Types of RNA

- 80% rRNA
- 15% tRNA
- 2% mRNA
- 2% non-coding RNA

- Eukaryotic RNA polymerase transcription
  - RNA polymersase I: pre-rRNA
  - RNA polymerase II: mRNA, siRNA(transcription control), miRNA(translation control), snRNA(Splicing control)
  - RNA polymerase III: tRNA, 5S & 7S rRNA (ribosomal subunit)
- Location of processing:
  - tRNA and rRNA in the cytoplasm
  - Most mRNA, tRNA, rRNA, snRNA in the nucleus
- Transcription coupled with modification: capping enzyme, splicosome complex and polyadenylation enzyme coupled on the polymerase.
  - Advantages: Quality control, prevent degradation, conserve cellular resources

mRNA Post transcriptional modification

- 5' capping: addition of 7-methyl guanosine (m7G)
  - γ-phosphate on the 5' end of the polynucleotide removed with RNA triphosphatase
  - α-phosphate of the guanosine triphosphate molecule linked with β-phosphate of 5' end nucleotide with guanylyltransferase, creating a unique 5 prime-5 prime bond
  - Methyl group added to guanosine N7 using methyltransferase.
- RNA splicing: Exon connected together, intron excised and degraded via transesterification.
  - snNRP(small nuclear nucleoriboproteins) made up of 100-200 nucleotides + proteins (U1,2,4,5,6 involved)
  - Intron sequence: 5' GU site, branching point adenine, pyrimidine tract near 3' end, 3' end AG site.
  - Binding and splicing sequence:
    - U1 bind to 5' end GU site.
    - Branch bridging protein (BBP) bind to branching point
    - U2 auxillary factor 65kDa (U2AF65) bind to pyrimidine tract, U2AF35 bind to 3' end AG site
    - U2 bind to branching point displace BBP
    - U4,5,6 binds, release U2 auxillary factors.
    - 1st transesterification at 5' Gu site, release U1 and U4, branching lariat form, exon 1 freed
    - Splicosome complex bring AG site closer to exon 1, 2nd transesterification, two exons joined. Lariat released.
  - Alternative splicing: In different tissues, different splice sites through enhancer/silencers, different position of poly A tail, different exon shuffling. Lead to expression of the same gene but different product
- Poly-A tail
  - Polyadenylation factor found with polymerase
  - When poly-A signal AAUAA detected, polyadenylation factor bind to signal, induce cleavage by endonuclease
  - Addition of a poly-A tail downstream of the signal, using polyadenine polymerase
  - Poly-A binding protein (PAB) binding prevent degradation of tail

tRNA rRNA processing

- tRNA processing
  - D-loop cleavage (5' end) and T-loop cleavage (3' end), addition of CAA site on 3' end for amino acid binding
  - Splicing remove introns
  - Aminoacyl synthetase ATP —> AMP

- rRNA processing
    - Self-spliced
    - Coordinated modification of nucleotides by small nucleolar RNA (snoRNA)
    - E.g. rRNA in S.cerevisae cleaved by RNAse III

Diseases related to RNA processing:

- mRNA Splicing - Spinal Muscular atrophy
- mRNA Splicing - Cystic fibrosis
- mRNA Polyadenylation - Alzheimer's
- mRNA Polyadenylation - Parkinson's
- tRNA processing - mitochondrial disorders
- tRNA processing - Neurodegenerative disorder
- rRNA processing - Developmental abnormalities
- rRNA processing - Skeletal dysplasia

Types of RNA
Types of polymerase, function
Processing locations
Coupling components position, advantages
mRNA processing three steps
Different tissue expressions
tRNA, rRNA
Diseases