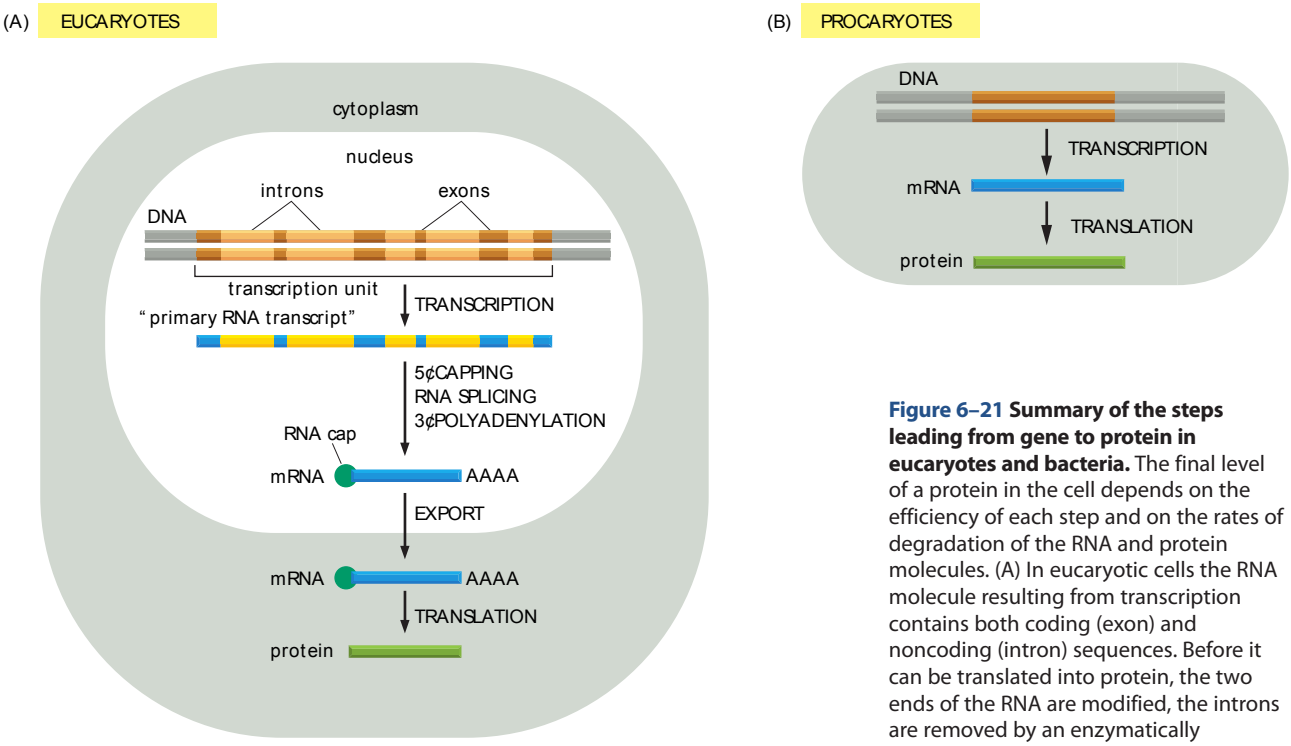

Figure 6–21 Summary of the steps leading from gene to protein in eucaryotes and bacteria. The final level of a protein in the cell depends on the efficiency of each step and on the rates of degradation of the RNA and protein molecules. (A) In eucaryotic cells the RNA molecule resulting from transcription contains both coding (exon) and noncoding (intron) sequences. Before it can be translated into protein, the two ends of the RNA are modified, the introns are removed by an enzymatically catalyzed RNA splicing reaction, and the resulting mRNA is transported from the nucleus to the cytoplasm. Although the steps in this figure are depicted as occurring one at a time, in a sequence, in reality they can occur concurrently. For example, the RNA cap is added and splicing typically begins before transcription has been completed. Because of the coupling between transcription and RNA processing, primary transcripts—the RNAs that would, in theory, be produced if no processing had occurred—are found only rarely. (B) In procaryotes the production of mRNA is much simpler. The 5¢end of an mRNA molecule is produced by the initiation of transcription, and the 3¢end is produced by the termination of transcription. Since procaryotic cells lack a nucleus, transcription and translation take place in a common compartment. In fact, the translation of a bacterial mRNA often begins before its synthesis has been completed.

positive superhelical tension in the DNA in front of it and negative helical tension behind it. For eucaryotes, this situation is thought to provide a bonus: the positive superhelical tension ahead of the polymerase makes the DNA helix more difficult to open, but this tension should facilitate the unwrapping of DNA in nucleosomes, as the release of DNA from the histone core helps to relax positive superhelical tension.

Any protein that propels itself alone along a DNA strand of a double helix tends to generate superhelical tension. In eucaryotes, DNA topoisomerase enzymes rapidly remove this superhelical tension (see p. 278). But in bacteria a specialized topoisomerase called DNA gyrase uses the energy of ATP hydrolysis to pump supercoils continuously into the DNA, thereby maintaining the DNA under constant tension. These are negative supercoils, having the opposite handedness from the positive supercoils that form when a region of DNA helix opens (see Figure 6–20B). Whenever a region of helix opens, it removes these negative supercoils from bacterial DNA, reducing the superhelical tension. DNA gyrase therefore makes the opening of the DNA helix in bacteria energetically favorable compared with helix opening in DNA that is not supercoiled. For this reason, it usually facilitates those genetic processes in bacteria, including the initiation of transcription by bacterial RNA polymerase, that require helix opening (see Figure 6–11).

Transcription Elongation in Eucaryotes Is Tightly Coupled to RNA Processing

We have seen that bacterial mRNAs are synthesized solely by the RNA polymerase starting and stopping at specific spots on the genome. The situation in eucaryotes is substantially different. In particular, transcription is only the first of several steps needed to produce an mRNA. Other critical steps are the covalent modification of the ends of the RNA and the removal of intron sequences that are discarded from the middle of the RNA transcript by the process of RNA splicing (Figure 6–21).