



Unit 3 Appendix A: MICROENVIRONMENT ARRAY INSTRUCTIONS

Instructions

This is a much simplified version of these signaling pathways, so remind your students that one signaling molecule may affect many genes (signal amplification). Producing one “red” protein will not cause a myeloid progenitor to immediately turn into an erythrocyte. In reality, many specific proteins must be expressed to influence the decision to make a red blood cell or a white blood cell. This simplified exercise demonstrates how a protein specific to one or another more specialized cell type is made from a common progenitor.

- Before students begin the activity, download program onto all student computers (or your computer if you are performing the demonstration) Link: [Another Plasmid Editor \(ApE\)](http://www.biology.utah.edu/jorgensen/wayned/ape/) (<http://www.biology.utah.edu/jorgensen/wayned/ape/>) Download for either PC or Mac by scrolling down on the page.
- Using this program, students can simulate the production of different types of mature cells from an adult stem cell depending on signals from the microenvironment.
- Tell students that they each have an identical copy of a short portion of the genome of a Common Myeloid Progenitor cell (CMPs). Whether daughter cells of CMPs become red blood cells or white blood cells depends on which genes are expressed (transcribed and translated into proteins that lead to different phenotypes.) This process can be dictated by factors in the extracellular environment, such as the introduction of Erythropoietin or Granulocyte-Colony Stimulating Factor.
 - Erythropoietin (Epo) and Granulocyte-Colony Stimulating Factor (G-CSF) are soluble factors that bind to their specific cell surface receptors, instigating a signaling cascade which ends with the binding of transcription factors to DNA, up- or down-regulating specific genes. For more about transcription factors and their role in hypoxia (low oxygen), as well as a list of known factors with links to pathway information, check out http://www.rndsystems.com/molecule_group.aspx?r=1&g=985.
 - Note: Depending on the depth of explanation you wish to provide your students, you can discuss transcription factors or say that Epo and G-CSF jumpstart the pathway leading to transcription of target genes.
- Give students a **raw DNA transcript** file which contains (in this order): promoter region 1, a start codon (ATG), the first gene’s DNA sequence including introns and exons, a stop codon (TAA), introns, promoter region 2, a start codon (ATG), the second DNA sequence including introns and exons, and another stop codon (TAA). This raw DNA transcript is found in the “From Genotype to Phenotypes Handout”, also in Unit Three Appendix A.



Assign students (or have them pick) either Epo or G-CSF (In Genotype to Phenotype Handout), which start signaling cascades leading to the expression of either gene 1 (Epo target) or gene 2 (G-CSF target). If students get Epo, start at promoter region 1. If G-CSF, start at promoter region 2.

Students will then transcribe into RNA the gene downstream of their promoter region (ATG....TAA).

They will then remove the introns from the RNA transcript to make mRNA (they will be told the sequences of the introns so they know what to splice out.)

From the mRNA transcript, students will use a codon chart to translate the mRNA bases into the primary amino acid sequence. The amino acid sequences will spell out either “RED” (target gene 1) or “WHITE” (target gene 2) depending on which gene was transcribed.

Use “From Genotype to Phenotype Handout in Appendix A for specific student instructions for the Microarray activity