

Figure 1. An overview of competence in *H. influenzae*

- 1. Regulation of competence:**
cya (HI0604)=adenylate cyclase
crp (HI0957)=cAMP regulatory protein
sxy (HI0601)=competence activator
murE (HI1133)=murein synthesis
purR (HI1365) = purine repressor
?trmE, rpoBC, topA, fis
- 2 & 3. Sequence-specific DNA binding and uptake:**
 recognizes **AAGTGGCGT**
comA, C, E (HI0439,0437,0435, CRE)?
comJ (HI0441)?
comE1 (HI1008, CRE)?
pilA (HI0299, CRE)
?pbpG, (CRE) isn (CRE)
- 4. Translocation of DNA:**
rec-2 (HI0061, CRE)
comF (HI0434, CRE)
dprA (HI0985, CRE)
- 5 & 6. DNA processing and recombination:**
comM (HI1117, CRE)
rec-1 (0600)=recA homolog
?ssb (HI0250, CRE)

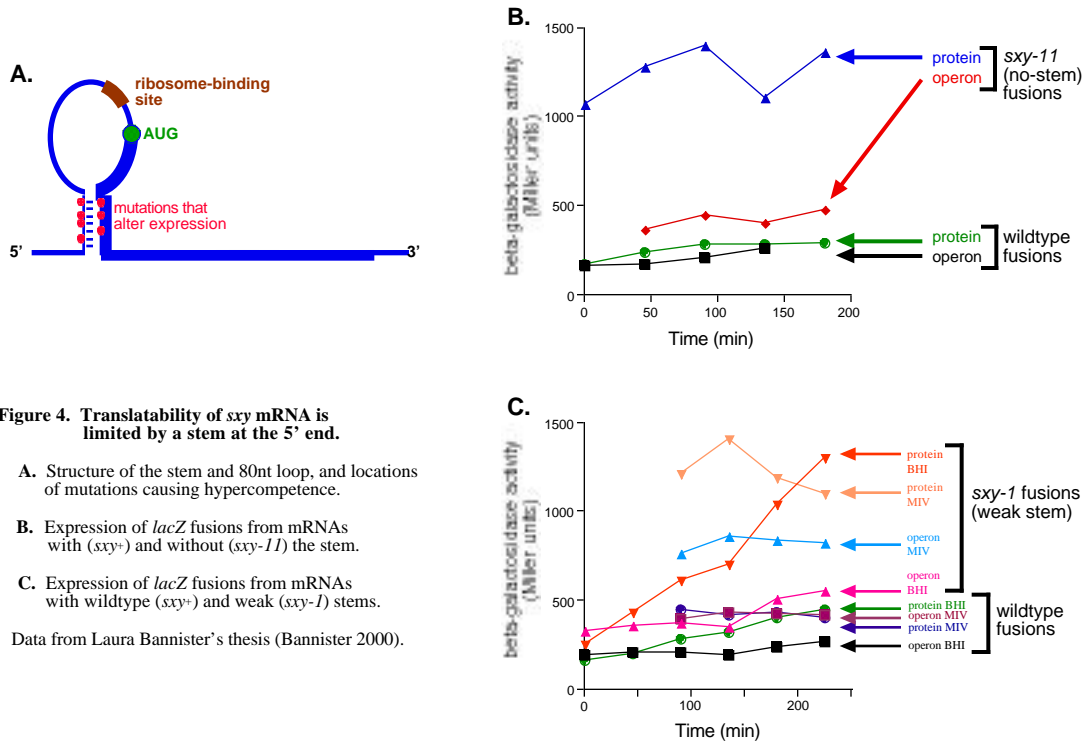


Figure 4. Translatability of *sxy* mRNA is limited by a stem at the 5' end.
 A. Structure of the stem and 80nt loop, and locations of mutations causing hypercompetence.
 B. Expression of *lacZ* fusions from mRNAs with (*sxy+*) and without (*sxy-11*) the stem.
 C. Expression of *lacZ* fusions from mRNAs with wildtype (*sxy+*) and weak (*sxy-1*) stems.
 Data from Laura Bannister's thesis (Bannister 2000).

Figure 5. Comparison of CRE and CRP sequences

Weighted matrices of CRE and CRP sequences. The CRE matrix was generated from the nine CRE sequences listed in Macfadyen (2000) (available at <http://www.zoology.ubc.ca/~redfield/CIHR>). The CRP matrix is from Macfadyen (2000) and was generated from the 49 CRP binding site sequences identified in *E. coli*. Pink boxes indicate nucleotides that are highly conserved. Consensus sequences are from Macfadyen (2000), where W=A or T and N=A,T,C, or G. Conserved motifs are highlighted by grey boxes. Asterisks indicate nucleotides that will be changed using site directed mutagenesis. Numbers in grey indicate nucleotide positions; sequences are aligned with promoters to the right.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	
CRE Matrix	A	0	0	0	0	0	0	100	0	0	22	56	0	100	0	0	0	11	100	78	100	78	
	T	100	100	100	0	0	0	0	100	11	45	11	22	0	100	0	0	22	0	11	0	22	
	C	0	0	0	0	0	100	0	0	0	89	22	0	22	0	0	100	0	67	0	0	0	
	G	0	0	0	0	100	0	100	0	0	11	33	56	0	0	0	100	0	0	11	0	0	
Consensus	T	T	T	T	G	C	G	A	T	C	N	N	G	A	T	C	G	C	A	A	A	A	
						*											*						
Consensus	W	W	W	T	G	T	G	A	N	N	N	N	N	N	T	C	A	C	A	W	W	W	
						*																	
CRP Matrix	A	47	47	37	1	4	2	8	88	12	18	18	31	20	33	12	14	71	20	67	24	37	29
	T	43	37	37	80	12	82	8	1	49	29	41	20	20	31	67	6	6	14	12	43	61	49
	C	2	4	8	16	2	16	1	6	20	35	31	14	16	22	6	80	2	65	8	18	2	14
	G	8	12	18	4	82	1	84	6	18	20	10	35	43	14	14	1	20	1	12	14	1	8