This paper presents a plain English map of the chromosomes of the fruit fly, *Drosophila melanogaster*. The fruit fly has been important in genetics since it was selected for study by Thomas Hunt Morgan in 1909.

Morgan chose to work with the fruit fly for many reasons. Fruit flies are small, and hundreds of them can be bred in a single small vial. Under ideal conditions, they have a generation time of 10 days, making it possible to study many generations in a year. Fruit flies are easy to study because they have only four pairs of chromosomes (2n = 8). Finally, the third instar larva, the largest larva, has giant "polytene" chromosomes that can be easily stained and studied. These chromosomes occur in many larval tissues where the DNA replicates repeatedly in the absence of cell division. When stained, the polytene chromosomes give reproducible bands that form the basis for the chromosomes in this map. A single polytene chromosome can contain as many as 1000 DNA molecules.

The fruit fly was one of the first organisms whose genetics was studied. Many of our basic ideas in genetics, such as sex-linkage and autosomal linkage come from early studies of fruit fly genetics. Indeed, the fruit fly was the first organism to have a chromosome map of any kind done. And the same characteristics that made the fruit fly useful for early genetics studies make it useful today for studies in development.

As a result, the chromosome map presented here contains genes from very different kinds of studies. Some of the genes, such as that for vestigial wings or white eyes, have been known for the better part of a century. Some of these were found by the early fruit fly workers as single flies, spontaneous mutants that appeared in the midst of wild-type cultures. Others were obtained with X-rays and other mutagens by early workers looking for inherited variations to study. Other genes such as the homeotic genes have been found more recently by researchers using sophisticated molecular tools to study development. And still other genes such as the gene for catalase or alcohol dehydrogenase have been mapped to the fruit fly chromosomes with modern molecular techniques.

The resulting map represents the work of nearly a century by thousands of researchers using a tremendous variety of techniques. In some of the most satisfying developments, the molecular basis for some of the old phenotypes, such as eyeless, have been elucidated by studying the genes with modern techniques. In other cases, the molecular basis of the phenotype remains unknown.

A look at the map shows extensive conservation of genes across animal phyla and even across kingdoms. Hexokinase, the gene that codes for the first enzyme of glycolysis and triose phosphate isomerase, the gene coding for another glycolytic enzyme, are found in the fruit fly. They are found in humans and virtually every known organism in all five kingdoms. Catalase, the gene that codes for the enzyme that detoxifies hydrogen peroxide, is found in the fruit fly, as it is in humans and an enormous variety of other organisms. This means that the catalase gene evolved before fruit flies and humans last had a common ancestor over half a billion years ago. By the Cambrian Explosion, 543 million years ago, all animal phyla were present on Earth. Therefore, the Chordate and Arthropod lineages diverged before that time, and humans and fruit flies last had a common ancestor before then. So these genes must have evolved more than 543 million years ago.

One of the surprises is finding an alcohol dehydrogenase gene on the fruit fly map. After all, fruit flies don't give beer parties, so why would the presence of an alcohol dehydrogenase gene be selected for? Alcohol dehydrogenase is the enzyme that detoxifies alcohol. Fruit flies eat decaying fruit. Therefore, they sometimes eat fruit that has been fermented by yeast. Thus, in the normal course of their lives, they occasionally ingest alcohol. It stands to reason that a fruit fly that could detoxify this alcohol would have a better chance at survival than one that flew around intoxicated until the alcohol could be excreted. This is confirmed by the fact that fruit flies lacking a gene for alcohol dehydrogenase become rapidly intoxicated and die when exposed to ethyl alcohol. Of course, humans had an alcohol dehydrogenase gene long before they learned how to make wine from grapes.
The usefulness of this gene in us is similar to that in the fruit fly—a person who inadvertently ate fermented fruit would be able to detoxify the alcohol quickly. The presence of this gene in such diverse organisms testifies to the ubiquity of alcohol in the natural world and the importance of its detoxification in organisms that consume it.

The chromosomes in the present map are diagrams of the giant salivary gland chromosomes, as stained from the third instar larva. They were originally drawn by Calvin Bridges (Bridges 1935) and were redrawn in Science in 1991 (Genome Map, 1991). The Y Chromosome does not polytenize and has not been included in the map. Fruit flies have four pairs of chromosomes. The X Chromosome is Number 1 and is large. Chromosomes Number 2 and 3 are also large, while Chromosome Number 4 is very small. Although different researchers have come up with slightly different numbers, in the polytene state there are approximately 1000 bands on the X Chromosome, about 2000 bands on Chromosome 2, approximately 2200 bands on Chromosome 3, and between 40 and 50 bands on Chromosome 4.

The fruit fly genome is smaller than the human genome. A haploid fruit fly genome (four chromosomes) contains about 165 million base pairs and is estimated to have about 17,000 genes (Halder et al. 1995). By contrast, a haploid human genome contains 3 billion base pairs and is estimated to have between 50,000 and 100,000 genes.

Sex determination in fruit flies differs somewhat from sex determination in humans. In fruit flies, as in humans, females are XX and males are XY. Also as in humans, the X Chromosome is much larger than the Y Chromosome and contains many genes not found on the Y. None of the genes on the X Chromosome of this map is found on the Y Chromosome. They are therefore inherited as sex-linked genes. The only exceptions are the ribosomal RNA genes which are also found on the Y Chromosome. However, in fruit flies, it is not the presence or absence of the Y Chromosome that determines sex, but the ratio of X Chromosomes to autosomes. Therefore, in fruit flies, XXX is female and XO is male since two Xs and one set of autosomes is female, whereas one X and one set of autosomes is male.

Gene explanations, unless otherwise stated, were obtained from Lindsley and Zimm (1992). This is an excellent book that gives both classical and molecular descriptions of all genes known in fruit flies as of 1989.

Genes were placed on the chromosome bands according to Genome Maps (1991) and O’Brien (1993).

It is hoped that this map of the fruit fly chromosomes will be useful, both in teaching fruit fly genetics and in teaching evolution.

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Figure 1. Fruit fly (Drosophila melanogaster) chromosomes.
**X Chromosome (Chromosome 1)**

**Yellow Body**—The bodies of wild-type fruit flies are gray in color. The bodies of yellow mutants are yellow. Yellow mutants were reported as early as 1916, and there are now over 100 independently isolated yellow mutants known. This gene codes for a protein involved in depositing melanin in the body of the fruit fly.

**Scute Bristles**—Genes here code for a series of proteins responsible for specifying many of the bristles found on the head and thorax. Over 50 independently isolated scute mutants are known. The most common of these has smaller bristles on the thorax than the wild-type fly.

**White Eye**—The white eye mutation was the first mutation ever found in fruit flies, arising spontaneously in the lab of Thomas Hunt Morgan. It was reported in 1910. There are now hundreds of independently isolated white eye mutants known. This gene codes for a protein whose exact function is unknown. However, it is believed to be involved in the production and distribution of the two pigments found in *Drosophila* eyes, a brown (omnochrome) and a red (pteridine) pigment. It may be a membrane protein that carries precursors of these pigments into the cell. The white locus is actually incompletely dominant—heterozygotes look as if they have red eyes, but they have less pigment than homozygotes.

**Singed Bristles**—Singed mutants have smaller, curled bristles on their thorax. The gene at this location has been studied and is believed to code for a protein with a molecular weight of 59,000 daltons. The function of this protein is unknown. Over 100 independently isolated singed mutations are known; the earliest was reported in 1912.

**Lozenge Eye**—The eyes of Lozenge eye mutants are greatly reduced in size. The function of this gene is unknown.

**Hexokinase**—This gene codes for hexokinase, the first enzyme in glycolysis, that catalyzes the reaction glucose + ATP to yield glucose-6-P + ADP. This gene is highly conserved in eukaryotes, and is derived from a related glucokinase gene in prokaryotes (see Offner, 1994, for a discussion).
Vermillion Eye—The wild-type fruit fly has a red eye color. Normal red eye color in fruit flies is due to the presence of brown (omnochrome) and red (pteridine) pigments. This gene codes for tryptophan oxidase, an enzyme involved in the production of the brown (omnochrome) pigment. The eye color of vermilion mutants is a brilliant red since it does not have any brown pigment. Miniature Wing—In wild-type flies, the wings extend well beyond the abdomen. In miniature wing flies, the wings are only slightly longer than the abdomen. Miniature wing flies were reported as early as 1916. The biochemical function of this gene is not known.

Pyruvate Kinase—This gene codes for pyruvate kinase, an enzyme in glycolysis that catalyzes the reaction, phosphoenolpyruvic acid + ADP to yield pyruvic acid + ATP. As is true of the other enzymes of glycolysis, this enzyme is widely distributed throughout the living world.

Scalloped Wings—The wing margins of wild-type fruit flies are smooth in shape. The wing margins of scalloped flies are uneven or scalloped. The function of this gene is not known.

Forked Bristles—Bristles on the thorax are greatly shortened and bent at the ends. Forked mutants were reported as early as 1916. The function of this gene is not known.

Bar Eye—Flies with Bar eye have eyes that are reduced to a narrow vertical slit. The phenotype is most extreme in males (hemizygous) and homozygous females. Heterozygous females have eyes that are about half the normal size. Bar eye is a dominant gene that is due to a duplication of a small part of the chromosome. The function of the gene(s) involved in the duplication is unknown.

Ribosomal RNA—This area of the chromosome, long known as “bobbed,” contains about 225 genes that code for ribosomal RNA. There is a homologous area on the Y chromosome that also contains many genes for ribosomal RNA. The two areas together combine to form the nucleolus, where ribosomal RNA is made by base pairing from the ribosomal RNA genes on the chromosomes. Phenotypically, bobbed mutants have bristles that are shortened and thinned. This is believed to be due to a reduced rate of protein synthesis in flies that have fewer ribosomal RNA genes than normal. The rate of protein synthesis would be reduced since the cell would have fewer ribosomes. This is because ribosomal RNA is a structural component of the ribosomes. It would affect the bristles since they are made of protein. Some bobbed mutations are lethal.

Chromosome 2

Curly Wing—Curly wing flies have their wings curled upward due to unequal contraction of the upper and lower wing epithelia when the newly hatched fly dries its wings after it emerges from the pupa. Curly is inherited as an autosomal dominant and is lethal as a homozygote. The first curly mutant was reported in 1923. The function of the curly gene is unknown.

Dumpy Wing—Flies with dumpy wings have smaller than normal wings. The wings are also shaped somewhat differently from wild-type wings. There are over 100 dumpy mutants known, and they vary in wing size and shape. The function of the dumpy gene is not known.

Beta-Galactosidase—This gene codes for beta-galactosidase, the enzyme that digests lactose to glucose and galactose. This enzyme is sometimes called lactase. Fruit flies missing this enzyme cannot live on a medium containing lactose as the sole source of carbon.

Sucrase—This gene codes for sucrase, the enzyme that digests sucrose to glucose and galactose.

Alcohol Dehydrogenase—This gene codes for alcohol dehydrogenase, the enzyme that breaks down alcohol. Fruit flies missing this enzyme become rapidly intoxicated and then die when exposed to ethyl alcohol (ordinary drinking alcohol). This gene is widely distributed in living organisms. It evidently protects fruit flies from ethanol they may inadvertently ingest while eating decomposing fruit, a staple of their diet.

Black Body—These flies have black pigment on their body, making it darker than the gray wild-type body color. The function of this gene is not known.

Myosin, Heavy Chain—This gene codes for the heavy chain of myosin, one of the important proteins found in skeletal muscle. A single myosin molecule is composed of six amino acid chains: two identical heavy chains, coded for by this gene, and two each of two light chains. The genes for the two light chains of the myosin molecules are on Chromosome 3. It is striking that both human and fruit fly muscles have myosin as one of their main proteins. This implies an ancient origin for this gene.

Histone Proteins—There is a cluster of genes here that codes for the positively charged histone proteins that DNA winds around during mitosis. This gene cluster includes genes for all five histone groups: H1, H2A, H2B, H3 and H4. There are between 100 and 200 histone genes in this cluster. This great number of genes is probably necessary because histone proteins need to be produced in large quantities. These histone genes are among the first to be transcribed in the fertilized egg.
**Apterous**—Apterous flies have virtually no wings. They are small, weak and short-lived. The first apterous mutants were reported in 1914. The function of this gene is unknown.

**Cinnabar Eye**—Cinnabar flies have brilliant red eye color, like vermilion. This gene codes for kynurenine 3-hydroxylase, the enzyme that converts kynurenine to 3-hydroxykynurenine. This reaction is required for the formation of ommochrome, the brown pigment in wild-type eyes. Therefore, flies with a mutation in this gene have no brown pigment in their eyes.

**Vestigial Wing**—Vestigial wing flies have tiny wings at right angles to the body. They are unable to fly. The first vestigial mutants were reported in 1919, and over 40 independently isolated mutants are known. The function of the gene is unknown.

**Lobe Eye**—Lobe eye mutants have greatly reduced eyes. Lobe eye is inherited as an autosomal dominant and is lethal when homozygous. The function of the gene is not known.

**Amylase**—This gene codes for amylase, the enzyme that digests starch into glucose. Amylase is a widely distributed gene since so many organisms use starch for energy. The fruit fly amylase protein, coded for by this gene, is 57% identical to mouse amylase protein.

**Brown Eye/Plum**—This gene is believed to code for a protein involved with the transport of some precursors of pteridine pigments into the cell. Pteridines are the red pigments in the eye. Therefore flies with a mutation in this gene have brown eyes since their eyes contain only brown (omnochrome) pigments. Flies that have mutations in the brown eye gene will have white eyes if they also have a mutation in any of genes required for production of the red eye pigment. Thus brown eye mutants that also have mutations in either vermilion, cinnabar or scarlet have white eyes. One particular strain of fly with a mutation in the brown eye gene has been named Plum; hence the double name of the gene.

**Chromosome 3**

**Lysozyme**—This gene codes for lysozyme, a protein expressed in the salivary glands and mid-gut of the fruit fly. Lysozyme is an enzyme that digests bacterial cell walls.

**Sepia Eye**—This gene codes for an enzyme called PDA synthetase. This enzyme is required to produce...
red drosophila pigments. Flies with a mutation in this gene have eyes that are dark brown and become darker as the fly gets older. The eyes have no red pigments, but do contain yellow pigments, in addition to the normal brown pigments. This could be due to an accumulation of the intermediate of the red pigment substrate of this enzyme.

**Frizzled Hairs**—Flies with frizzled hairs have hairs on the thorax directed irregularly towards the midline of the thorax rather than posteriorly. There are other abnormalities in orientation of hairs on the wings and legs. This gene codes for a protein 581 amino acids long. The function of this protein is unknown.

**Scarlet Eyes**—These flies have bright vermilion eyes. This gene codes for phenoaxazine synthetase, an enzyme required to produce the brown eye pigment. Flies with a mutation in this gene therefore have no brown pigment in their eyes. This means there is only red pigment in their eyes. Flies that have mutations in both the scarlet gene and the brown eye gene have white eyes since they have neither brown nor red pigment in their eyes.

**Catalase**—This gene codes for catalase, the enzyme that breaks hydrogen peroxide into water and oxygen. This gene is widely distributed in living organisms.

**Homeotic Gene Cluster ANT-C**—There are four homeotic genes in this cluster. All contain a common, highly conserved region that codes for what is called a “homeobox”—a sequence of 60 amino acids arranged in three alpha helices of 20 amino acids each. This protein segment binds to DNA and is highly conserved in homeotic genes in a very wide range of organisms. There are seven homeotic genes in Drosophila. Four are here, and three are in the Homeotic Gene Cluster BX-C found elsewhere on Chromosome 3. The homeotic genes function during the development of the fruit fly and determine the appendages that will develop in each segment. Flies with mutations in individual homeotic genes have unusual phenotypes such as legs growing where antennae should be, or four wings instead of the normal two. During development, different homeotic genes are turned on in different segments. If the “correct” gene is turned on in all the segments, all the segments will develop the normal wild-type appendages. However, if the wrong homeotic gene is turned on in a segment, that segment will develop the wrong appendage, such as a leg growing where an antenna should be. The homeotic genes in this cluster regulate the development of the posterior segments of the head and the anterior regions of the thorax. The 1995 Nobel Prize was given to Edward Lewis, Eric Wieschaus and Christiane Nüsslein-Volhard for their discovery of genes controlling the early development of the fruit fly. The homeotic genes are among these genes. The Nobel Committee noted that these genes are especially significant because they function in humans and many other animals as well as in fruit flies.

**Tubulin**—Microtubules are made of the globular (spherical) proteins alpha and beta tubulin. Microtubules are major structural components of the mitotic spindle, cilia, flagella, and the cytoskeleton. There are eight genes known to code for the tubulin proteins in the fruit fly. Four of them map in this cluster. Three of them are genes for alpha tubulin; one is a gene for beta tubulin. Tubulin genes are widely distributed in living organisms.

**Rosy Eye**—This gene codes for xanthine dehydrogenase, an enzyme involved in the production of eye color pigments. Flies with a mutation in this gene have reddish-brown eyes due to an accumulation of xanthine and 2-amino-4-hydroxypteridine, the substrates of the enzyme. This gene has been the subject of very extensive molecular studies. Hundreds of mutants have been isolated.

**Acetylcholinesterase**—This gene codes for acetylcholinesterase, the enzyme that hydrolyzes the neurotransmitter acetylcholine after it has been released into the synapse. This is necessary so that the nerve signal can be stopped. This enzyme is widely distributed in living organisms. It is remarkable that the mechanism of nerve transmission should be so similar in vertebrates and invertebrates that the same enzymes are used.

**Stubble Bristles**—Flies with stubble bristles have bristles on their thorax that are shorter and thinner than wild-type bristles. Stubble is inherited as an autosomal dominant. Some of the stubble mutations are lethal as homozygotes. The function of the gene is not known.

**Spineless Bristles**—Flies with spineless bristles have small bristles on their thorax. The function of this gene is not known.

**Homeotic Gene Cluster BX-C**—Three of the homeotic genes described above are in this cluster. The genes in this cluster regulate the development of the posterior segments of the thorax and the segments of the abdomen. The fact that nearly all animals have a segmented form with distinct anterior and posterior ends early in development is believed to be due to these homeotic genes.

**Rhodopsin**—This gene codes for rhodopsin, the light-sensitive protein found in the fruit fly’s eyes. This rhodopsin protein, 373 amino acids long in the fruit fly, is homologous to the rhodopsin protein in humans, the light sensitive pigment in the rods of our eyes. This indicates that we both inherited the rhodopsin gene from our last common ancestor, over half a billion years ago.

**Hairless**—Flies with a mutation in this gene have greatly reduced or absent bristles on their head and
Hairless is inherited as an autosomal dominant. Many mutations in this gene are homozygous lethal. The function of the gene is not known.

**Ebony Body**—Flies with a mutation in this gene have dark black bodies. This gene codes for beta-alanyl dopamine synthetase, an enzyme required for the reaction beta alanine + dopamine to yield N-beta-alanyl dopamine.

**tRNA Aspartic Acid**—Transfer RNAs are small RNA molecules that carry amino acids to the ribosome and put them in the proper place on the growing protein. About 90 different tRNAs have been identified in the fruit fly. Each of these tRNAs is coded for by between 8 and 12 separate genes. This means there are approximately 900 different genes coding for tRNA molecules. These genes are found throughout the fruit fly genome. As with mRNA, these large numbers are probably necessary because the cell needs to produce very large numbers of tRNA molecules. This gene codes for a transfer RNA for aspartic acid, one of the 20 amino acids found in protein.

**Triose Phosphate Isomerase**—This gene codes for triose phosphate isomerase, the enzyme in glycolysis that catalyzes the reaction that converts dihydroxyacetone phosphate to glyceraldehyde-3-phosphate. This is one of the most ancient enzymes known and is widely distributed in all five kingdoms. There is a homologous gene in humans on Chromosome 12.

**Myosin, Light Chain**—There are two genes here that code for the two different small chains of amino acids found in myosin, an important protein in muscle. The gene for the heavy chain of the myosin molecule is found on Chromosome 2.

**Chromosome 4**

**Eyeless**—This gene codes for a protein, PAX-6, that directs the formation of the fruit fly eye. Flies with a mutation in this gene have very tiny eyes. Eyeless flies have been reported since 1915. However, it is only very recently that the molecular basis of the mutation has been understood (Quiring et al. 1994). PAX-6 is homologous to the human PAX-6 gene found on human Chromosome 11. In humans, the PAX-6 gene also directs the formation of the eye. People with mutations in the PAX-6 gene have aniridia, a condition characterized by tiny eyes. This implies that the gene that directs the formation of both human and fruit fly eyes evolved in a common ancestor over 570 million years ago. A homologous gene has been found in squids, and in several other animal phyla, making it likely that this gene is involved in eye formation across the animal kingdom. For a summary, see Gould 1994. In a remarkable series of experiments, Halder et al. (1995) were able to get relatively normal eyes to form on fruit fly wings, legs and antennae by artificially activating the eyeless gene in the embryonic tissue of these organs. They even transferred the homologous mouse gene to the embryonic tissue of a fruit fly leg and found that a fruit fly eye formed on the leg. This shows that the mouse gene can function in the fruit fly, and implies that this gene has the same function in both vertebrates and invertebrates. There are about 2500 genes believed to be involved in the formation of a fruit fly eye (Halder et al. 1995). Eyeless seems to be the gene that begins the whole process of directing these other genes to form eyes.

**Sparkling Eyes**—Flies with mutations in this gene have rough, bulging eyes. The function of the gene is not known.