**The Detection of Genetically Modified Organisms in Everyday Foods**

**Introduction**

Since the early 1900s, farmers have manipulated their crops to improve their yield, quality, nutritional value, and resistance to various stressors. As stated in OpenStax College (2013), this process was commonly known as hybridizing plants, or manipulating the plant’s genes to reach a desirable phenotype. The phenotype of an organism is its observable characteristics that result from its genotype and environment. By the late 1900s, the concept of recombinant DNA entered society by an experiment performed by two scientists, Herbert Boyer and Stanley Cohen. Recombinant DNA is a DNA molecule created in a lab by a molecular geneticist joining together several pieces of different genomes in a novel combination. These two men are important in science due to their experiment that demonstrated genetically engineered cells may be cloned into foreign cells (415). This led to a development of a new branch of science commonly known today as molecular biology. Since then, numerous advancements in technology and science have aided and improved society in pharmaceuticals, agriculture, and animals. For instance, the mass production of insulin through molecular biology techniques has increased its availability in large amounts, which has helped increase the health of many patients suffering from diseases like diabetes (457).

 Noted by Simms (2016) in the handout “Detection of Genetically Modified Organisms (GMOs) in Different Food Items,” genetic engineering is the process of transferring DNA segments between organisms to reach a desirable phenotype in an individual organism. Specifically, a gene of interest, or one that is more favorable due to its characteristics, is removed from one organism’s DNA and placed into another organism’s DNA (1). Thus, a genetically modified organism is an organism that has had its DNA modified by genetic engineering techniques to have more advantageous or favorable characteristics. The process is not quite this simple, though. Explained by Simms (2016), for an organism to express a foreign gene, two regulatory sequences are needed: a promotor and a terminator. Promotors are sequences of DNA located before the start of a gene that allow the enzyme RNA polymerase to bind. This enzyme is important for the transcription, or copying, of DNA into RNA that is necessary for a gene to attain its product, a protein (2). Without this production of protein, there would be no significant purpose for genes, which leads back to the importance of the promotor. The most common promotor is isolated from the cauliflower mosaic virus (CaMV). Terminators are also DNA sequences, but they are located at the end of a gene to signal its end. They terminate the end of transcription by dislodging RNA polymerase from the DNA template. Nopaline synthase (NOS) is a common terminator that is isolated from the bacterium *Agrobacterium tumefaciens* (3). To determine of an organism has been genetically modified, one can detect the promotor (CaMV), gene, or terminator (NOS) in a DNA segment to conclude if a change in the DNA has occurred. In this experiment, only the promotor will be examined to save time and materials.

 There are many processes that need to take place before it can be noted if an organism has been genetically modified. It begins with DNA being extracted from the host organism. This experiment deals directly with food items, therefore DNA extraction is the processes of grinding the food with a mortar & pestle, mixing it with chemicals, specifically InstaGene Matrix, in a test tube, and centrifuging it to separate the DNA from the rest of the materials. InstaGene Matrix is a solution comprised of negatively charged microscopic beads that function to remove any positively charged divalent metal ions found in the food slurry. Removal of these metal ions is crucial, for they serve as cofactors for DNases, enzymes that degrade DNA, making it difficult to amply with PCR. Since the amount of DNA at this point is very small, it needs to be amplified through polymerase chain reaction (PCR). This will generate millions of copies of a segment of DNA. Simms (2016) describes in the handout “Detection of Genetically Modified Organisms (GMOs) in Different Food Items” that there are three main steps to PCR: denaturation, annealing, and extension. Denaturation is heating the DNA template to 94°C to allow the separation of the two strands in the DNA double helix. Annealing occurs when the temperature is lowered to 59°C to allow the primers, short sequences of DNA that are complementary to the DNA template stand, to bind to the DNA. In the extension step, the temperature is increased to 72°C to allow the enzyme DNA polymerase to attach to the DNA template strand. This enzyme adds nucleotides to the ends of the primers to generate a copy of the original DNA strand. These three steps need to be repeated 30-40 times to exponentially amplify the DNA, which will allow the DNA to be seen with the naked human eye (6). For this process to be successful, several ingredients are needed. This includes a 10x buffer solution, equal concentrations of all four nucleotides (dNTPs, deoxynucleotide triphosphates), two primers that are complementary to the DNA template, and the DNA polymerase enzyme. The specific polymerase enzyme used is *Taq* polymerase. It is isolated from the thermophilic bacterium *Thermus aquaticus,* which resides in hot springs or steam vents (7-8). This enzyme is especially useful in this experiment for it can withstand the extreme temperature of 94°C without being denatured. If denaturation occurs, the enzyme would not be able to do its job, therefore no DNA would be made and the experiment would be a fail.

 After the polymerase chain reaction is completed, the DNA fragments go through gel electrophoresis. As Simms (2016) reports in “Detection of Genetically Modified Organisms (GMOs) Part II: Agarose Gel Electrophoresis,” this is a molecular biology technique that separates DNA fragments based on charge and size that is made possible by using an electrical charge to draw the fragments through a porous material. Agarose is a polysaccharide extracted from seaweed that contains pores created by the binding of various polymers to each other in the gel. It is used as the material for the DNA fragments to weave their way through and around. The porosity of the agarose in a gel is impacted by the concentration of the agarose solution. A gel with a higher percentage of agarose results in smaller pore sizes, whereas a gel with a lower percentage of agarose results in larger pore sizes. Because of the need to restrict the passage of DNA fragments, a higher percentage of agarose gel is commonly used (1). As an electrical current is applied to the gel, the fragments will begin to move towards the positive end, or the anode. This is because DNA is a negative molecule, and the fragments will move in the direction of opposite charge. The smaller the DNA fragment, the faster it will be able to move through the porous material and reach the positive electrode. The larger the DNA fragment, the slower it will navigate through the pores, and the farther it will be from the positive electrode.

 DNA fragments that have been separated by gel electrophoresis appear as bright bands. Analyzing these DNA fragments is made possible by DNA ladders. These are DNA sequences that are cut into known sizes with a specific number of base pairs. They appear as bands that can be compared to the DNA fragments one is testing. As concluded by Simms (2016) in “Detection of Genetically Modified Organisms (GMOs) Part II: Agarose Gel Electrophoresis,” since only the promotor is being amplified and gel electrophoresed in this experiment, for an organism to be considered as genetically modified, their DNA fragments need to contain the 190 base pairs that is specific to the promotor CaMV. There are two methods in which one can determine if their band of DNA has the 190 base pairs that are needed to be considered genetically modified: 1) making a direct comparison to the DNA ladder and/or 2) creating a semi log graph that plots of the size of the DNA fragments in the DNA ladder (log base pairs) versus the distance that the fragments traveled (3-4). Both methods are important to use to be confident in one’s data and conclusions.

 In this experiment, everyday food items are tested to see if they have been genetically modified. The foods go through the processes of DNA extraction, polymerase chain reaction, and gel electrophoresis, in that precise order, to conclude if the DNA has been modified to include a region of DNA from a different organism. Genetically modified organisms will contain foreign DNA in the promotor, gene, and terminator. In this specific experiment, only the DNA in the promotor will be examined. If an organism is genetically modified, it will contain the specific promotor cauliflower mosaic virus that can be detected by the presence of 190 base pairs after gel electrophoresis. If an organism is not genetically modified, it will not contain this specific promotor, and therefore will not contain the specific 190 base pairs.

**Materials and Methods**

*The Food Items*

Three different food items were tested in this experiment: a potato, pretzels, and sausage. No detailed information was given about the potato. The pretzels were Snyder’s of Hanover and directly stated as non-GMO on the package. The sausage was Banquet brand and fully-cooked. Nothing about GMOs were specifically stated on the sausage package.

*DNA Extraction*

The potato was cut into a piece about 1 cm thick with a knife on a rectangular cutting board. A plastic tray was placed on the Scout Pro electronic scale and zeroed out. The piece of potato was then placed on the plastic tray and weighed. Precisely 2.0 grams of each food item was needed, so pieces of potato were either added or taken away until the scale read 2.0 grams. The potato was then taken out of the plastic tray and placed in a 100-mL mortar to be grinded for 1 minute with a pestle. A glass 10-mL pipette was used to obtain 10 mL of distilled water from a beaker, which had been poured from a bottle while the potato was being weighed. The 10 mL of distilled water was added to the mortar. The food-water mixture was then grinded for an additional 2 minutes to break down the cells walls and release the DNA. Another 10 mL of distilled water was obtained with the glass pipette and added to the food-water slurry in the mortar. The slurry was grinded for about 3 more minutes, or until it was smooth enough to pipette. It was more important to pay attention to the consistency of the mixture rather than the exact amount of time that had passed. The 20-200 μL VWR micropipette was prepared to obtain 50 μL of the food-water slurry from the mortar. This was an important procedure that needed to be performed accurately to avoid erroneous results. The micropipette was first set to 50 μL by turning the top buttons until it read this precise number. A sterile cap was then placed on the tip. The top button on the micropipette was pressed until it stopped, or fully resisted. It was then placed into the slurry, and the individual using the pipette slowly raised his or her thumb until it was completely off the button. The mixture was released into one of the 1.5 mL tubes that contained 500 μL of InstaGene Matrix (prepared by the instructor) by pressing the top button of the pipette past the click. Once this was completed, the tip of the micropipette was removed by pressing the farthest back button and releasing it into the container waste. This tube was then labeled #1 for the first food item (potato), #3 for group number, and another #3 for lab section. The tube was parafilmed, or covered, with sheet wax to prevent heat evaporation. The remaining slurry in the mortar was discarded down the sink. The mortar and pestle were thoroughly cleaned with water and 10% beach solution to prevent contamination of the food items. These same steps were repeated for the remaining food items, the pretzels and sausage. Two grams of each food item was measured, grinded, and placed into a tube that contained 500 μL of InstaGene Matrix. The tube containing the pretzels was labeled #2, and the tube with the sausage was labeled #3. Each tube was also again labeled #3 for group number and another #3 for lab section.

Once each of the food items had been grinded and placed into their 1.5 mL tubes containing 500 μL of InstaGene Matrix, the three tubes were placed into a 78°C water bath for 24 minutes. Once the tubes were taken out of the bath, the temperature had risen to 92°C. This step was performed to destroy any proteins and enzymes associated with the DNA that could potentially degrade it. The tubes were dried off with a dry paper towel and placed in an Eppendorf centrifuge for a maximum speed of 13,200 revolutions/minute for 5 minutes. After the 5 minutes passed, the tubes were carefully removed from the centrifuge. Two layers could be observed in the tubes: a supernatant/liquid portion at the top containing the DNA, and the food particles and pellet of beads at the bottom. The tubes were placed in a tube rack for the next procedure to be performed.

*Polymerase Chain Reaction*

The 20-200 μL VRW micropipette was used to remove 7 μL of the supernatant portion, or DNA portion, of each individual test tube. The DNA from test tube #1, which contained the potato, was pipetted for 7 μL and placed into the 0.2 mL tube labeled #1 that was already provided on the lab table. The same procedures for using the pipette were followed as in DNA extraction. The micropipette was first set to 7 μL by turning the top buttons until it read this precise number. A sterile cap was then placed on the tip. The top button on the micropipette was pressed until it stopped, or fully resisted. It was then placed into the supernatant portion of the tube, and the individual using the pipette slowly raised his or her thumb until it was completely off the button. The mixture was released into the 0.2 mL tube by pressing the top button of the pipette past the click. Once this was completed, the tip of the micropipette was removed by pressing the farthest back button and releasing it into the container waste. This process was repeated for test tubes #2 (pretzels) and #3 (sausage). An extra test tube, test tube #4, was used as a negative control for later procedures. Since this test tube contained no DNA but still needed the same number of ingredients, 7 μL of water were added with the micropipette. After the DNA was extracted from each food item and placed into the 0.2 mL tubes, the primers for the promotors needed to be obtained. Using the Gilson pipetman P20 pipette, 2 μL of the promotor solution provided by the instructor was placed into each of the four 0.2 mL tubes. Once this was completed, the master mix was placed into each of the 0.2 mL tubes that now contained the DNA (or water for test tube #4) and primer solution. The master mix is a solution that contained the 10x PCR buffer, two primers targeting the CaMV promotor region, dNTPs (deoxynucleotide triphosphates) and *Taq* polymerase. Using the 20-200 VWR micropipette and applying the same techniques as mentioned earlier, 8 μL were extracted from the tube containing the master mix and placed into test tube #1. This was repeated for the rest of the three test tubes. Once all the test tubes contained the DNA (or negative control), promotor solution, and master mix, the tubes were ready to be run in a machine called a thermocycler. This procedure was performed by the lab instructor outside of class. The thermocycler amplified the DNA to generate millions of copies of the DNA segment in each test tube.

*Gel Electrophoresis*

Gel Preparation

After the DNA was extracted and amplified, it was run through gel electrophoresis to be separated by charge and size. This process allowed the DNA fragments to be analyzed to conclude if they were genetically modified. Before the gel could be ran, it had to be prepared. Outside of lab, the instructor had prepared the agarose solution. A weigh boat was used to measure 2 grams of agarose. This agarose was added to a 300-mL flask. 100 mL of 1X TAE buffer was also added to the flask. The flask was covered and heated in a water bath to boiling point (100°C) and then maintained at a temperature of about 60°C. A 10 μL micropipettor was used to add 4 μL of 10,000 x Gel Green. This is an intercalator that is used to insert molecules between the planar bases of DNA. Once lab started, the first step was placing a sample comb at one end of the gel tray in the casting apparatus. The 2% agarose solution was then poured into the gel. About 100 mL, or enough to cover the bottom of the tray, was poured into the gel. To have the gel solution polymerize, the gel tray sat at room temperature for about 20 minutes. Afterwards, the comb was carefully removed from the gel to expose the sample wells. The gel tray was then placed into the electrophoresis chamber, with it positioned so that the end of the gels with the wells was nearest to the negative electrode. This allowed the DNA to flow toward its opposite charge, the positive electrode. More 1X TAE electrophoresis buffer was the added to the chamber so that the gel was completely covered.

Loading the Gel

The test tubes that were prepared earlier were now placed into the wells in the gel chamber. The 20-200 μL VWR micropipette was used to load 15 μL of each food item into a sample well. Each group had their own four designated wells for food item #1, food item #2, positive control food item, and PCR negative control. A DNA ladder was loaded in four wells, adding 10 μL of the unique DNA ladder to each of the wells. To load a well, the very top of the pipette tip was placed into the buffer just above the well. The sample in the micropipette was released very slowly to ensure it was entering the well. When the entire sample had been released from the pipette tip, the micropipettor was pushed down to the second stop and carefully raised straight out of the buffer.

Running the Gel

 After all the samples and ladders were loaded, the cover was placed onto the electrophoresis chamber. The red and black electrode connectors were plugged into their appropriate sockets located directly on the chamber. The red electrode was the positive electrode (anode). The black electrode was the negative electrode (cathode). The other end of the electrode connecters was plugged into the electrophoresis power supply. The red connector was located at the end of the gel opposite the wells containing the DNA samples so that the DNA could move from the cathode to the anode. The power supply was turned on and set to a current of 140 mV. Bubbles were observed to ensure the current was flowing through the buffer. The DNA samples ran through this gel until the red band was situated at about 1/3 of the way from the bottom of the gel, which took about 60 minutes.

Visualizing the DNA Fragments

Once the electrophoresis was complete, the power to the chamber was turned off and the electrode connectors were unplugged. The gel was carefully removed from the chamber and placed on a plastic tray for imaging. The blue LED light was turned on while all the other lights in the room were turned off. The GelGreen that was associated with the DNA fluoresced when viewed with the safety glasses.

Analyzing the Gel

 A ruler was used to measure the distance (in cm) the fragments had traveled in both the 100-base pair (bp) ladder and ladder kit. The distance for the positive control food item and any other present bands for each group were also measured. A table was made on Excel that contained this information. Also, a semi-log graph was constructed that plotted the log of the size of the DNA fragments in the size standard (in log bp) as a function of the distance that the fragment traveled (in cm). The distance traveled was placed on the x-axis while the size of the DNA fragment was placed on the y-axis. The log of the base pairs was calculated by using the formula: log10(size in bp). Once the graph was constructed, a linear trendline was added that provided an equation. This equation was used to determine the log of the size of the fragments in food items #1, #2, and positive control. The log bp of the fragment was used to switch the number back to just bp by using the formula: 10^ (answer from above).

**Results**

Everyday food items were tested to see if they had been genetically modified. The food items had their DNA extracted, amplified through polymerase chain reaction (PCR), and sorted by charge and size through gel electrophoresis. As stated in the hypothesis, if the food items were genetically modified, they would contain foreign DNA in the promotor, gene, and terminator. In this specific experiment, only the DNA in the promotor was tested. If an organism was genetically modified, it would contain the specific promotor cauliflower mosaic virus that can be detected by the presence of 190 base pairs. If an organism was not genetically modified, it would not contain this specific promotor, and would not have the specific 190 base pairs.

****Figure 1 displays the gel electrophoresis image, which contains several components. Each well is labeled numerically from left to right. As seen in this figure, there are two types of DNA ladders: the ladder kit in wells 1 and 24 and the 100 bp ladder in wells 10 and 19. These DNA fragments represent controls that be used as a comparison tool for one’s own data. Wells 11, 12, 13, and 14 contain the food items specific to my group. Well 11 contains the potato, well 12 the pretzels, well 13 the positive food control (sausage), and well 14 the PCR negative control. The lab instructor’s positive food control is in well 25 while the negative food controls are in wells 26 and 27.

**Figure 1.** Gel image created by gel electrophoresis. 100 bp ladder in wells 10 and 19. Ladder kit in wells 1 and 24. Group’s DNA fragments in wells 11 (potato), 12 (pretzels), 13 (positive control- sausage), and 14 (PCR negative control). Lab instructor positive food control in well 25. Lab instructor negative food control in wells 26 and 27.

It can be seen in Figure 1 that the DNA ladders are clearly marked with the number of base pairs that represents each band. Table 1 contains information about the 100 bp ladder in wells 10 and 19 while Table 2 contains information about the ladder kit in wells 1 and 24. The size (in bp) of the fragments was known information that was provided by the instructor. The log of these bases was found by taking the log10(size in bp). Finally, the distance of each fragment (in cm) was found by measuring from the bottom of the well to the top of the fragment with a ruler. Figure 2 is a scatter plot graph with a linear trendline that represents the 100 bp ladder while Figure 3 represents the ladder kit. A negative slope was created by both DNA ladders. The size, or molecular weight, of the DNA fragments decreased as they moved farther away from the wells (the negative electrode) and closer to the end of the gel (the positive electrode).

**Table 1.** The size (measured in base pairs) of the DNA fragments, the log of these base pairs, and the total distance traveled by the fragments in the 100 bp ladder.

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| --- |
| **100 Base Pair Ladder** |
| **Size (in base pairs) of DNA Fragments** | **Log of Base Pairs** | **Distance Traveled (cm)** |
| 1517 | 3.180985581 | 3.2 |
| 1200 | 3.079181246 | 3.5 |
| 1000 | 3 | 3.9 |
| 900 | 2.954242509 | 4.2 |
| 800 | 2.903089987 | 4.4 |
| 700 | 2.84509804 | 4.5 |
| 600 | 2.77815125 | 4.7 |
| 500 | 2.698970004 | 4.9 |
| 400 | 2.602059991 | 5.1 |
| 300 | 2.477121255 | 5.3 |
| 200 | 2.301029996 | 5.9 |
| 100 | 2 | 6.6 |

**Figure 2.** Semi log graph that shows the size (log bp) of the DNA fragments over distance traveled (cm) for the 100 bp ladder.

|  |
| --- |
| **Ladder Kit** |
| **Size (in base pairs) of DNA Fragment** | **Log of Base Pairs** | **Distance Traveled (cm)** |
| 1000 | 3 | 3.3 |
| 700 | 2.84509804 | 3.9 |
| 500 | 2.698970004 | 4.3 |
| 200 | 2.301029996 | 5.6 |
| 100 | 2 | 6.3 |

**Table 2.** The size (measured in base pairs) of the DNA fragments, the log of these base pairs, and the total distance traveled by the fragments in the DNA ladder kit.

**Figure 3.** Semi log graph that shows the size (log bp) of the DNA fragments over distance traveled (cm) for the ladder kit.

As can be seen back in Figure 1, my group’s samples were in wells 11, 12, 13 and 14. There are no clear bands for these food items. Well 12 contains some smeared DNA, but that is the only visible marks in the specific wells designated for my group. Since no brands are present, the distance traveled, size of DNA fragment using equation of line, and size of fragment compared to DNA ladder are all 0. Table 3 visually represents this data, or therefore lack of.

**Tested Items**

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| --- |
| **Tested Items** |
| **Food Item** | **Name** | **Distance Traveled (cm)** | **Size (in bp) of DNA Fragment using Equation of Line**  | **Size (in bp) of Fragment Compared to DNA Ladder**  |
| Food Item #1 | Potato | 0 | 0 | 0 |
| Food Item #2 | Pretzels | 0 | 0 | 0 |
| Positive Control Food Item | Sausage | 0 | 0 | 0 |
| PCR Negative Control | Water | 0 | 0 | 0 |

**Table 3.** The label for each food item, the name of each food item, the distance the DNA fragment traveled, the size of the fragment using the equation of line, and the size of fragment compared to DNA ladder for each item tested in this lab.

Referring back to Figure 1, the lab instructor’s positive control food item located in well 25 contains a clear band located close to the 200 bp fragment in the DNA ladder kit. This well also contains a band below the 100 bp ladder kit fragment. The negative control food items in wells 26 and 27 both contain bands that are located below the 100 bp ladder kit fragment.

**Discussion**

 Each food item had its DNA extracted, amplified, and separated on the basis of charge and size. The smaller the DNA fragment, the faster it was able to move through the porous material of the agarose in the gel and reach the positive electrode. The larger the DNA fragment, the slower it navigated through the pores, and the farther it was from the positive electrode. According to the hypothesis, if the food items were genetically modified, they would contain the specific promotor cauliflower mosaic virus that can be detected by the presence of 190 base pairs after electrophoresis. If an organism was not genetically modified, it would not contain this specific promotor, and therefore would not have the specific 190 base pairs.

 There were no bands present for any of the food items that had been in my specific group, wells 11, 12, 13, and 14. Because of this, one could assume that the organisms were not genetically modified since they did not contain the specific 190 base pairs. It is hard to make this assumption, though, for there were several sources of error. Food item #1 never entered the well due to a problem that occurred in the micropipetting process. Food Item #2 was slightly diluted due to the solution containing extra water. Besides mechanical errors, it also appears that the food items contained little to no primers due to no band appearing on the bottom of the gel. The lab instructor’s positive and negative control did contain this band at the bottom of the gel, which indicates some type of mistake. Another source of error could have resided in the DNA. There are instances where DNA is of poor quality and cannot be amplified. A mechanism to ensure the DNA is of good quality should be implemented, such as using the molecule actin as a control to ensure the DNA is functioning properly.

 If these errors would not have occurred and the organisms were indeed genetically modified, the DNA fragments would have bands of 190 base pairs. To find out how far the fragments would have traveled if they had been genetically modified, the 190 base pairs can be put in the formula log 10(190) and then substituted for *y* in the equation of the line found in both ladders kits. The equation can then be solved for *x*, which is how far the fragments would have traveled if the food items had been genetically modified. If solved in the equation of the line for the DNA ladder kit, the fragments would have traveled 5.56 cm. If solved for the equation of the line in the 100 bp ladder, the fragments would have traveled 5.99 cm. Although the difference of these numbers is very minimal, it still shows that the DNA ladders are not precisely the same.

 Since this experiment had many sources of error, it would be wise to redo it with more checkpoints to ensure things were going right. For instance, adding in a procedure to test the quality of DNA would be very helpful. Adding in more primers and making sure they are the correct ones for the promotor would also be very important. A future experiment may not contain a negative result, which is the fact that nothing appears if it is not genetically modified. This makes it hard to pinpoint if the organism was truly not genetically modified or if something went wrong. If a further study contained these procedures and variables, it would be more reliable and produce more trustworthy results.

Numerous studies have been performed similar to this experiment to test the presence of GMOs in various foods. A recent study (2013) done by Maryam Rabiei et. al tested processed foods sold commercially in Iran by using qualitative PCR. The scientists tested corn flakes, frozen maize, corn puffs, corn seeds, canned corn, corn chips, and pop corns by using the same methods performed in this experiment: DNA extraction, PCR, and agarose gel electrophoresis. The specific promotors used differed quite greatly, for these scientists used primers such as zein, CaMV35s, Bt-11, Bt-176 and MON810. This study resulted in 5 of the 25 total food items being genetically modified, which led to the conclusion that genetically modified organisms are becoming increasingly popular in today’s society.

 Genetically modified organisms are a controversial issue that many individuals debate whether they are beneficial or harmful to society. It is important that scientists continue to study these processes and ensure they are healthy for humans to consume. As society and technology continue to advance, one can assume this subject will only become more popular and relevant in both science and the public. Therefore, it is crucial for one to understand how genetically modified organisms are made and be aware of what is going in the food items one consumes.

**References**

OpenStax College. (2013). *Biology.* Houston, Texas: Rice University.

Rabiei, M., Mehdizadeh, M., Rastegar, H., Vahidi, H., & Alebouyeh, M. (2013). Detection of Genetically Modified Maize in Processed Foods Sold Commercially in Iran by Qualitative PCR. *Iranian Journal of Pharmaceutical Research: IJPR*, *12*(1), 25–30.

Simms, T. M. (2016). Detection of Genetically Modified Organisms (GMOs) in Different Food Items handout for Biology 105 labs, retrieved from <https://mnsu.ims.mnscu.edu/d2l/le/content/3361863/viewContent/28594236/View>.

Simms, T. M. (2016). Detection of Genetically Modified Organisms (GMOS) Part II: Agarose Gel Electrophoresis handout for Biology 105 labs, retrieved from <https://mnsu.ims.mnscu.edu/d2l/le/content/3361863/viewContent/28638023/View>.