

Hamilton Smith - *H. influenzae*

(AKA SLOW)

- grows only in humans
- genome = AT rich (62%)

### Library Isolation

plasmid → 50-100 kb → shearing

Bal 31  
gel purify

1.6-2.0 kb  
fragments

ligation to  
puc18

cut out  
→  
linear of  
right size

T4 polymerase  
→  
ligase

### Gaps

- many in regions w/ RNA promoters

#### Closing Gaps

- combinatorial PCR
- Southern
- X Clones
- Peptide links



- w/ 6 ID - RNA -- how align  
- plasmids?  
dual functions?

SLOW

### HI1056

- Rest. enzyme w/ AGTC repeat
- deletion of 1 or 2. leads to frameshift

There is the Thai on  
lytton

JING JING

SIAM

Methano thermo

Mycoplasma

Pyrobaculum

Aquifer

Pyrococcus

Trichonema

Synechocystis

Streptococcus

Neisseria

E. coli

B. subtilis