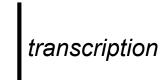
Today's Objectives

- Provide a context for appreciating RNA as a macromolecule capable of specific interactions
 - Small molecules
 - Proteins
- Appreciate that:
 - Atomic level interactions underlie these binding events
 - Binding reactions occur in 3-dimensional space

The Central Dogma





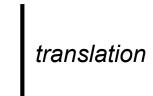


Information storage

- Double stranded
- Helical structure
- Encodes genes









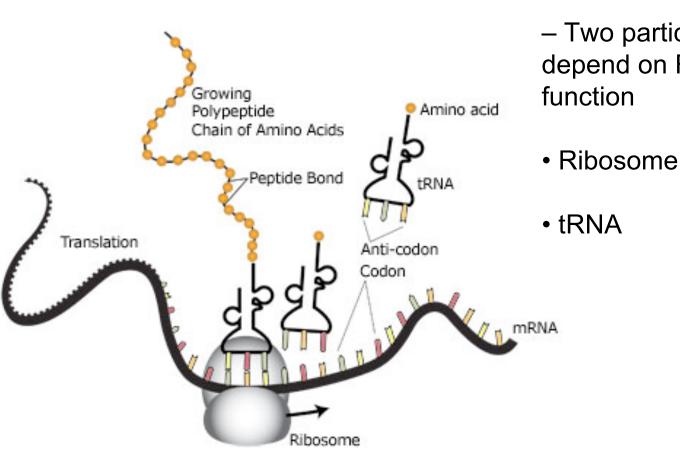
What is RNA good for?

Diverse Functions

- Enzymes
 - DNA replication
 - Energy production
- Transport
 - Cell membrane
- Motility
 - Actin, myosin



RNA has diverse functions, too!



How is mRNA decoding take place during translation?

 Two particularly critical players depend on RNA for proper

Image adapted from: National Human Genome Research Institute.

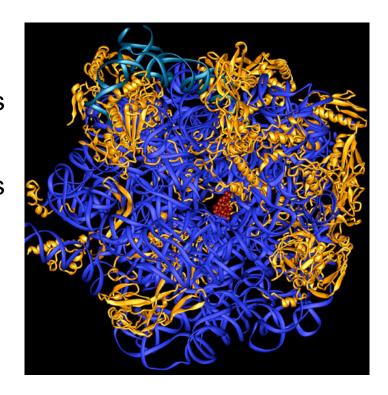
Ribosome composition and structure

Two subunits

- Large
 - 50S in prokaryotes/ 60S in eukaryotes
- Small
 - 30S in prokaryotes/ 40S in eukaryotes

Composition

- 60% RNA!
 - 5S rRNA (LSU)
 - 23S rRNA (LSU)
 - 16S rRNA (SSU)

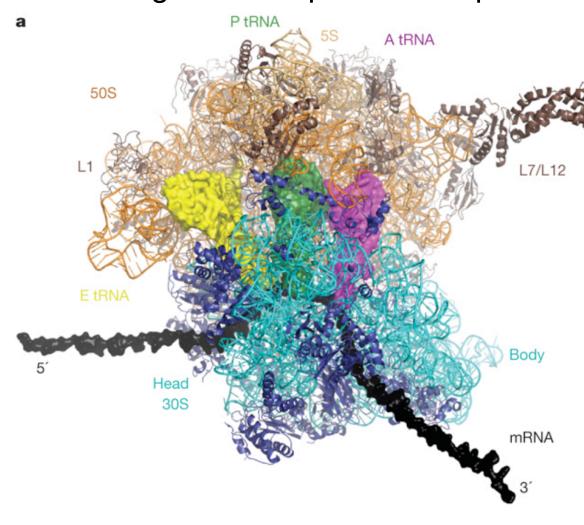


50S ribosomal subunit (*D. radiodurans*)
Blue = ribosomal RNA (rRNA)
Gold = protein

Ribosomal RNA functions

Structural

- Organize the protein components in the ribosome

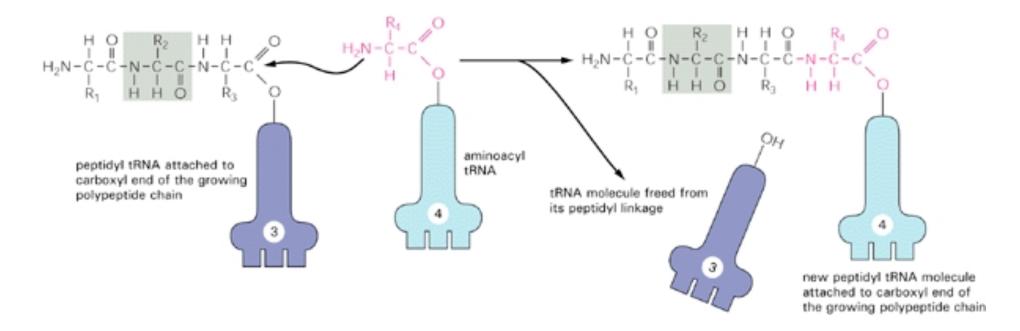


- rRNA serves as a scaffold for the associated protein components
- Proper assembly requires establishing very specific atomic contacts between the RNA and protein components

Ribosomal RNA functions

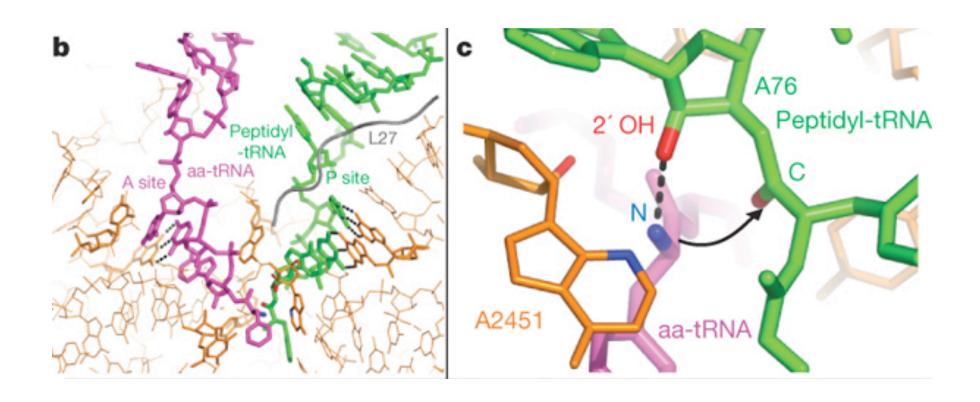
Enzymatic

- 23S rRNA involved in catalyzes the peptidyl transfer reaction step during translation
 - Binding site for the aminoacyl tRNA is located in the 23S rRNA
- Rate enhancement over non-enzymatic reaction: ~ 10⁵!



Ribosomal RNA functions

 Specific atomic contacts are made between rRNA residues and the amino acyl-tRNA



rRNA enzymatic activity as a drug target

Antibiotics

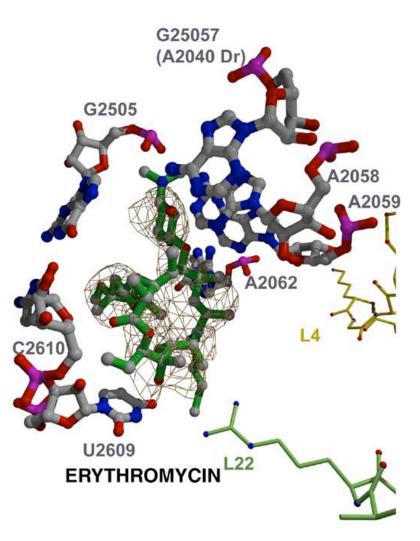
- Used to treat microbial pathogens
- Several different classes
- Target different cellular processes
- Selectively inhibit pathogen but not host pathways
- Chloramphenicol
 - Inhibit ribosomal peptidyl transferase activity!

Macrolides

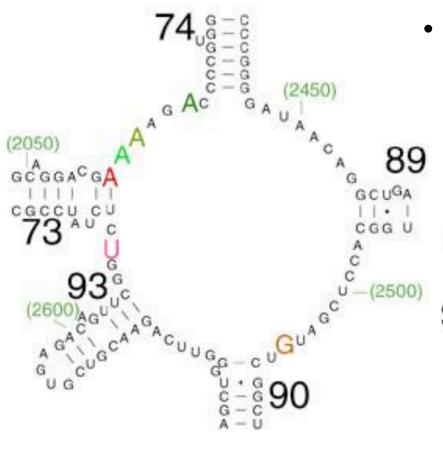
- E.g. erythromycin, clarithromycin
- Inhibit nascent peptide transfer away from the peptidyl transferase site

Exploiting rRNA enzymatic activity

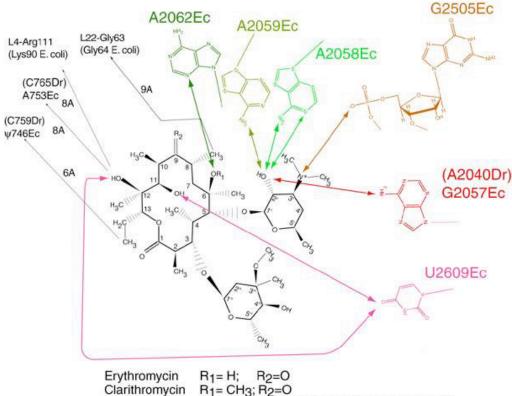
- Erythromycin binds directly to the 50S ribosome
 - Interacts <u>exclusively</u> with the 23S rRNA!
 - No contacts between drug and any ribosomal protein
 - Bind in the peptidyl transferase cavity
 - Interferes with nascent peptide channeling from the PT cavity
 - Specific rRNA-erythromycin atomic level interactions stabilize the complex
 - Inhibits protein synthesis



Exploiting rRNA enzymatic activity



 Specific atomic level interactions underlie erythromycin interaction with the rRNA



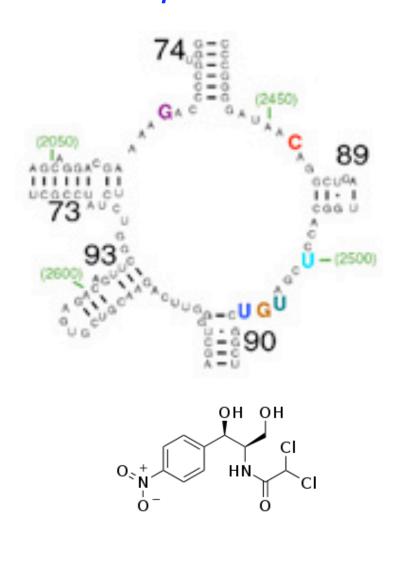
Roxithromycin

R₁= H; R₂= N-O-CH₂-O-CH₂-CH₂-O-CH₃

Structurally distinct antibiotics can bind to the same rRNA

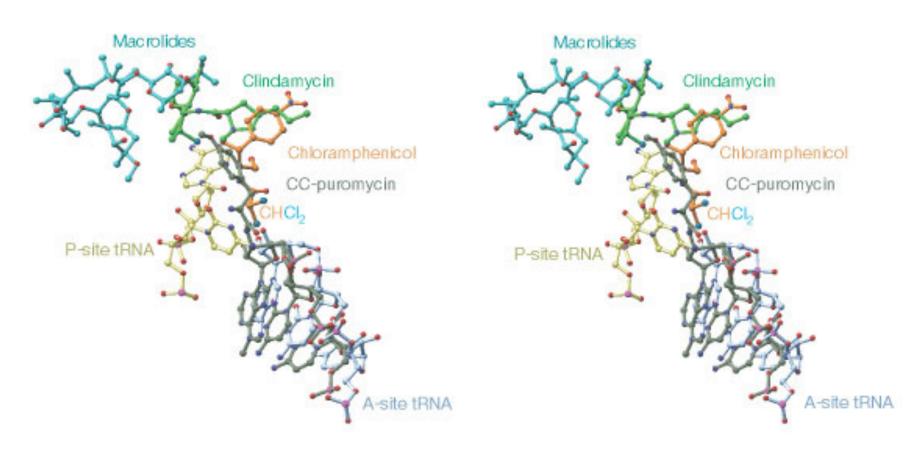
Erythromycin contacts

Chloramphenicol contacts



F. Schlunzen et al, Nature 413, 814-821 (2001)

Structurally distinct antibiotics can bind to the same rRNA



- Different compounds can interact with a single RNA target
 - Overlapping or distinct molecular contacts with the RNA
- What are some potential resulting consequences when thinking of RNA as a binding reagent?

Now what about tRNA?

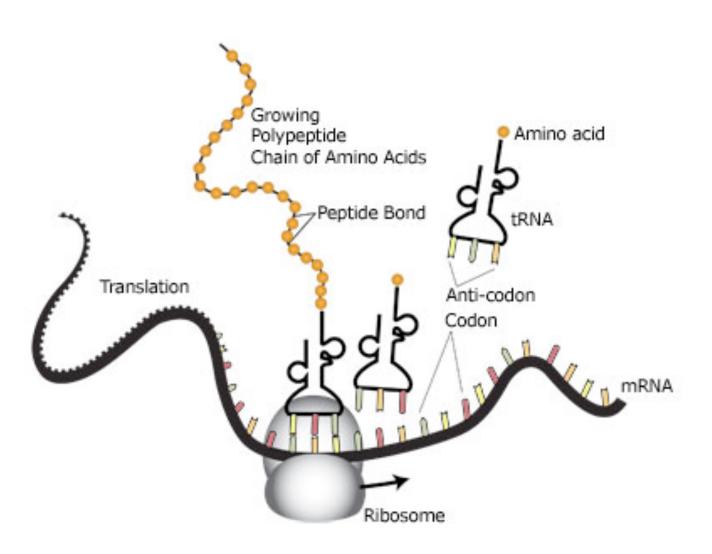
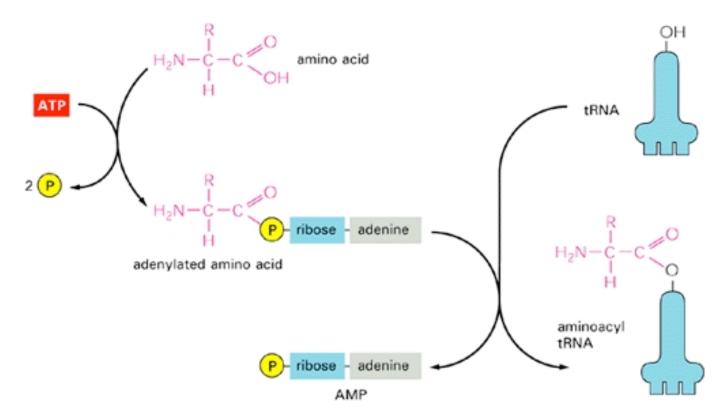


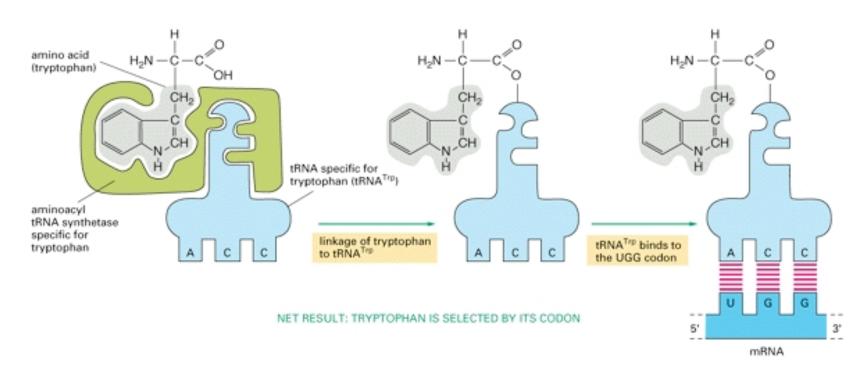
Image adapted from: National Human Genome Research Institute.

- Each tRNA must be "charged" with its cognate amino acid
- Reaction carried out enzymatically
 - Aminoacyl tRNA synthetase (aaRS)

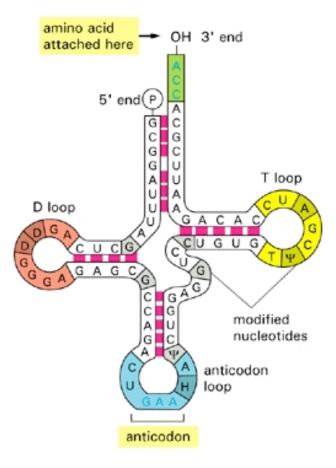


Bruce Alberts et al, Molecular Biology of the Cell (NCBI Bookshelf)

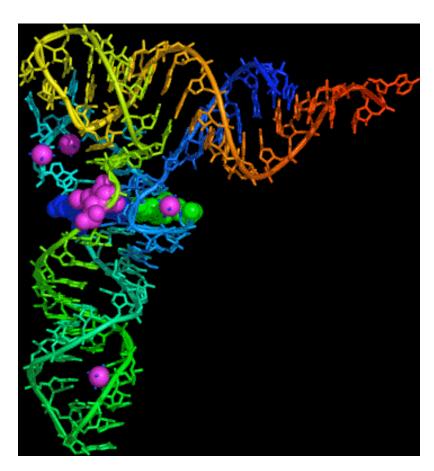
- Specificity of aminoacylation reaction
 - Charging a tRNA with the right amino acid
 - How might this be achieved?
 - Each tRNA is recognized by a specific aminoacyl tRNA synthetase



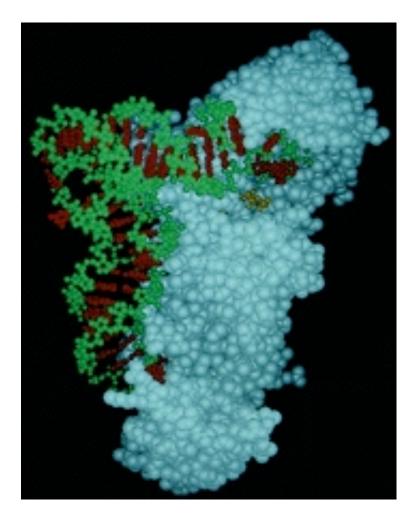
How is this possible?



2D tRNA view



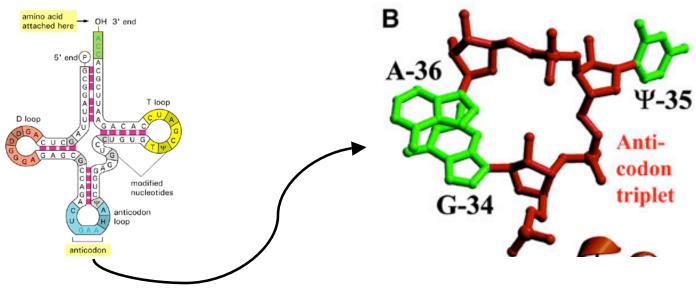
3D tRNA view

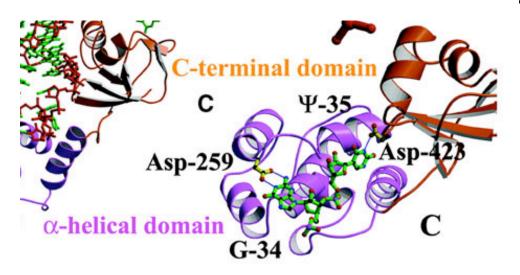


Aminoacyl tRNA synthetase in complex with tRNA

 Aminoacyl tRNA synthetases very <u>specifically</u> recognize the 3D structure adopted by their cognate tRNA

– How is this achieved?

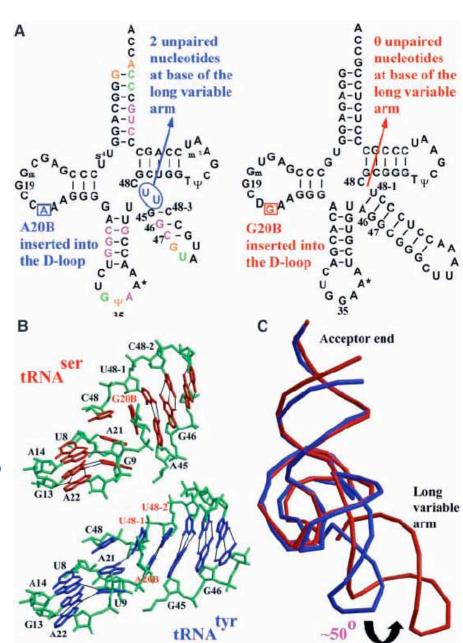




- Specific tRNA recognition occurs due to atomic level interactions between the tRNA and enzyme
 - H-bonding
 - Electrostatic
 - Van der Waals

Yaremshuk et al, EMBO J, (2002) 21:3829-3840

- tRNAs differ in their sequence
- This translates into differences in structure
 - 2D structure
 - 3D structure
- Atomic level contacts only possible if the tRNA structure fits exactly with the aminoacyl tRNA synthetase structure



Summary

- RNA plays very dynamic roles in biology:
 - Intricately involved in protein synthesis
 - Structural function
 - Enzymatic/catalytic functions
- These roles are facilitated by RNA's ability to:
 - Adopt very defined structures
 - Form molecular interactions with small molecules and proteins
 - Highly specific
 - High affinity
 - Facilitated by complementarity of the interacting partners
 - Atomic level interactions dictate these properties
- As achieved by Nature, can we take advantage of RNA's plasticity to derive new functions?

Module Workflow

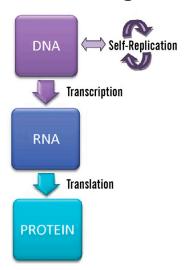
Phase I Objective

Reconstitute an RNA SELEX library

Skills

- 1. PCR to generate DNA library template
- 2. RNA synthesis (in vitro transcription)
 - RNA handling precautions
- 3. Nucleic acid purification methods

Central Dogma





BioRad Thermal Cycler

Module Workflow

Phase II Objective

Subject RNA library to selection pressure

Skills

- 1. RNA refolding method
- Restoring proper 3D RNA structure for appropriate function
- 2. Affinity based library enrichment
- Controlling stringency during selection
- 3. RT-PCR: converting RNA into DNA
- Expanding your post-selection library
- Enriched for target aptamers (hopefully)



Module Workflow

Phase III Objective

Analyzing the success of your aptamer selection process



Skills

- 1. UV-visible spectroscopy
- Take advantage of unique heme spectral characteristics
- 2. Data analysis
- Post-acquisition spectral analysis
- Pooled lab data (hopefully) to understand how selection stringency impacts enrichment efficiency

