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Interactive Computer Program for Learning Genetic Principles of Segregation and Independent Assortment through Meiosis

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***Abstract*— Teaching fundamental principles of genetics such as segregation and independent assortment of genes could be challenging for high school and college biology instructors. Students without thorough knowledge in meiosis often end up of frustration and failure in genetics courses.**

Although all textbooks and laboratory manuals have excellent graphic demonstrations and photographs of meiotic process, students may not always master the concept due to the lack of hands-on exercise. In response to the need for an effective lab exercise to understand the segregation of allelic genes and the independent assortment of the unlinked genes, we developed an interactive program for students to manually manipulate chromosome models and visualize each major step of meiosis so that these two genetic principles can be thoroughly understood.

I. Introduction

Meiosis is a cellular process which leads to the formation of gametes [1]. During meiosis, allelic genes are segregated and non-allelic genes on non-homologous chromosomes (unlinked genes) assorted independently. Segregation and independent assortment of genes are two fundamental principles in genetics [2, 3]. Genetic recombination, which results in the richness of gene pool, is caused by either independent assortment of unlinked genes (genes on different chromosomes) or by crossing over of linked genes due to exchanges of non-sister chromatids [4, 5].

Although the principles of segregation and independent assortment are fundamentally important for understanding genetics, it is always challenging for some beginning biology students. The objectives of this project are to model eukaryotic chromosomes and develop an interactive computer program for learning these principles through meiotic process. Two chromosome pairs were used as a model system for two consecutive cell divisions of meiosis. Each member of the chromosome pair represents paternal or maternal in origin. Each chromosome pair is labeled with a pair of heterozygous genes (e.g., *A/a* or *B/b*). Users may focus on the mechanisms of segregation and independent assortment in this exercise.

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II. Software Development

A. Functions

Two fundamental genetic principles to be explained from the developed interactive tutorial software are:

1) Segregation of allelic genes and reduction of gene copies are due to the separation of homologous chromosomes in anaphase I and the separation of sister chromatids in anaphase II, respectively.
2) Genetic recombination of unlinked genes is due to different chromosome confirmations in metaphase I, leading to independent assortment of chromosomes.

There are five main functions implemented in the program to help students understand these principles:

1) With "virtual tweezers", users will be able to move/manipulate the chromosomes, as if they were working with the real ones.
2) Users will be able to manually pair the homologous chromosomes during prophase I instead of automatic pairing.
3) Users may continue to move the chromosomes, step by step, until the completion of meiosis. Descriptions for controlling each step are provided.
4) In case of mistakes made by users, a correction system is available for explanation and correction.
5) Users will be able to track the chromosomes and their associated genes throughout the process.

B. Chromosome Model

To provide students with hands-on experience in tracking the meiotic process, we built chromosome models that simulate the shape of the G-banded chromosomes in OpenGL [6, 7] (Fig. 1).

The model is in a solid color and can be labeled with specific genes at different loci. A centromere, which separates *p* (short) and *q* (long) arms on the model, can be located at different positions characteristic of each chromosome. The model was built with many independent elements of ball shapes [8, 9]. Each element has its position, color, radius, and connections with others. To avoid the

appearance of discontinuous segments on the model, a smoothing algorithm is implemented to fill the gap between every two ball shape elements (Fig. 2) by adding a square outline.

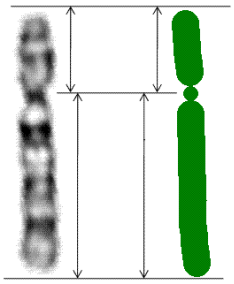

Fig. 1. Chromosome model based on G-banded chromosome

To simulate the meiotic process, chromosome model should be manipulated easily and moved freely according to users' input. The 2D-Ragdoll Physics method [8, 9] is embedded in every element to create smooth model movements. Elements are connected together and kept a desired distance from one another. The system ensures that elements do not scramble together once the model starts moving.

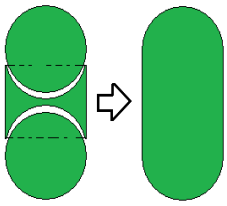

Fig. 2. Basic elements of chromosome model

C. *Meiotic process*

In the system, users can interact with the cell and chromosome models through the graphical user interface under the mouse control [10]. Main functions include meiosis control and splitting control. For the meiosis control, users can resolve each chromosome into two sister chromatids and set spindle fibers connecting to centromeres. The splitting control allows users to control the behavior of chromosomes during such transitional phases as anaphase I to telophase I and anaphase II to telophase II.

Prophase I: In early prophase I (Fig. 3), the cell (primary spermatocyte or oocyte) with the genotype *A/a*; *B/b* contains two homologous chromosome pairs. Gene *A* is located on paternal chromosome 1 and its allelic gene *a* on maternal chromosome 1. Gene *B* is located on paternal chromosome 2 and its allelic gene *b* on maternal chromosome 2. In this stage, the chromosomes are long the thin. Each chromosome is seen as a single structure even through each chromosome consists of two sister chromatids [2]. In late prophase I, the chromosomes are condensed, and each can be seen to contain two sister chromatids shared by a functional centromere. Also, homologous chromosomes are physically paired to form two bivalents (chromosome pairs). Since each chromatid carries a copy of the genes, the genotype is actually *A/a; A/a; B/b; B/b* (Fig. 4). The text explanation of each step is displayed on the right top of the screen.

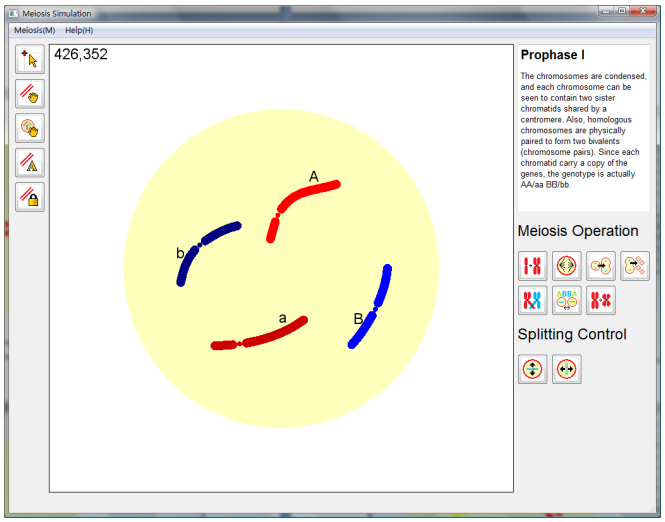

Fig. 3. Early prophase I with viewport and a simple control panel

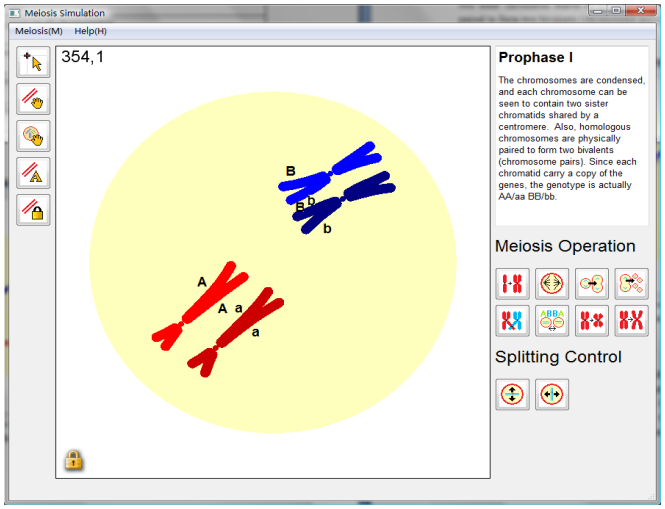

Fig. 4. Late Prophase I

Metaphase I: Each bivalent is moved (by spindle fibers) to the equatorial plane of the cell. For two bivalents, each with a heterozygous gene pair, there are two possible chromosome configurations in metaphase I: Configuration I is referred to a situation where paternal chromosomes are on one side and maternal chromosomes on the other side. Configuration II has mixed paternal and maternal chromosomes on each side of the equatorial plane (Fig. 5).

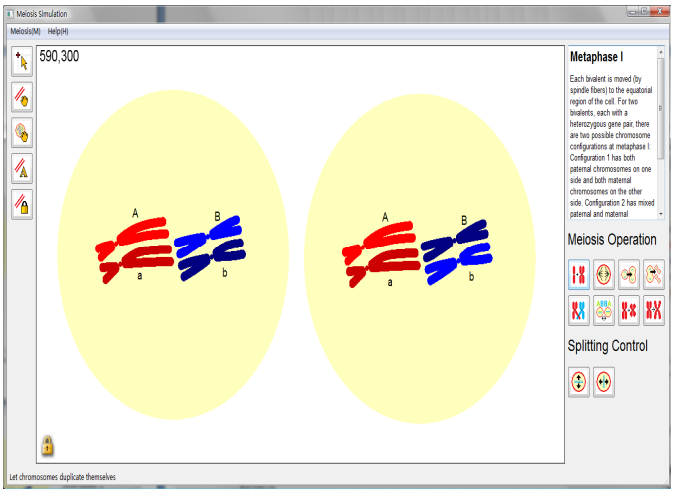

Fig. 5. Metaphase I, showing two configurations of chromosome and gene pairs

Anaphase I: Homologous chromosomes are pulled by spindle fibers toward the opposite poles of the cell. This process can be performed by clicking the "select" button to show spindle fibers. Users then click the spindle fiber button and use the vertical splitting control button to pull the chromosomes. Fig. 6 shows anaphase I following configuration I in metaphase I. It should be noted that anaphase I from configuration II is not shown. In the actual lab exercise, students will practice chromosome separation for both types of chromosome configurations.

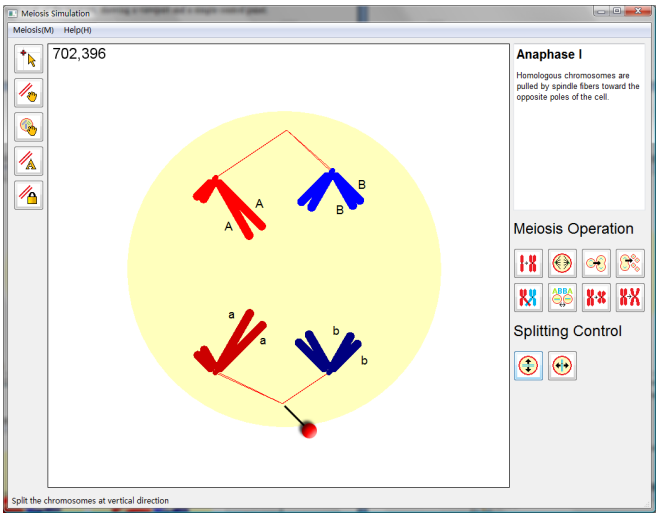

Fig. 6. Anaphase I, showing the pulling of homologous chromosomes toward two opposite poles by spindle fibers

Telophase I: Chromosomes continue to stretch and the cell is in the process of dividing into two, a process called cytokinesis (division of cytoplasm) (Fig. 7).

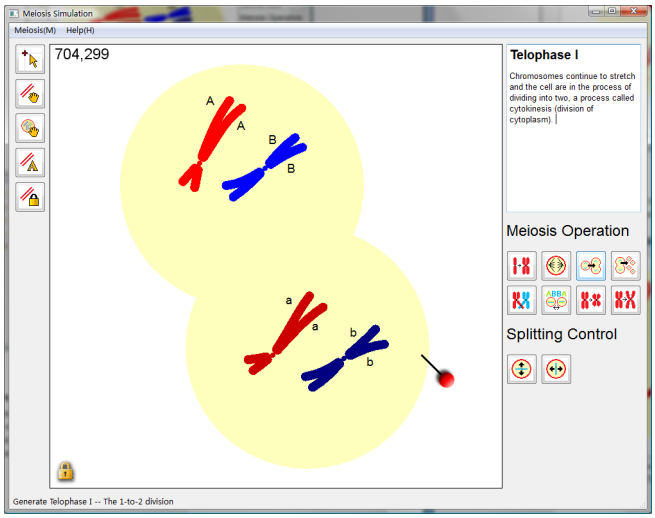

Fig. 7. Telophase I

Prophase II: Chromosomes in each daughter cell start to condense and may eventually become invisible under the light microscope. The genotypes of the two daughter cells resulted from configuration I are *AB* and *ab* (actually they are *AABB* and *aabb* because of two chromatids per chromosome) (Fig. 8). On the other hand, the genotypes of the two daughter cells resulted from configuration II are *Ab* and *aB* (actually *AAbb* and *aaBB*) (not shown).

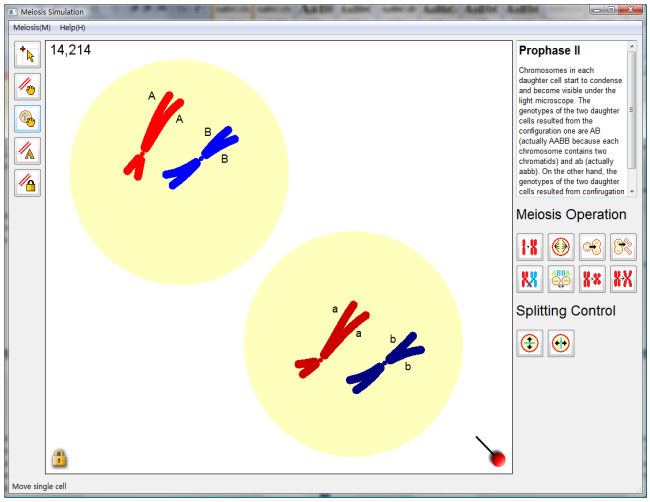

Fig. 8. Prophase II

Metaphase II: Each chromosome (univalent) is moved to the equatorial plane of the daughter cell (Fig. 9). Again, the metaphase from the original configuration II is not shown.

Anaphase II: Upon separation of the centromere into two separate functional units, the sister chromatids are moved to the opposite poles of the cell entering anaphase II (Fig. 10) Each chromatid is now called a chromosome since each contains a functional centromere.

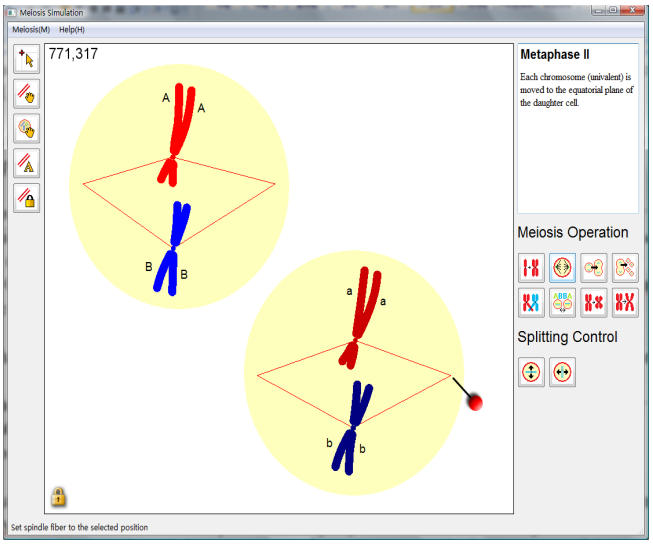

Fig. 9. Metaphase II

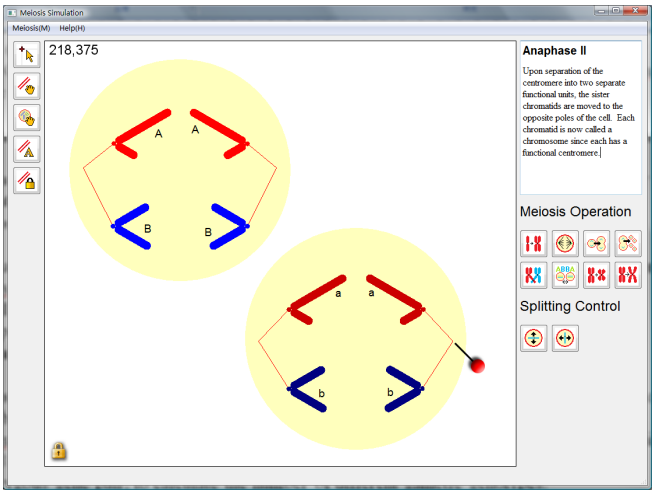

Fig. 10 Anaphase II

Telophase II: Chromosomes continue to stretch and become longer and the thinner. At the same time, cytokines for each cell takes place, forming 4 gametes from each configuration. The original cell with the chromosome configuration I in meetaphase I results in 4 gametes of the genotypes *AB, AB, ab*, and *ab* (Fig. 11). Likewise, the original cell chromosome configuration II results in 4 gametes of the genotype *Ab, Ab, aB,* and *aB* (not shown). Summing up, gametes of four genotypes are produced: AB, ab, Ab, and aB.

III. Conclusion and Future Work

Since we are only interested in the kinds of genotypes of the gametes, there are only 4 possible gamete genotypes after meiosis for two heterozygous gene pairs. These are *AB, ab, Ab,* and *ab*, each with ¼ chances. Students may use the formula 2^N, where N equals the number of independently assorted heterozygous gene pairs, to calculate the number of different gamete genotypes.

In conclusion, primary spermatocytes or oocytes with two heterozygous pairs of unlinked genes produce four genotypes of gametes due to independent assortment of non-homologous chromosomes during meiosis. At the same time, allelic genes (*A* and *a* or *B* and b*)* are segregated in the gamete which contains only one copy of the allelic genes.

We tested this program on different computers with different setups and found no problem running the software even on low-end computers. QT simply has quite good platform flexibility, and OpenGL provides the fast rendering speed. This software has been introduced to a genetics lab exercise in the Department of Biological Sciences, Purdue university calumet. The feedback was positive.

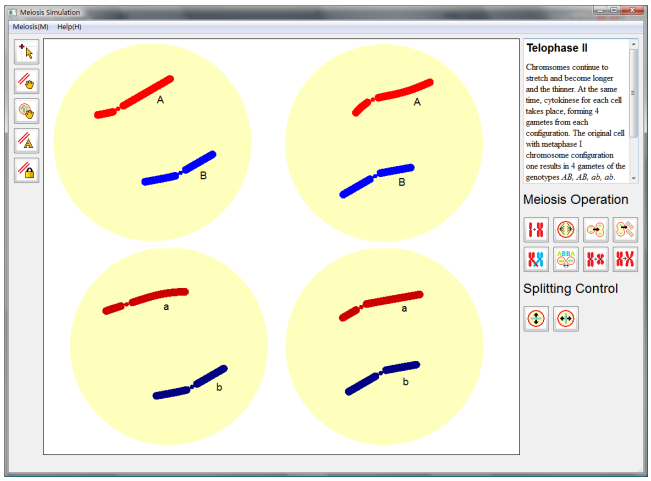

Fig. 11. Telophase II

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