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Figure Legends

Figure 1. Genetic map of regulatory region of λ (not drawn to scale). Shown are relevant, promoters (P), operators (O), terminators (t, filled squares intrinsic and filled circles Rho-dependent), nut (put), and qut. Below are shown transcription patterns in the absence and presence of N and Nus factors and in the presence and absence of Q. Narrowing of lines provides an indication of reduced levels of transcription.

Figure 2. Features of antitermination sites in early operons of lambdoid phages. A. Comparison of nut regions (L and R) of λ and H-19B with components elements identified below (52,120). The arrows indicate regions of hyphenated dyad symmetry that are sources of stem-loop structures. B. The PUT stem-loop structures of phage HK022 (6). C. The GNRA fold-like structure formed by λ BOXB upon interaction with N, shown here for the NUTR-BOXB, is based on the structure determined for NUTL-BOXB (101,162). Bases, sugars, and phosphates are represented respectively by rectangles (with base indicated within), ovals, and squares. Dashed lines shows hydrogen bonds of Watson-Crick pairing and heavy dashed line shows sheared G(6)-A(10) base pair. Bases are numbered from 3’ end of upstream stem to 5’ end of downstream stem. The purine ring of adenine 7 stacks with the indole ring of Trp18 of N and adenine 9 is extruded from the structure.
Figure 3. The N-leader transcript beyond $p_L$. The sequence is shown starting at the BOXA sequence of NUTL; numbers indicate distance from RNA start of $p_L$. The structure of the RNaseIII site (RTS) is shown with the position of cleavage sites marked by arrows. The N ribosome-binding site (SD) and fMet codon are identified by underlines.

Figure 4. Assembly of transcription antitermination complex: N translation repression modes. RNA Pol is shown transcribing from the $p_L$ promoter through nutL and the RNase III site (RTS) into the N gene. The antitermination complex is formed first at NUTL (to the right of step 1) and the RTS is transcribed and assembles beyond step 2. If RNaseIII is not immediately present the SD (Shine-Dalgarno) sequence is protected in some way (?) from ribosome binding. If RNaseIII is present, the RTS is processed and allows optimal translation of N. Note the antitermination complex may remain bound to RNA Pol.