

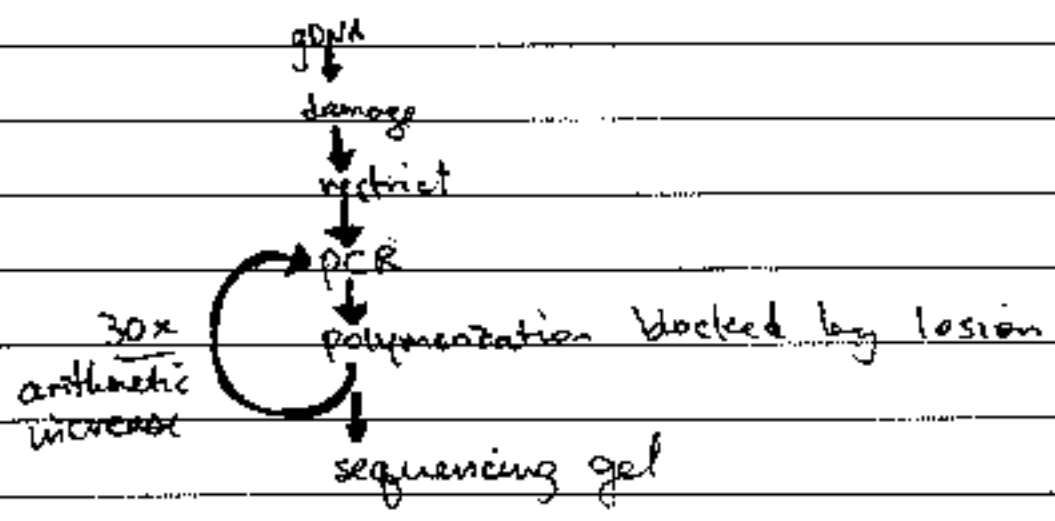
LAB MEETING

Triedon

no tx coupled repair in XP-G

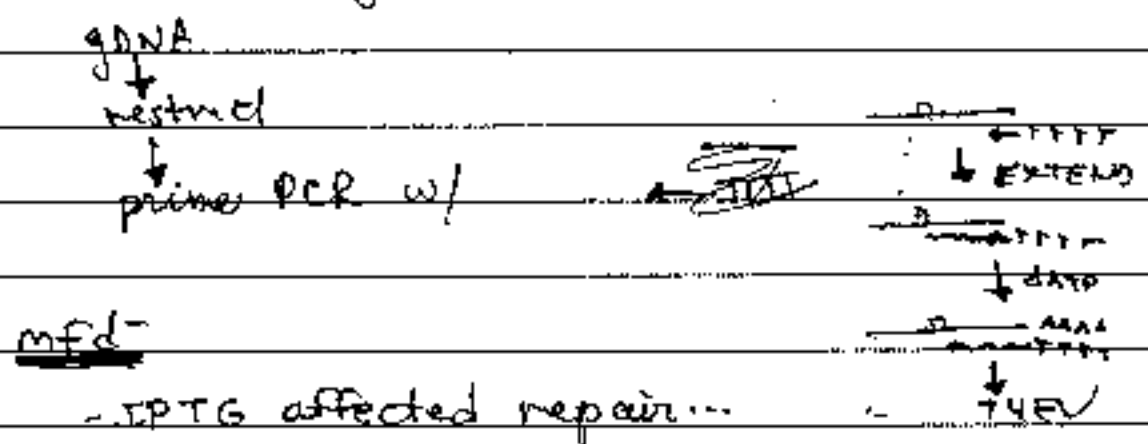
Ann Ganesan ... meeting update ... fine structure

Van Houten ... iterative PCR ... (repeated primer extension)



- so examine size distribution of bands
- coming out in JMB
- linear increase w/ UV dose
- not a good correlation of initial damage w/ mutations ^{in tx. strand}
- may apply to large fragments

Kuneda & Brash - oligonucleotide directed end-labelling

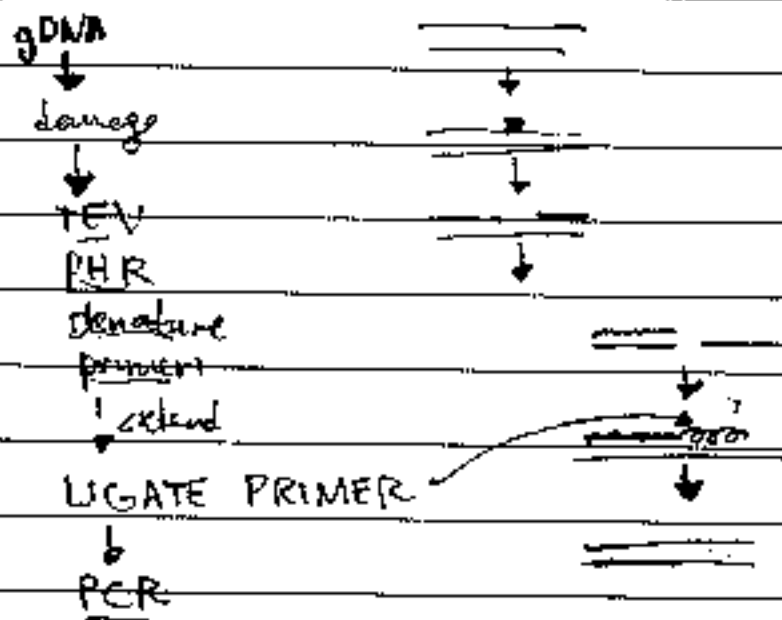


mfd

- IPTG affected repair ...
- low regions of repair ... increased

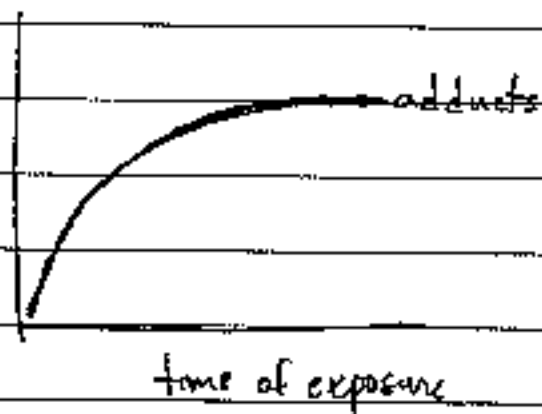
-near promoter -- not much strand specificity

③ LMPCR - Pfeifer



④ LMPCR - Holmquist

- Repair equilibrium
- Mutation may be more related to equilibrium



⑤ Maher - BPDE adducts

- ① damage, repair, & mutation
- treats sperch. cells in G1
- HPRT --

- ② UVR ABC -- purified -- cuts at all BPDE sites -- 4 bases away from stop site
- tag vs. sequence -- gave similar lesion values

-> var. in signal of some bands w/ time

LAB MEETING CONTD.

① M. Sidman - sequence context of UV induced damage

- PS189 --- plasmid

- - XPA cells (no repair)
- score for mutations
- hotspots for mutation

- TCGA

↖ hotspot in SUPF but cold spot in SUPARG

- ...-TC... hotspot for mutation ; same damage
 ↓
 - ...-CC... no hotspot " ; same damage

② Brian A. Donahue

ⓐ RNA pol. stalls at TT

- SII induced cleavage but ~~not~~ TT not more accessible to PHR

↓ load initiation factor
 ↓ add polymerase

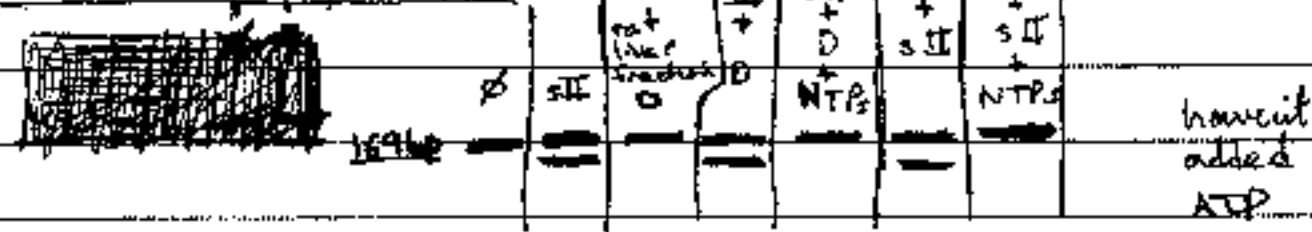
RUN RXN

↓ purify RNA

TX CLEAVAGE

↓ +/- SII
 ↓ +/- Fraction D

ⓑ TX ASSAY w/ TFIIH



fraction D contains TFIIH

Sweder - Factor b mutants

TFIIH... deficient in all repair

Δ ERCC6 \rightarrow homolog in yeast

--- ts vs. nts. equal in repair in mutant

--- Δ deficient in ts coupling

--- UV survival v. sim to WT

--- overall repair sim. to WT.