



Simple vs. complex gene organization

**Figure 21.** Pie charts of organismal genome organization. Genome sizes are indicated for the major model organisms used in epigenetic research at the top of each pie chart. The enlargement in genome size correlates with the increase of noncoding (i.e., intronic, some regulatory elements) and vast expansion of repetitive (i.e., retrotransposons [LINEs and ERVs (endogenous retroviruses) and other repeats [SINEs (short interspersed elements) and satellite repeats]) sequences in more complex multicellular organisms. This expansion is accompanied with an increase in the number of epigenetic mechanisms (particularly repressive) that regulate the genome (see the table on the inside front cover of this book). Expansion of the genome also correlates with an increase in size and complexity of transcription units, with the exception of plants; they have evolved mechanisms that are intolerant to insertions or duplications within the transcription unit. For *Tetrahymena*, the composition of the micronuclear genome is shown, whereas the common gene structure (asterisk) refers to the gene arrangement in the macronucleus, where gene expression occurs. P, promoter DNA element.