

Table 5.1 Metazoan genomes

Organism predicted	Genome	No. of genes
Phylum Cnidaria		
Class Anthozoa		
<i>Nematostella vectensis</i> (starlet sea anemone)	450 Mb	18 000
Phylum Nematoda		
Class Secernetea		
<i>Caenorhabditis elegans</i>	97 Mb	19 000
<i>Caenorhabditis briggsae</i> (for comparison with <i>C. elegans</i>)	104 Mb	19 500
Phylum Arthropoda		
Class Insecta		
<i>Aedes aegypti</i> (Yellow fever mosquito)	1376.0 Mb	15 419
<i>Anopheles gambiae</i> (Malaria mosquito)	272.9 Mb	13 111
<i>Apis mellifera</i> (Honeybee)	236 Mb	10 157
<i>Bombyx mori</i> (Moth)	530 Mb	18 500
<i>Drosophila melanogaster</i> (Fruit fly) ^a	117 Mb	13 718
Phylum Echinodermata		
Class Echinoidea		
<i>Strongylocentrotus purpuratus</i> (sea urchin)	814 Mb	23 300
Phylum Chordata		
Subphylum Tunicata		
Class Ascidiacea		
<i>Ciona intestinalis</i>	116.7 Mb	16 000
Subphylum Gnathostomata		
Class Osteichthyes		
<i>Danio rerio</i> (Zebra fish)	1.7 Gb	—
<i>Takifugu rubripes</i> (Puffer fish)	390 Mb	22–29 000
<i>Tetraodon nigroviridis</i> (Puffer fish)	385 Mb	—
Class Aves		
<i>Gallus gallus</i> (Chicken)	1 Gb	20–23 000
Class Mammalia		
Subclass Metatheria		
<i>Mondodelphus domestica</i> (Opossum)	3.475 Gb	18–20 000
Subclass Eutheria		
<i>Mus musculus</i> (Mouse)	2.5 Gb	24 174
<i>Rattus norvegicus</i> (Rat)	2.75 Gb	21 166
<i>Canis familiaris</i> (Dog)	2.4 Gb	19 300
<i>Macaca mulatto</i> (Rhesus monkey)	2.87 Gb	20 000
<i>Pan troglodytes</i> (Chimpanzee)	3.1 Gb	—
<i>Homo sapiens</i> (Human)	3.2 Gb	22 000

Further detail is given in the papers cited in the Bibliography.

^aThe genomes of 12 other species of *Drosophila* have been sequenced ranging from *D. grimshawi* with six chromosomes and 201 Mb of DNA to *D. pseudoobscura* with four chromosomes (the more usual complement) and 156 Mb of DNA.