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NEW DNA Standard ladder sizes:
6751, 3652, 2827, 1568, 1118, 825, 630



Edvo-Kit #

114

Edvo-Kit #114

DNA Paternity Testing Simulation

Experiment Objective:

The objective of this experiment module is to introduce students to the use of DNA Fingerprinting in a hypothetical paternity determination.

See page 3 for storage instructions.

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Experiment Components

READY-TO-LOAD™ SAMPLES FOR ELECTROPHORESIS

Store QuickStrip™ samples in the refrigerator immediately upon receipt.
All other components can be stored at room temperature.

Components (in QuickStrip™ format)

- A Standard DNA Marker
- B Mother DNA cut with Enzyme
- C Child DNA cut with Enzyme
- D Father 1 DNA cut with Enzyme
- E Father 2 DNA cut with Enzyme

Check (✓)

- ☐
- ☐
- ☐
- ☐
- ☐

REAGENTS & SUPPLIES

- UltraSpec-Agarose™
- Electrophoresis Buffer (50x)
- Practice Gel Loading Solution
- FlashBlue™ DNA Stain
- InstaStain® Blue cards
- 1 ml pipet
- Microtipped Transfer Pipets

- ☐
- ☐
- ☐
- ☐
- ☐
- ☐
- ☐

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Experiment #114 is designed for 8 gels if stained with FlashBlue™ or InstaStain® Blue (both included) or 16 gels if stained with SYBR® Safe or InstaStain® Ethidium Bromide (not included).

Store QuickStrip™ samples in the refrigerator immediately upon receipt. All other components can be stored at room temperature.

All experiment components are intended for educational research only. They are not to be used for diagnostic or drug purposes, nor administered to or consumed by humans or animals.

Requirements

- Horizontal gel electrophoresis apparatus
- D.C. power supply
- Automatic micropipets with tips
- Balance
- Microwave, hot plate or burner
- Pipet pump
- 250 ml flasks or beakers
- Hot gloves
- Safety goggles and disposable laboratory gloves
- Small plastic trays or large weigh boats (for gel destaining)
- DNA visualization system (white light)
- Distilled or deionized water

Background Information

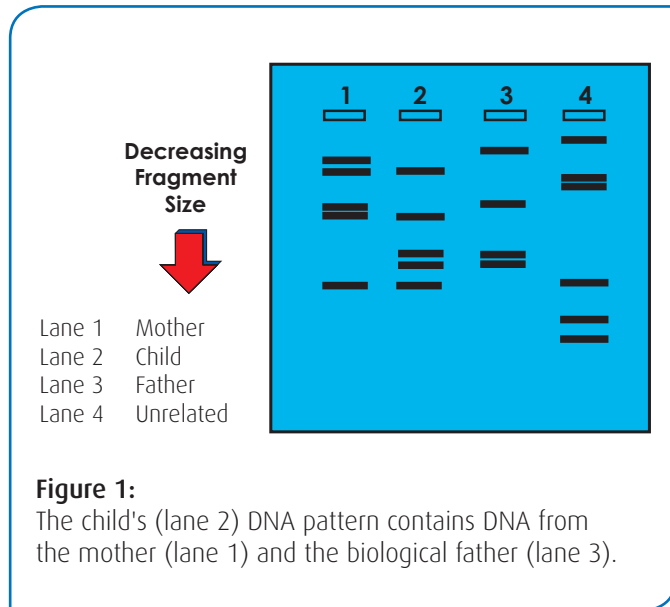
DNA fingerprinting (also called DNA typing) allows for the identification of the source of DNA samples. The method has become very important to provide evidence in paternity and criminal cases. In contrast to the more conventional methodologies, such as blood typing, which can only exclude a suspect, DNA fingerprinting can provide positive identification with great accuracy.

Paternity determination based on DNA analysis (genetic DNA fingerprinting) has become an important procedure for matching children with biological fathers and mothers. Examples of recent court cases that have utilized this procedure have included rape, incest, immigration, citizenship of children to the United States and matching of children with parents who were mismatched at birth due to hospital errors. This type of testing is also used during unrest as in nations in civil war where children are often separated from parents and subsequently reunited.

For paternity DNA fingerprinting, samples obtained from the mother, the child, and possible fathers are analyzed. A child's DNA is a composite of its parent DNAs. Therefore, comparison of DNA fragmentation patterns obtained from the mother and child will give a partial match. Bands in the child's DNA fingerprint that are not present in the mother's must be contributed by the father. Because of allelic differences, the DNA bands present in the child's fingerprint must be found in either the father's or mother's fingerprint.

Prior to the advent of the Polymerase Chain Reaction (PCR), DNA fingerprinting involved the electrophoretic analysis of DNA fragment sizes generated by restriction enzymes followed by Southern Blot Analysis. Restriction enzymes are endonucleases which catalyze the cleavage of the phosphate bonds within both strands of DNA. They require Mg^{+2} for activity and generate a 5 prime (5') phosphate and a 3 prime (3') hydroxyl group at the point of cleavage. The distinguishing feature of restriction enzymes is that they only cut at very specific sequences of bases called recognition sites. Restriction enzymes are produced by many different species of bacteria (including blue-green algae). Over 3,000 restriction enzymes have been discovered and catalogued.

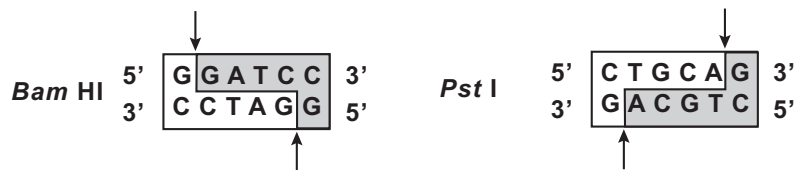
Restriction enzymes are named according to the organism from which they are isolated. This is done by using the first letter of the genus followed by the first two letters of the species. Only certain strains or substrains of a particular species may be a producer of restriction enzymes. The type of strain or substrain sometimes follows the species designation in the name.



Finally, a Roman numeral is always used to designate one out of possibly several different restriction enzymes produced by the same organism or by different substrains of the same strain.

Restriction enzymes recognize specific double stranded sequences in DNA. Most recognition sites are 4 to 8 base pairs in length. Cleavage occurs within or near the site. The cleavage positions are indicated by arrows. With some exceptions, recognition sites are frequently symmetrical, i.e., both DNA strands in the site have the same base sequence when read 5' to 3'. Such sequences are called palindromes. It is these sites in DNA that are substrates for restriction enzymes. In DNA paternity and fingerprinting laboratories, the commonly used restriction enzymes are *Hae* III (GG'CC) and *Hinf* I (G'ANTC), which are 4-base and 5-base cutting enzymes respectively.

In this experiment, the DNAs from a hypothetical paternity case are cut by a restriction enzyme, which is a six-base cutting enzyme. Examples of six-base cutting enzymes include *Bam* HI and *Pst* I. The recognition sites for these restriction enzymes are:



The size of the DNA fragments generated by restriction enzyme cleavage depends on the distance between the recognition sites. No two individuals have exactly the same pattern of restriction enzyme recognition sites. There are several reasons for this fact. A large number of alleles exist in the population. Alleles are alternate forms of a gene. It is estimated that about 25% of all human genes occur in multiple alleles which are called polymorphisms. Alleles result in alternative expressions of genetic traits which can be dominant or recessive and are inherited in a Mendelian pattern just as genes.

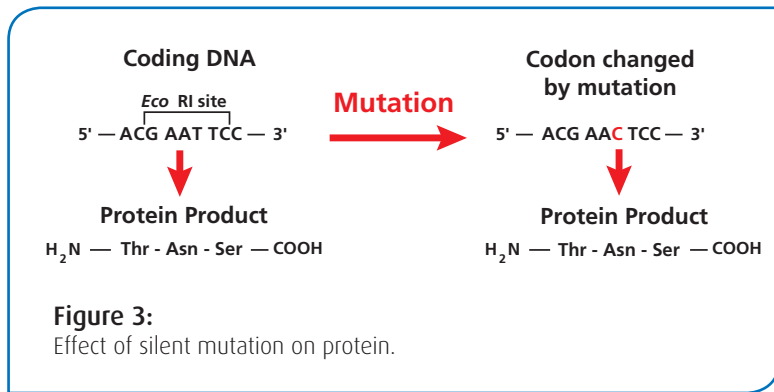
Restriction Enzyme

Chromosomes occur in matching pairs, one of maternal and the other of paternal origin. The two copies of a gene (which can be alleles) at a given chromosomal locus, and which represent a composite of the parental genes, constitutes the unique genotype for an offspring. It follows that alleles have differences in their base sequences which consequently creates differences in the distribution and frequencies of restriction enzyme recognition sites. Other differences in base sequences between individuals can occur because of mutations and deletions. Such changes can also create or eliminate a recognition site.

Restriction Enzyme	Organism
<i>Bam</i> HI	<i>Bacillus amyloliquefaciens</i>
<i>Hae</i> III	<i>Haemophilus aegyptius</i>
<i>Eco</i> RI	<i>Escherichia coli</i> , strain RY13
<i>Hinf</i> I	<i>Haemophilus influenzae</i> Rf

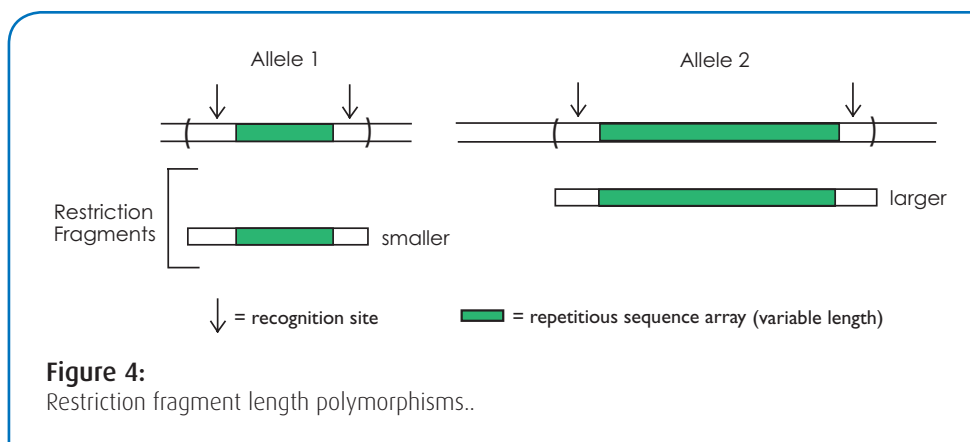
Figure 2:
Restriction enzyme names and bacterial sources.

The example in Figure 3 shows how a silent mutation can eliminate a recognition site but leave a protein product unchanged. Individual variations in the distances between recognition sites in chromosomal DNA are often caused by intervening repetitive base sequences. Repetitious sequences constitute a large fraction of the mammalian genome and have no known genetic function. These sequences can occur between genes or are adjacent to them. They are also found within introns. Ten to fifteen percent of mammalian DNA consists of sets of repeated, short sequences of bases that are tandemly arranged in arrays. The length of these arrays (the amount of repeated sets) varies between individuals at different chromosomal loci.



TGTTTA | TGTTTA | TGTTTA |variable number

When these arrays are flanked by recognition sites, the length of the repeat will determine the size of the restriction enzyme fragment generated. Variations in the length of these fragments between different individuals, in a population, are known as restriction fragment length polymorphisms, RFLPs. Several hundred RFLPs have been mapped on all 23 chromosomes. RFLPs are a manifestation of the unique molecular genetic profile, or "fingerprint", of an individual's DNA. As shown in Figure 4, there are several types of these short, repetitive sequences that have been cloned and purified. In Southern blot analysis, DNA probes are used to detect the length differences between these repetitive sequences. DNA probes are short fragments of single stranded DNA that are isotopically or non-isotopically labeled. DNA probes will complement and hybridize (attach) to single stranded DNA. Southern blot analysis requires electrophoresis, denaturation of the DNA fragments, transfer of DNA to a membrane, and exposure to probes to detect DNA Fingerprints.



There are two types of probes commonly used for genetic identification. The single-locus probes (SLPs) which detect a single segment of the repetitive DNA located at a specific site on a single chromosome. This will result in one or two DNA bands corresponding to one or both chromosome segments recognized. If the segments on the chromosome pairs are the same, then there will be one band. On the other hand, if they are different, it will appear as two bands. Several SLPs are available and are used less frequently since more than one person can exhibit the same exact pattern for a specific SLP. Multiple-Locus probes (MLPs) detect multiple repetitive DNA segments located on many chromosomes yielding 20-30 bands. Because of the multi-band patterns, the chances of two people chosen at random having the same pattern is enormously remote. For example, it is calculated that two unrelated individuals having the identical DNA pattern detected by MLPs as an average is 1 in 30 billion. It should be kept in mind that the total human population on earth is between 5-6 billion.

Currently, the polymerase chain reaction (PCR) is routinely used in forensics to analyze DNA (Figure 4). This technique requires about 500-fold less DNA than Southern blot RFLP analysis and is less time-consuming. PCR amplification (Figure 5) uses an enzyme known as Taq DNA polymerase. This enzyme, originally was purified from a bacterium that inhabits hot springs and is stable at very high (near boiling) temperatures. Also included in the PCR reaction mixture are two synthetic oligonucleotides known as "primers" and the extracted DNA. The region of DNA to be amplified is known as the "target".

In the first step of the PCR reaction, the template complementary DNA strands are separated (denatured) from each other at 94°C, while the Taq polymerase remains stable. In the second step, known as annealing, the sample is cooled to 40°-65°C, to allow hybridization of the two primers, one to each of the two strands of the template DNA. In the third step, known as extension, the temperature is raised to 72°C and the Taq polymerase adds nucleotides to the primers to synthesize the new complementary strands. These three steps - denaturation, annealing, and extension - constitute one PCR "cycle". This process is typically repeated for 20-40 cycles, amplifying the target sequence within DNA exponentially (Figure 5). PCR is performed in a thermal cycler, an instrument that is programmed to rapidly heat, cool and maintain samples at designated temperatures for varying amounts of time. The PCR products are separated by agarose gel electrophoresis and DNA fingerprints are analyzed.

In forensics and DNA paternity testing, PCR is used to amplify and examine highly variable (polymorphic) DNA regions. These are regions that vary in length from individual to individual and fall into two categories: 1) variable number of tandem repeats (VNTR) and 2) STR (short tandem repeats). A VNTR is a region that is variably composed of a 15-70 base pair sequence, typically repeated 5-100 times. An STR is similar to a VNTR except that the repeated unit is only 2-4 nucleotides in length. By examining several different VNTRs or STRs from the same individual, investigators obtain a unique DNA profile for that individual which is unlike that of any other person (except for identical twins).

In this simulation experiment, DNA was extracted from samples obtained from the mother, child and two possible fathers. The objective is to analyze and match the DNA fragment patterns after agarose gel electrophoresis and determine if Father 1 or Father 2 is the biological parent of the child.

THIS EXPERIMENT DOES NOT CONTAIN HUMAN DNA.

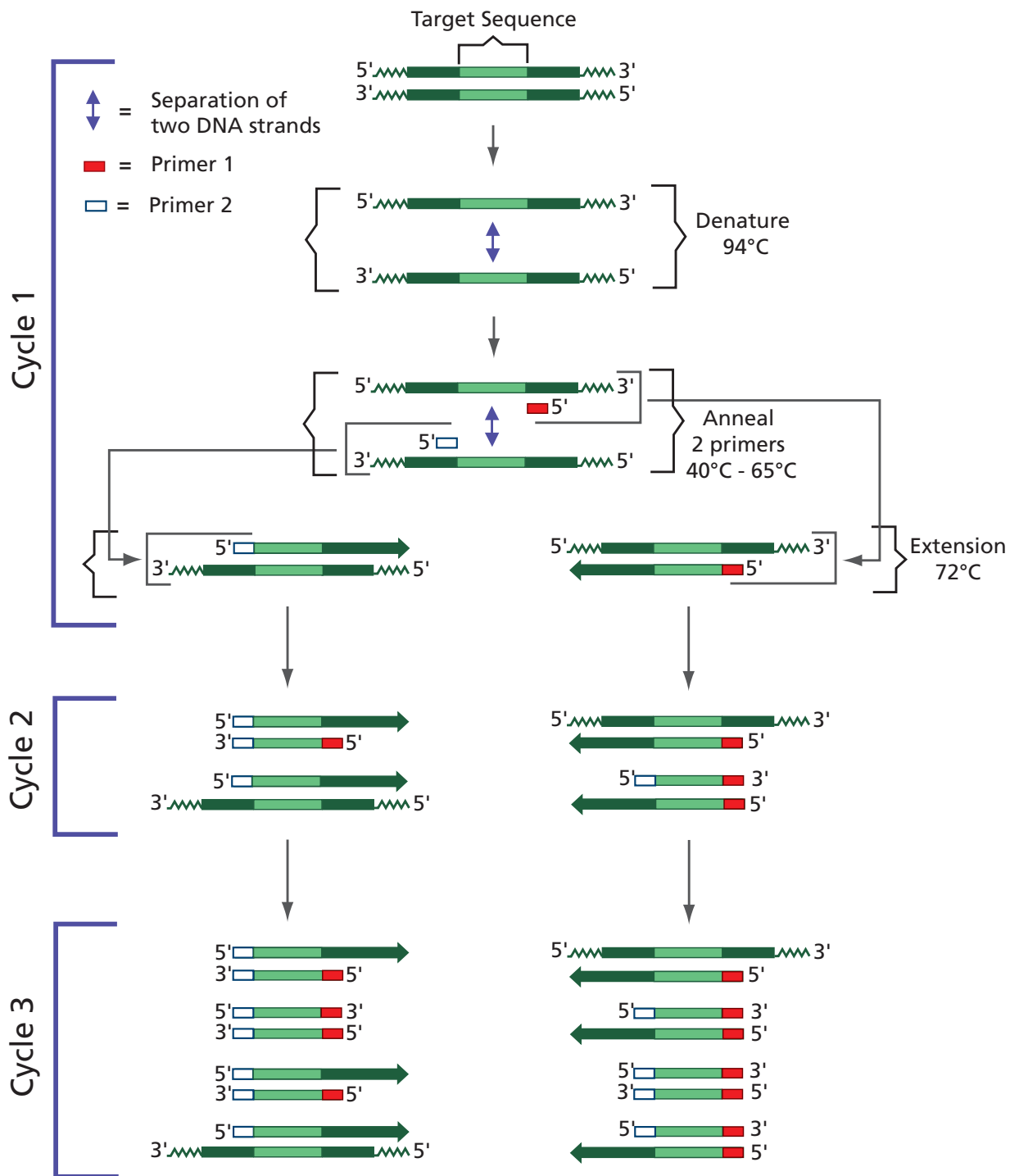


Figure 5:
DNA Amplification by the Polymerase
Chain Reaction

Experiment Overview

EXPERIMENT OBJECTIVE:

The objective of this experiment module is to introduce students to the use of DNA Fingerprinting in a hypothetical paternity determination.

LABORATORY SAFETY

1. Gloves and goggles should be worn routinely as good laboratory practice.
2. Exercise extreme caution when working with equipment that is used in conjunction with the heating and/or melting of reagents.
3. DO NOT MOUTH PIPET REAGENTS - USE PIPET PUMPS.
4. Exercise caution when using any electrical equipment in the laboratory.
5. Always wash hands thoroughly with soap and water after handling reagents or biological materials in the laboratory.



LABORATORY NOTEBOOKS:

Scientists document everything that happens during an experiment, including experimental conditions, thoughts and observations while conducting the experiment, and, of course, any data collected. Today, you'll be documenting your experiment in a laboratory notebook or on a separate worksheet.

Before starting the Experiment:

- Carefully read the introduction and the protocol. Use this information to form a hypothesis for this experiment.
- Predict the results of your experiment.

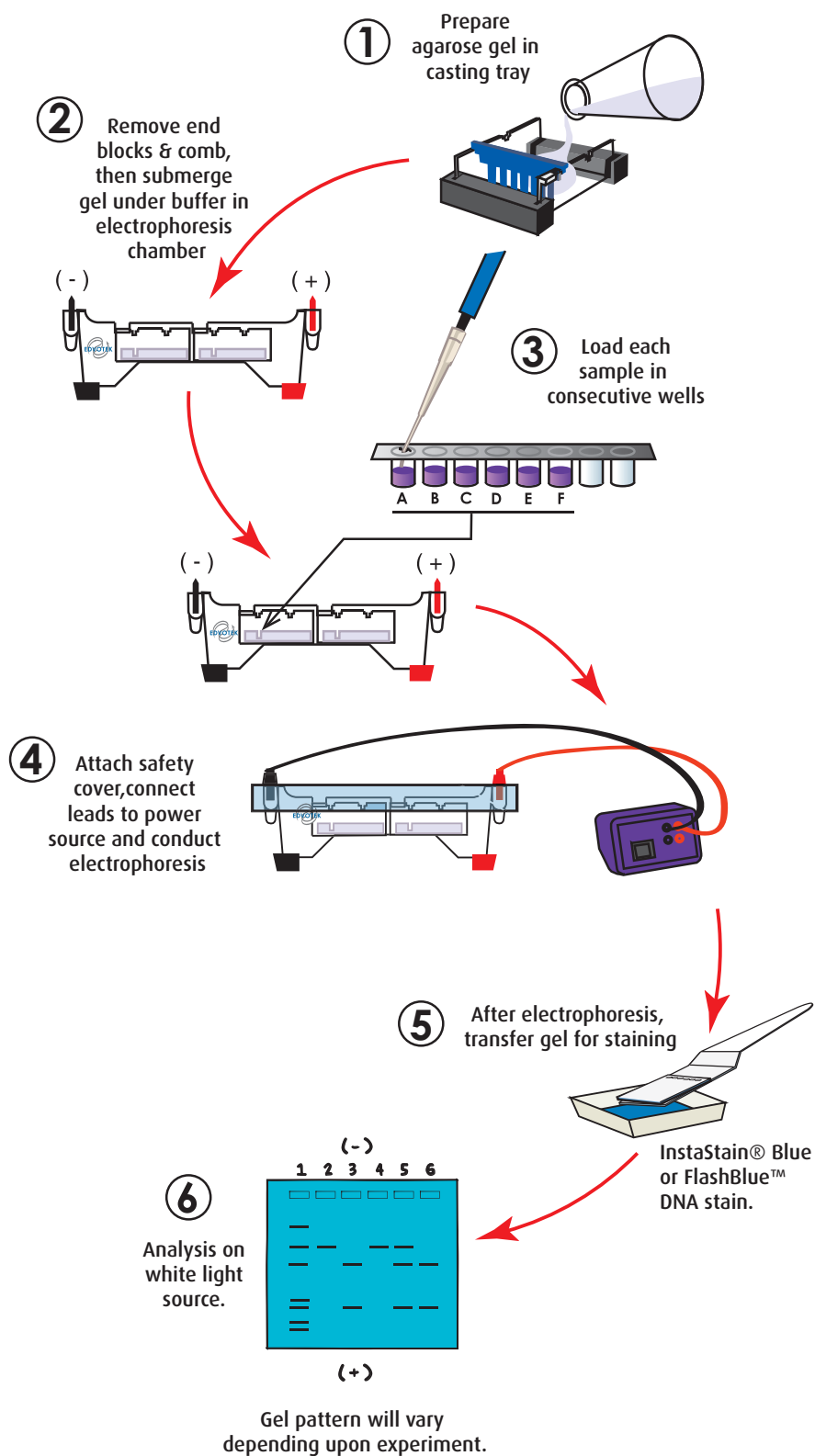
During the Experiment:

- Record your observations.

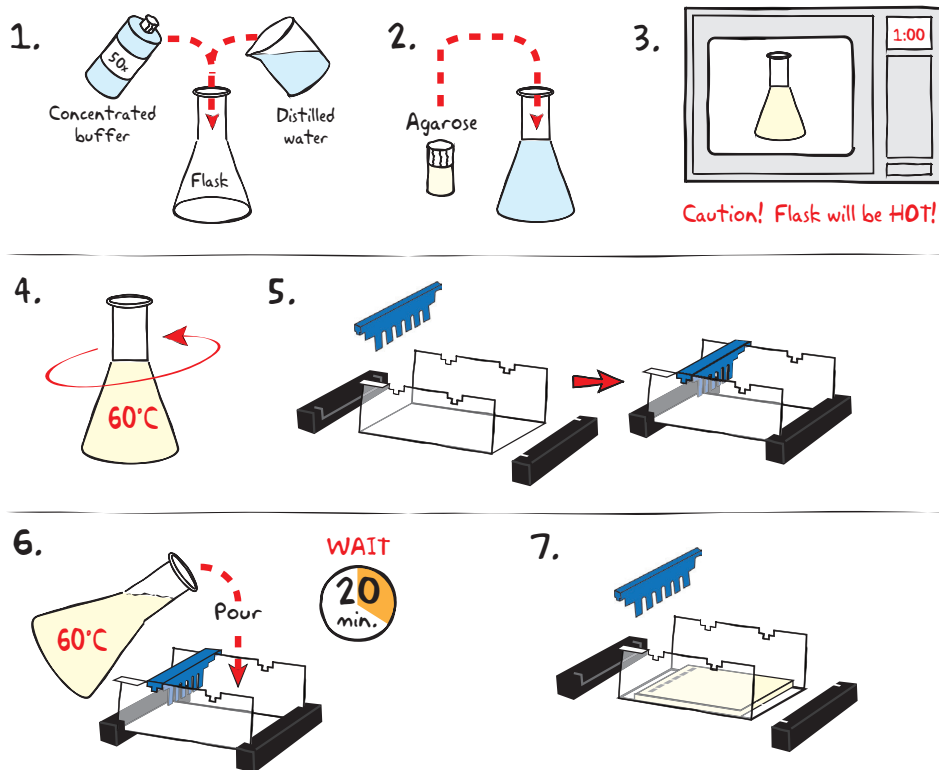
After the Experiment:

- Interpret the results – does your data support or contradict your hypothesis?
- If you repeated this experiment, what would you change? Revise your hypothesis to reflect this change.

Experiment Overview



Module I: Agarose Gel Electrophoresis



IMPORTANT:

If you are unfamiliar with agarose gel prep and electrophoresis, detailed instructions and helpful resources are available at www.edvotek.com



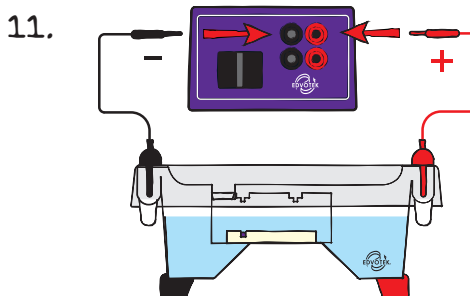
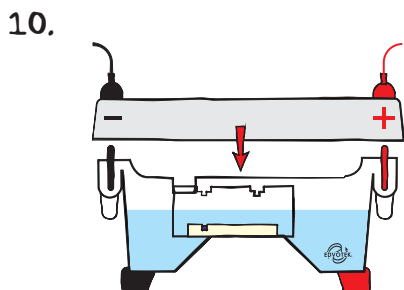
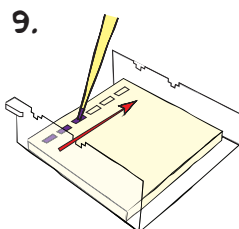
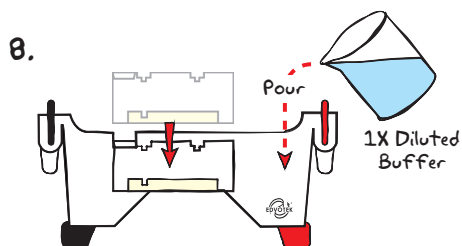
Wear gloves and safety goggles

CASTING THE AGAROSE GEL

- DILUTE** concentrated 50X Electrophoresis buffer with distilled water (refer to Table A for correct volumes depending on the size of your gel casting tray).
- MIX** agarose powder with buffer solution in a 250 ml flask (refer to Table A).
- DISSOLVE** agarose powder by boiling the solution. **MICROWAVE** the solution on high for 1 minute. Carefully **REMOVE** the flask from the microwave and **MIX** by swirling the flask. Continue to **HEAT** the solution in 15-second bursts until the agarose is completely dissolved (the solution should be clear like water).
- COOL** agarose to 60° C with careful swirling to promote even dissipation of heat.
- While agarose is cooling, **SEAL** the ends of the gel-casting tray with the rubber end caps. **PLACE** the well template (comb) in the appropriate notch.
- POUR** the cooled agarose solution into the prepared gel-casting tray. The gel should thoroughly solidify within 20 minutes. The gel will stiffen and become less transparent as it solidifies.
- REMOVE** end caps and comb. Take particular care when removing the comb to prevent damage to the wells.

Table A	Individual 0.8% UltraSpec-Agarose™ Gel			
	Size of Gel Casting tray	Concentrated Buffer (50x)	Distilled Water + Agarose	TOTAL Volume
	7 x 7 cm	0.6 ml	29.4 ml	30 ml
	7 x 10 cm	1.0 ml	49.0 ml	50 ml
	7 x 14 cm	1.2 ml	58.8 ml	60 ml

Module I: Agarose Gel Electrophoresis



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- Easier band measurements
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Wear gloves
and safety goggles

REMINDER:

Before loading the samples, make sure the gel is properly oriented in the apparatus chamber.

RUNNING THE GEL

- PLACE** the gel (still on the tray) into the electrophoresis chamber. **COVER** the gel with 1X Electrophoresis Buffer (See Table B for recommended volumes). The gel should be completely submerged.
- PUNCTURE** the foil overlay of the QuickStrip™ with a pipet tip. **LOAD** the entire sample (35 µl) into the well in the order indicated by Table 1, at right.
- PLACE** safety cover on the unit. **CHECK** that the gel is properly oriented. Remember, the DNA samples will migrate toward the positive (red) electrode.
- CONNECT** leads to the power source and **PERFORM** electrophoresis (See Table C for time and voltage guidelines). Allow the tracking dye to migrate at least 3.5 cm from the wells.
- After electrophoresis is complete, **REMOVE** the gel and casting tray from the electrophoresis chamber and proceed to instructions for **STAINING** the agarose gel.

Table 1: Gel Loading

Lane	Tube	Sample
1	Tube A	Standard DNA Marker
2	Tube B	Mother DNA cut with Enzyme
3	Tube C	Child DNA cut with Enzyme
4	Tube D	Father 1 DNA cut with Enzyme
5	Tube E	Father 2 DNA cut with Enzyme

Table B

1x Electrophoresis Buffer (Chamber Buffer)

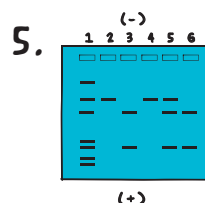
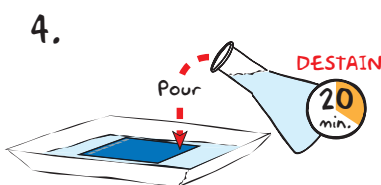
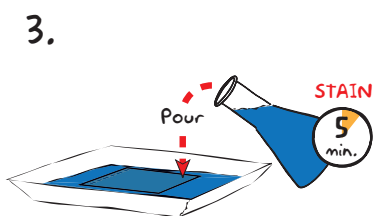
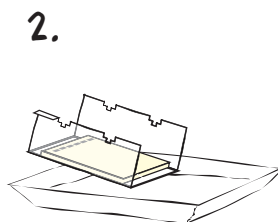
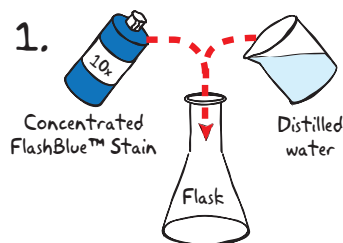
EDVOTEK Model #	Total Volume Required	50x Conc. Buffer	Dilution + Distilled Water
M6+ & M12 (new)	300 ml	6 ml	294 ml
M12 (classic)	400 ml	8 ml	392 ml
M36	1000 ml	20 ml	980 ml

Table C

Time & Voltage Guidelines (0.8% Agarose Gel)

Volts	Electrophoresis Model		
	M6+ Min. / Max.	M12 (new) Min. / Max.	M12 (classic) & M36 Min. / Max.
150	15/20 min.	20/30 min.	25 / 35 min.
125	20/30 min.	30/35 min.	35 / 45 min.
75	35 / 45 min.	55/70 min.	60 / 90 min.

Module II-A: Staining Agarose Gels Using FlashBlue™

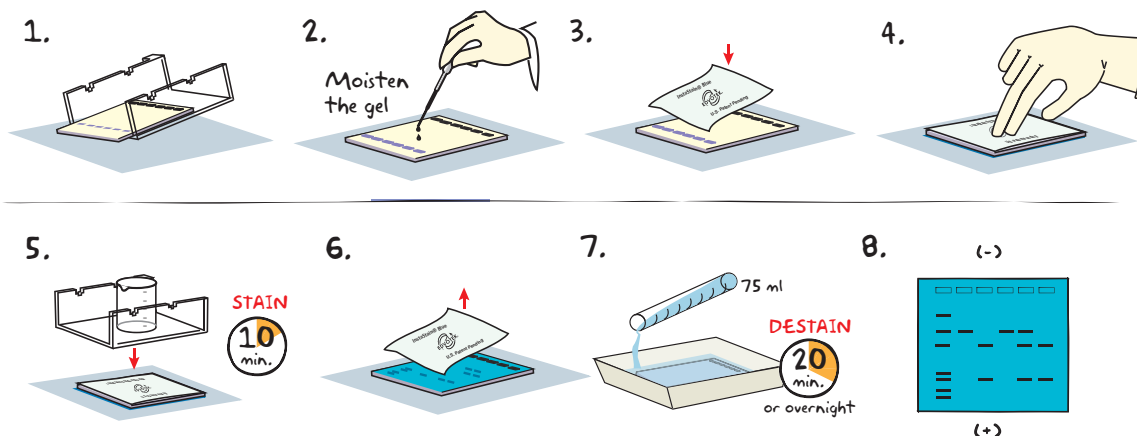


1. **DILUTE** 10 ml of 10x concentrated FlashBlue™ with 90 ml of water in a flask and **MIX** well.
2. **REMOVE** the agarose gel and casting tray from the electrophoresis chamber. **SLIDE** the gel off of the casting tray into a small, clean gel-staining tray.
3. **COVER** the gel with the 1x FlashBlue™ stain solution. **STAIN** the gel for 5 minutes. For best results, use an orbital shaker to gently agitate the gel while staining. **STAINING THE GEL FOR LONGER THAN 5 MINUTES WILL REQUIRE EXTRA DESTAINING TIME.**
4. **TRANSFER** the gel to a second small tray. **COVER** the gel with water. **DESTAIN** for at least 20 minutes with gentle shaking (longer periods will yield better results). Frequent changes of the water will accelerate destaining.
5. Carefully **REMOVE** the gel from the destaining liquid. **VISUALIZE** results using a white light visualization system. DNA will appear as dark blue bands on a light blue background.

ALTERNATIVE PROTOCOL:

1. **DILUTE** one ml of concentrated FlashBlue™ stain with 149 ml dH₂O.
2. **COVER** the gel with diluted FlashBlue™ stain.
3. **SOAK** the gel in the staining liquid for at least three hours. For best results, stain gels overnight.

Module II-B: Staining Agarose Gels Using InstaStain® Blue



1. Carefully **REMOVE** the agarose gel and casting tray from the electrophoresis chamber. **SLIDE** the gel off of the casting tray on to a piece of plastic wrap on a flat surface.
2. **MOISTEN** the gel with a few drops of electrophoresis buffer.
3. Wearing gloves, **PLACE** the blue side of the InstaStain® Blue card on the gel.
4. With a gloved hand, **REMOVE** air bubbles between the card and the gel by firmly running your fingers over the entire surface. Otherwise, those regions will not stain.
5. **PLACE** the casting tray on top of the gel/card stack. **PLACE** a small weight (i.e. an empty glass beaker) on top of the casting tray. This ensures that the InstaStain® Blue card is in direct contact with the gel surface. **STAIN** the gel for 10 minutes.
6. **REMOVE** the InstaStain® Blue card. If the color of the gel appears very light, reapply the InstaStain® Blue card to the gel for an additional five minutes.
7. **TRANSFER** the gel to a small, clean gel-staining tray. **COVER** the gel with about 75 mL of distilled water and **DESTAIN** for at least 20 minutes. For best results, use an orbital shaker to gently agitate the gel while staining. To accelerate destaining, warm the distilled water to 37°C and change it frequently.
8. Carefully **REMOVE** the gel from the destaining liquid. **VISUALIZE** results using a white light visualization system. DNA will appear as dark blue bands on a light blue background.



Wear gloves
and safety goggles

NOTE:
DO NOT STAIN
GELS IN THE
ELECTROPHORESIS
APPARATUS.

ALTERNATIVE PROTOCOL:

1. Carefully **SLIDE** the agarose gel from its casting tray into a small, clean tray containing about 75 ml of distilled/deionized water or used electrophoresis buffer. The gel should be completely submerged.
2. Gently **FLOAT** the InstaStain® Blue card(s) on top of the liquid with the stain (blue side) facing toward the gel. Each InstaStain® Blue card will stain 49 cm² of gel (7 x 7 cm).
3. **COVER** the tray with plastic wrap to prevent evaporation. **SOAK** the gel in the staining liquid for at least 3 hours. The gel can remain in the liquid overnight if necessary.
4. Carefully **REMOVE** the gel from the staining tray. **VISUALIZE** results using a white light visualization system. DNA will appear as dark blue bands on a light blue background.

Study Questions

1. Why do different individuals such as siblings have different restriction enzyme recognition sites?
2. What is the function of PCR primers used in DNA paternity analysis?
3. Why is there more than one single locus used in an actual paternity DNA test?
4. Why do we not use probes in this DNA paternity simulation and still obtain results?

Instructor's Guide

ADVANCE PREPARATION:

Preparation for:	What to do:	When?	Time Required:
Module I: Agarose Gel Electrophoresis	Prepare QuickStrips™	Up to one day before performing the experiment	45 min.
	Prepare diluted electrophoresis buffer		
	Prepare molten agarose and pour gels		
Module II: Staining Agarose Gels	Prepare staining components	The class period or overnight after the class period	10 min.

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Pre-Lab Preparations: Module I

AGAROSE GEL ELECTROPHORESIS

This experiment requires a 0.8% agarose gel per student group. You can choose whether to prepare the gels in advance or have the students prepare their own. Allow approximately 30-40 minutes for this procedure.

Individual Gel Preparation:

Each student group can be responsible for casting their own individual gel prior to conducting the experiment. See Module I in the Student's Experimental Procedure. Students will need 50x concentrated buffer, distilled water and agarose powder.

Batch Gel Preparation:

To save time, a larger quantity of agarose solution can be prepared for sharing by the class. Electrophoresis buffer can also be prepared in bulk. See Appendix B.

Preparing Gels in Advance:

Gels may be prepared ahead and stored for later use. Solidified gels can be stored under buffer in the refrigerator for up to 2 weeks.

Do not freeze gels at -20° C as freezing will destroy the gels.

Gels that have been removed from their trays for storage should be "anchored" back to the tray with a few drops of molten agarose before being placed into the tray. This will prevent the gels from sliding around in the trays and the chambers.

NOTE:

Accurate pipetting is critical for maximizing successful experiment results. EDVOTEK Series 100 experiments are designed for students who have had previous experience with micropipetting techniques and agarose gel electrophoresis.

If students are unfamiliar with using micropipets, we recommend performing Cat. #S-44, Micropipetting Basics or Cat. #S-43, DNA DuraGel™ prior to conducting this advanced level experiment.

FOR MODULE I Each Student Group should receive:

- 50x concentrated buffer
- Distilled Water
- UltraSpec-Agarose™
- QuickStrip™ Samples

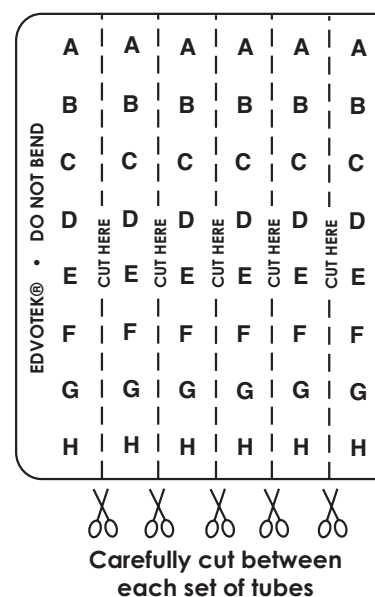
SAMPLES FORMAT: PREPARING THE QUICKSTRIPS™

QuickStrip™ tubes consist of a microtiter block covered with a protective overlay. Each well contains pre-aliquoted DNA.

Using sharp scissors, carefully divide the block of tubes into individual strips by cutting between the rows (see diagram at right). Take care not to damage the protective overlay while separating the samples.

Each lab group will receive one set of tubes. Before loading the gel, remind students to tap the tubes to collect the sample at the bottom of the tube.

If using SYBR® Safe or InstaStain® Ethidium Bromide for DNA visualization, each QuickStrip™ is shared by two groups. 18 µl of the DNA sample will be loaded into each well. Proceed to visualize the results as specified by the DNA stain literature.



Pre-Lab Preparations: Module II

MODULE II-A: STAINING WITH INSTASTAIN® BLUE

The easiest and most convenient DNA stain available is InstaStain® Blue. InstaStain® Blue does not require the formulation, storage and disposal of large volumes of liquid stain. Each InstaStain® Blue card contains a small amount of blue DNA stain. When the card is placed in water, the DNA stain is released. This solution simultaneously stains and destains the gel, providing uniform gel staining with minimal liquid waste and mess.

You can use a White Light Visualization System (Cat. #552) to visualize gels stained with InstaStain® Blue.

MODULE II-B: STAINING WITH FLASHBLUE™

FlashBlue™ stain is optimized to shorten the time required for both staining and de-staining steps. Agarose gels can be stained with diluted FlashBlue™ for 5 minutes and destained for only 20 minutes. For the best results, leave the gel in liquid overnight. This will allow the stained gel to “equilibrate” in the destaining solution, resulting in dark blue DNA bands contrasting against a uniformly light blue background. A white light box (Cat. #552) is recommended for visualizing gels stained with FlashBlue™.

- Stained gels may be stored in destaining liquid for several weeks with refrigeration, although the bands may fade with time. If this happens, re-stain the gel.
- Destained gels can be discarded in solid waste disposal. Destaining solutions can be disposed of down the drain.

MODULE II: PHOTODOCUMENTATION OF DNA (OPTIONAL)

Once gels are stained, you may wish to photograph your results. There are many different photodocumentation systems available, including digital systems that are interfaced directly with computers. Specific instructions will vary depending upon the type of photodocumentation system you are using.

**FOR MODULE II-A
Each Student Group
should receive:**

- 1 InstaStain® card per 7 x 7 cm gel

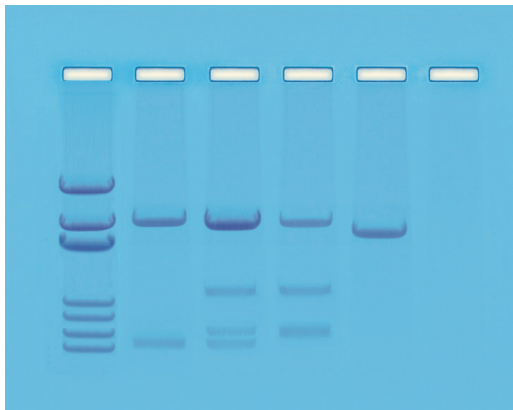


Wear gloves
and safety goggles

**FOR MODULE II-B
Each Student Group
should receive:**

- 10 ml 10X concentrated FlashBlue OR 100 mL 1x diluted FlashBlue
- Small plastic tray or weight boat
- Distilled or deionized water

Experiment Results and Analysis



Includes EDVOTEK's All-NEW DNA Standard Marker

- Better separation
- Easier band measurements
- No unused bands

NEW DNA Standard ladder sizes:

6751, 3652, 2827, 1568, 1118, 825, 630



In the idealized schematic, the relative positions of DNA fragments are shown but are not depicted to scale.

Lane	Tube	Sample	Molecular Weights (in bp)
1	A	DNA Standard Markers	-----
2	B	Mother DNA cut with Enzyme	3652, 630
3	C	Child DNA cut with Enzyme	3652, 1300, 700, 630
4	D	Father 1 DNA cut with Enzyme	3652, 1300, 700
5	E	Father 2 DNA cut with Enzyme	3000

Parentage (meaning maternity and paternity) can be determined from a child's DNA profile. By comparing the DNA profile of a mother and her child it is possible to identify DNA fragments in the child which are absent from the mother. Therefore, these polymorphisms have been inherited from the biological father. In this case, the two bands in the child's DNA profile that are not explained by the mother's profile are found in father #1.

**Please refer to the kit
insert for the Answers to
Study Questions**

Appendices

- A EDVOTEK® Troubleshooting Guide
- B Bulk Preparation of Electrophoresis Buffer and Agarose Gels
- C Data Analysis Using a Standard Curve

Safety Data Sheets can be found on our website: www.edvotek.com/safety-data-sheets

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Appendix A

EDVOTEK® Troubleshooting Guides

PROBLEM:	CAUSE:	ANSWER:
Bands are not visible on the gel.	The gel was not prepared properly.	Ensure that the electrophoresis buffer was correctly diluted.
	The gel was not stained properly.	Repeat staining.
	Malfunctioning electrophoresis unit or power source.	Contact the manufacturer of the electrophoresis unit or power source.
After staining the gel, the DNA bands are faint.	The gel was not stained for a sufficient period of time.	Repeat staining protocol.
	The background of gel is too dark.	Destain the gel for 5-10 minutes in distilled water.
DNA bands were not resolved.	Tracking dye should migrate at least 3.5 cm (if using a 7x7 cm tray), and at least 6 cm (if using a 7x14 cm tray) from the wells to ensure adequate separation.	Be sure to run the gel at least 6 cm before staining and visualizing the DNA (approximately one hour at 125 V).
DNA bands fade when gels are kept at 4°C.	DNA stained with FlashBlue™ may fade with time	Re-stain the gel with FlashBlue™
There is no separation between DNA bands, even though the tracking dye ran the appropriate distance.	The wrong percent gel was used for electrophoretic separation.	Be sure to prepare the correct percent agarose gel. For reference, the Ready-to-Load™ DNA samples should be analyzed using a 0.8% agarose gel.
There's not enough sample in my QuickStrip™.	The QuickStrip™ has dried out.	Add 40 µL water, gently pipet up and down to mix before loading.

Appendix B

Bulk Preparation of Electrophoresis Buffer and Agarose Gels

To save time, the electrophoresis buffer and agarose gel solution can be prepared in larger quantities for sharing by the class. Unused diluted buffer can be used at a later time and solidified agarose gel solution can be remelted.

Bulk Electrophoresis Buffer

Quantity (bulk) preparation for 3 liters of 1x electrophoresis buffer is outlined in Table D.

Table D Bulk Preparation of Electrophoresis Buffer			
50x Conc. Buffer	+	Distilled Water	Total Volume Required
60 ml		2,940 ml	3000 ml (3 L)

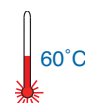
Batch Agarose Gels (0.8%)

For quantity (batch) preparation of 0.8% agarose gels, see Table E.

1. Use a 500 ml flask to prepare the diluted gel buffer.
2. Pour 3.0 grams of UltraSpec-Agarose™ into the prepared buffer. Swirl to disperse clumps.
3. With a marking pen, indicate the level of solution volume on the outside of the flask.
4. Heat the agarose solution as outlined previously for individual gel preparation. The heating time will require adjustment due to the larger total volume of gel buffer solution.
5. Cool the agarose solution to 60°C with swirling to promote even dissipation of heat. If evaporation has occurred, add distilled water to bring the solution up to the original volume as marked on the flask in step 3.
6. Dispense the required volume of cooled agarose solution for casting each gel. Measure 30 ml for a 7 x 7 cm tray, 50 ml for a 7 x 10 cm tray, and 60 ml for a 7 x 14 cm tray. **For this experiment, 7 x 7 cm gels are recommended.**
7. Allow the gel to completely solidify. It will become firm and cool to the touch after approximately 20 minutes. Then proceed with preparing the gel for electrophoresis.

Note:

The UltraSpec-Agarose™ kit component is usually labeled with the amount it contains. Please read the label carefully. If the amount of agarose is not specified or if the bottle's plastic seal has been broken, weigh the agarose to ensure you are using the correct amount.



60°C

Table E Batch Prep of 0.8% UltraSpec-Agarose™					
Amt of Agarose (g)	+	Concentrated Buffer (50X) (ml)	+	Distilled Water (ml)	Total Volume (ml)
3.0		7.5		382.5	390

Appendix C

Data Analysis Using a Standard Curve

Agarose gel electrophoresis separates biomolecules into discrete bands, each comprising molecules of the same size. How can these results be used to determine the lengths of different fragments? Remember, as the length of a biomolecule increases, the distance to which the molecule can migrate decreases because large molecules cannot pass through the channels in the gel with ease. Therefore, the migration rate is inversely proportional to the length of the molecules—more specifically, to the \log_{10} of molecule's length. To illustrate this, we ran a sample that contains bands of known lengths called a "standard". We will measure the distance that each of these bands traveled to create a graph, known as a "standard curve", which can then be used to extrapolate the size of unknown molecule(s).



Figure 6:
Measure distance migrated from the lower edge of the well to the lower edge of each band.

1. Measure and Record Migration Distances

Measure the distance traveled by each Standard DNA Fragment from the lower edge of the sample well to the lower end of each band. Record the distance in centimeters (to the nearest millimeter) in your notebook. Repeat this for each DNA fragment in the standard.

Measure and record the migration distances of each of the fragments in the unknown samples in the same way you measured the standard bands.

2. Generate a Standard Curve.

Because migration rate is inversely proportional to the \log_{10} of band length, plotting the data as a semi-log plot will produce a straight line and allow us to analyze an exponential range of fragment sizes. You will notice that the vertical axis of the semi-log plot appears atypical at first; the distance between numbers shrinks as the axis progresses from 1 to 9. This is because the axis represents a logarithmic scale. The first cycle on the y-axis corresponds to lengths from 100-1,000 base pairs, the second cycle measures 1,000-10,000 base pairs, and so on. To create a standard curve on the semi-log paper, plot the distance each Standard DNA fragment migrated on the x-axis (in mm) versus its size on the y-axis (in base pairs). Be sure to label the axes!

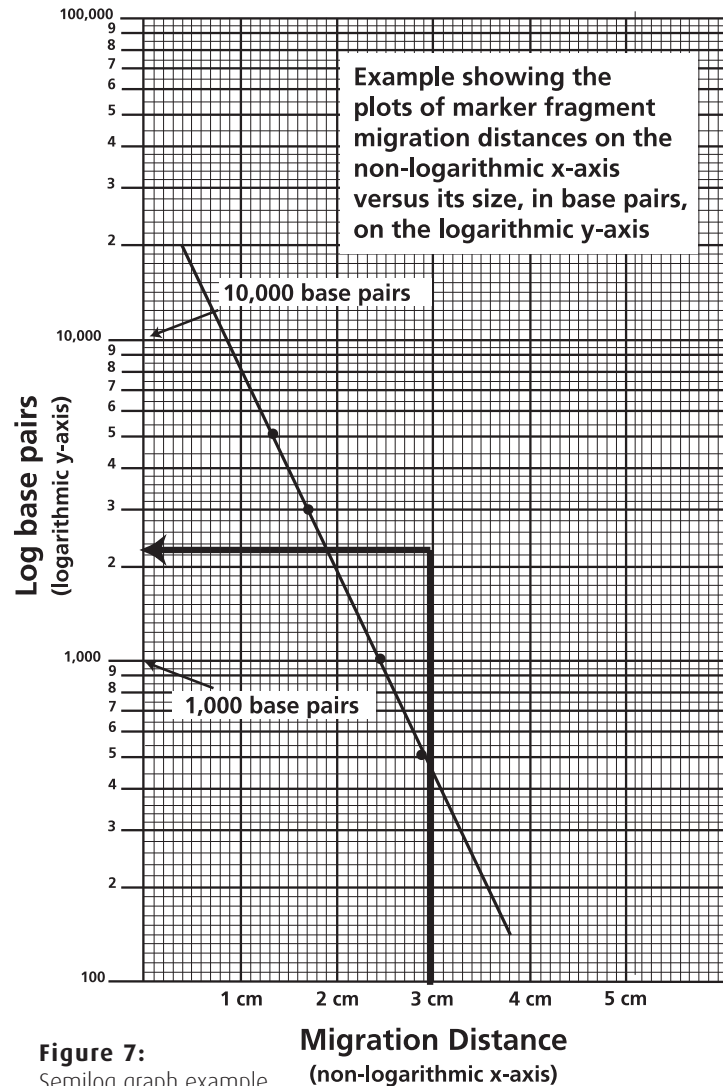


Figure 7:
Semilog graph example

Appendix C

Data Analysis Using a Standard Curve

After all the points have been plotted, use a ruler or a straight edge to draw the best straight line possible through the points. The line should have approximately equal numbers of points scattered on each side of the line. It is okay if the line runs through some points (see Figure 7 for an example).

3. Determine the length of each unknown fragment.

- Locate the migration distance of the unknown fragment on the x-axis of your semi-log graph. Draw a vertical line extending from that point until it intersects the line of your standard curve.
- From the point of intersection, draw a second line, this time horizontally, toward the y-axis. The value at which this line intersects the y-axis represents the approximate size of the fragment in base pairs (refer to Figure 7 for an example). Make note of this in your lab notebook.
- Repeat for each fragment in your unknown sample.

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Appendix C

