

Syllabus

- DNA structure and organisation
- RNA and non-coding RNAs
- Basics of replication, transcription, & translation
- DNA recombination & repair

Evaluation

- Midsem (20)
- Endsem (50)
- Internal (30) —
 - Class tests & Assignments
 - 15 + 15

References :

- Griffiths

DNA, RNA, 4 nitrogenous bases
difference b/w nucleotide & nucleoside

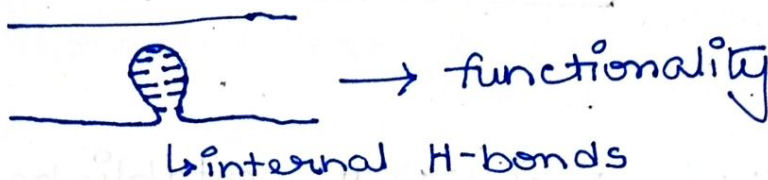
2/01/2023

Learn structures for these. *

→ You cannot break the phosphodiester bonds at boiling temp, as they are strong, covalent bonds

Boiling → disintegration ×
denaturation ✓

→ Internal structures of RNA



→ Alkaline hydrolysis of RNA

2' OH → deprotonation → O⁻ attacks Phosphodiester bond → one base removed.

does not happen for DNA as no 2' OH

→ reason why RNA was chosen for genetic material *

Info

Kosel → responsible for chemical structure of DNA & RNA

→ Three experiments for establishing DNA as genetic material

→ Cells (1st innate immunity)

3/01/2023

→ Fidelity in replication

→ Scope for mutation

→ Proteins cant replicate → not ~~DNA~~ gen. mat.

→ Chargaff's rule

- base comp. varies with organism
- base comp. same all across org. & age
- base comp. $A + G = T + C.$

Alexander Todd → chemically established nature of phosphodiester bond.

Criss-cross str. in X-ray crystallography → helical

HO 2 or so AND not regular for side # does not happen for DNA as for RNA
reason why RNA was chosen for genetic material
⊙

DNA & RNA
→ advantage for physical structure of

- 1) DNA strand which is Gi-C rich takes higher temperatures to denature → more stable
- 2) A-C incompatibility due to H-bond formation absence.

+ Chargaff's A=T & G=C data

→ complementary base pairing

⊛ to be verified

3) G-C : A-T ratios > 1 → in most prokaryotes
 (is it because they have stable genome)

4) Z-DNA found in recombining & genetically suppressed parts of DNA ; A-DNA is very hard to find

5) Primer designing theory:

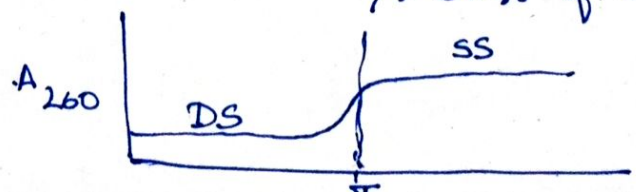
(a) melting temperature of DNA depends on:

- length of strand
- GC ratio

→ change in solvent (not physiologically relevant)

(b) Accuracy of renaturation after removal of denaturant is inversely proportional to length of DNA

6) Double-stranded DNA has OD < single ssDNA, because bases face inwards (minimal exposure) → 50% of DNA is denatured



7) 100-base long ORF → protein coding gene
(at least 30 amino acids are reqd. → assumed)
→ difference b/w start and stop codons

8) No. of protein-coding genes cross-checked
by proteomic profiling of 30 histologically
normal human tissue samples (adult + foetal)
→ 84% of total annotated protein coding
genes accounted for.

Actually somewhere in between → because of
small amounts of certain protein + maybe
short half lives (?)

→ different in abnormal human tissue,
proteome varies.

9) Looping in bacteria — 10 fold compaction
1000-fold compaction → supercoiled DNA.

Double-stranded DNA has 2.0 nm length
→ 50% of DNA is supercoiled
because of torsional stress

DNA looping & supercoiling

9/01/2024

1) Helps in 1000-fold compaction.

10 fold - looping
rest - supercoiling

2) Superhelix - when axis of DNA double helix coils on itself → new helix.

↓
also, supercoil → otherwise, DNA in relaxed state

↓
due to structural strain.

3) Purified ccd → rarely relaxed.

4) What is responsible for folding and maintenance of DNA supercoiling!

a) Linking no: defined as no. of complete revolutions one DNA strand makes around the other.

b) Supercoiling: when Linking no. differs from no in the relaxed state (+ve/-ve)

c) Negative supercoil → right handed

Positive supercoil → left handed.

d) Topoisomerases → cuts & reseals DNA to change Linking number
↳ in our body, helps in reducing supercoiling during replication.

Chromosome Discovery → Walther Flemming.

Lys & Arg → large proportion of histone amino acids → why? (20-40%)

→ Linker region varies from sp. to sp, 10/01/2024
but, no. of bp in core region remains same (147 bp)

→ Noll-Kornberg experiment

→ Difference b/w exonuclease and endonuclease

→ Difference b/w extensive and light digestion forms the basis for the Noll-Kornberg experiment (# read the paper)

→ Why Is there any correlation b/w linker DNA length & species?

→ Most of the interactions b/w histones and DNA happen in the minor groove region,

↳ A-T rich (#)

major grooves → G-C rich ↳ why?

→ Tight wrapping of DNA around histone core requires removal of about one helical turn in the DNA (required to relax DNA during packing)

→ DNA needs to be accessible to RNA polymerases for transcription (is this why A-T seq. bind to histone)

→ Bacterial gene density >>> us
↳ non-coding DNA

→ Gene - A region in DNA that encodes a gene product, either RNA/protein

→ RNA binds to basal transcr. factors on non-coding strands,

→ Enhancer → enhances gene expression by looping and sitting on promoter, and ↑ strength of binding of RNA polymerase, when influenced by a particular protein.

→ Gene = ORF + Regulatory sequence
↳ RNA much shorter

→ pseudogenes → missing a promoter

→ does LINE/SINE help in plasticity?

