

Skin Deep — Race & Disease

Secrets of the Sequence Video Series on the Life Sciences • Grades 9 — 12

Teaching materials developed by VCU Life Sciences

V i r g i n i a C o m m o n w e a l t h U n i v e r s i t y

Classroom Tested Lesson

Video Description

“Secrets of the Sequence,” Show 139, Episode 3

“Skin Deep? – Race and Disease” – approximately 10 minutes viewing time

What’s the connection between genes and race? It’s a loaded issue but one which scientists – and society – will have to deal with as genetic research advances. Many scientists believe geographical origins are more relevant to variations in human genomes than racial makeup. Nevertheless, researchers are finding genetic diseases that are more prevalent in particular racial groups. And drug research has shown that reactions to certain medications differ between racial groups.

Ward Television

Producer: Naomi Spinrad

Associate Producer: Mara Mlyn

Featuring: Sally Satel, Psychiatrist, American Enterprise Institute, Shomarka Keita, National Human Genome Center, Howard University, Dr. Neal Benowitz, Medicine, University of California-San Francisco

Lesson Author; Reviewers: Kathlyn Van Hoeck; Catherine Dahl, Dick Rezba

Trial Testing Teachers: Brooke Williams

National and State Science Standards of Learning

National Science Education Standards Connection

Content Standard C: Life Science

As a result of their activities in grades 9-12, all students should develop understanding of Molecular basis of heredity

- Biological evolution
- Behavior of organisms

Content Standard F: Science in Personal and Social Perspectives

As a result of their activities in grades 9-12, all students should develop understanding of

- Personal and community health

Selected State Science Standards Connections

Use <http://www.eduhound.com> (click on “Standards by State”) or a search engine to access additional state science standards.

Virginia

BIO.2 The student will investigate and understand the history of biological concepts. Key concepts include

b) scientific explanations of the development of organisms through time (biological evolution);

BIO.5 The student will investigate and understand life functions of archaeobacteria, monerans (eubacteria), protists, fungi, plants, and animals including humans. Key concepts include

- b) comparison of their metabolic activities;
- c) analyses of their responses to the environment;
- e) human health issues, human anatomy, body systems, and life functions; and

BIO.6 The student will investigate and understand common mechanisms of inheritance and protein synthesis. Key concepts include

- c) cell specialization;
- d) prediction of inheritance of traits based on the Mendelian laws of heredity;
- e) genetic variation (mutation, recombination, deletions, additions to DNA);
- h) use, limitations, and misuse of genetic information; and
- i) exploration of the impact of DNA technologies.

California

Grades Nine Through Twelve

Biology/Life Sciences

Science Content Standards

Genetics

4. Genes are a set of instructions encoded in the DNA sequence of each organism that specify the sequence of amino acids in proteins characteristic of that organism. As a basis for understanding this concept:

- c. Students know how mutations in the DNA sequence of a gene may or may not affect the expression of the gene or the sequence of amino acids in an encoded protein.

8. Evolution is the result of genetic changes that occur in constantly changing environments. As a basis for understanding this concept:

- d. Students know reproductive or geographic isolation affects speciation.

Overview

Humans are 99.9% genetically identical. However, within the remaining 0.1% are some of the genes responsible for the differences among the races. Some of these genes may also be associated with other traits that suggest some modifications or adjustments in medications. Researchers have shown that some races are more sensitive to certain drugs and these differences in response have led to the development of medicines that are tailored towards a specific race. Racially profiling a patient for medications is seen by some as controversial but clearly there are benefits to be had. Research has shown that just as some families share similar medical histories, so do certain races, which can be viewed as "bigger families". "Family history" has long been an important component of treating an individual.

Testing: A sample related multiple choice item from State Standardized Exams

A team of six scientists is conducting a study of the potential health hazards of a new chemical used in making house paints. One team member's results show the possibility of a slight hazard, although this does not show up in any of the studies performed by the other team members. The team decides to publish all the results and suggest the need for further investigation into the possibility of a health hazard. Why would they make this decision?

- a. The other studies are incorrect because they did not show evidence of a hazard.
- b. The team members all believe the results of the study showing a slight hazard.
- c. The group funding the research wanted to find evidence of a health hazard.
- d. Even if the studies did not all agree, it is important for the scientific community to have the complete results of the research.*

Source: Illinois PSAT Science Sample Test 2003

Video Preparation

Preview the video and make note of the locations at which you will later pause the video for discussion.

Before Viewing

1. Ask: What diseases are you aware of that are predominantly associated with a specific race or ethnicity? Then, ask: Why do you think these diseases tend to be concentrated in these groups? Students may know of these associated diseases; if not, mention the following:
 - *Sickle Cell Anemia- African-American*
 - *Tay Sachs – Jewish*
 - *Cystic Fibrosis – European Caucasian*
2. Inform students that African-Americans suffer from heart failure at twice the rates of other racial groups.
Ask: "What does that suggest for the treatment of African-Americans with regard to their hearts?"
Ask: "How might the knowledge of higher risk factors among certain groups be beneficial to members of those groups?"

During Viewing

1. **START** the video.
2. **PAUSE** the video (8.38 minutes into the video) after Dr. Satel says "...bits of genetic material to manifest as profound differences."

Review with the students the basic facts of race genetics:

- Only 0.1% of our genetic makeup is different among individuals and only a portion of these differences are associated with race
- Because there are approximately 3 billion nucleotides associated with the human genome, it appears that on average only about 3 million are related to differences between any two people.
- It only takes a change in 1 nucleotide to produce a disease as devastating as Tay Sachs or Sickle Cell Anemia.
- It is still unclear how many of the 0.1% differences in nucleotides are associated with race and ethnicity.

3. RESUME the video and play to the end.

After Viewing

1. The ultimate goal of researchers is to help physicians treat every patient as an individual. However, racial ancestry may suggest a specific drug or treatment based on a patient's membership in a particular group.

Ask: "What do you think are the pros and cons in designing drugs for a specific race?"

Pros:

- *Because it has already been determined that some races react differently to certain drugs; for example, African-Americans are more sensitive to Prozac and therefore suffer more unpleasant side effects than Caucasians. Clearly a doctor would not want to prescribe similar dosages of this drug to all individuals and should be willing to lower it immediately based on racial ancestry for the safety of the patient.*

Cons:

- *The government recognizes 63 racial combinations so it will likely be difficult to produce drugs with this degree of specificity. Unless all four grandparents were of the same race, racially influenced prescriptions might not have the expected and desired results.*
- *Racial profiling for whatever reasons raises concern for the repeat of past history that resulted in inhuman treatment of certain races. The video illustrates this point by contrasting the treatment of Japanese-Americans during WWII as compared to German-Americans.*

2. The video points out that Asians have a much lower degree of lung problems due to their slower metabolism. They take in about 35% less nicotine than Caucasians. African-Americans, however, have a normal rate of metabolism and take in about 30% more nicotine than Caucasians.

Ask: "If you were a young African-American considering taking up smoking, would you want to know that your risk of lung cancer was vastly greater than your Caucasian or Asian peers? "

Ask: "When differences in responses to drugs and treatments are known, should such differences be discussed in schools, which have been increasing politically sensitive in recent years?"

Ask: "What about children with parents from different races? How will their genetic makeup be different?"

(See the Secrets of the Sequence video on 'Quick Fix-Smoking in the Genes' at www.vcu.edu/lifesci/sosq for more information about differences in response to smoking by different races. A Trial Test teacher also suggested showing students the SOSq video, 'For Personal Use Only')

Teacher Notes for the Student Activity: SNP's - Race and Smoking

Materials needed

- Computers and Internet access for each pair or small group of students
- Printed copy of the Student Handout
- Digital copy of the Student Handout so students can copy and paste the sequences into the BLAST search

Introduction

If time allows and you have access to computers, you may wish to begin by having students do the activity on SNP's called *SNiPping Away at the Problem* on the Genetics Science Learning Center site at <http://gslc.genetics.utah.edu/units/pharma>

This will introduce them to the topic as well as provide them with an understanding of how the Human Genome Project could change the face of medicine. Otherwise you will need to go over the introduction in the Student Handout and carefully explain the meaning of a SNP and its significance.

SNP, pronounced "snip", is an acronym for Single Nucleotide Polymorphism. SNP's are single-nucleotide substitutions of one base for another. Each SNP location in the genome can have up to four versions: one for each nucleotide, A, C, G, and T. However, not all single-nucleotide changes are SNP's. To be classified as a SNP, two or more versions of a sequence must each be present in at least 1% of the general population.

Students working in pairs will take on the roles of two pharmacogenomics researchers looking for SNP's in populations. They will also want to know if an SNP might be associated with differences in biochemical responses to any of the drugs their company is developing.

In Part I students will first examine two sequences to see if there is a Single Nucleotide Polymorphism (SNP). A Trial Test teacher suggested that students need to be reminded that a nucleotide consists of three parts: Phosphate group, Sugar, and Nitrogen base. Some students may 'count' incorrectly by reading in codon form instead of nucleotides.

Then they will use an online bioinformatics tool called BLAST to determine if the SNP they found is part of a known gene and what that gene may be. BLAST is a database used daily by scientists to expand the results of their study. Students will have the opportunity to do exactly what scientists do when they use the BLAST database to search the human genome.

You will want to help the students with some of the scientific language that is found in the abstracts in PubMed during their BLAST search. These are written by scientists for their academic peers, but are available at any time to anyone. Expect students to be frustrated when attempting to read the abstract. Let them know this upfront and suggest that to non-scientists the abstract appears to be written in code. Ask: How much of the abstract can you de-code? What did you understand from reading the abstract? Suggest that they read it more than once to de-code more.

Alternately, you may just want students to conduct a BLAST search so they can see if a particular genetic sequence has been studied. After entering Sequence A or B, students will see that there have been numerous studies on this part of the human genome. Many of these studies are related to enzyme activity on nicotine.

Part I should take about 30 minutes and can probably be done right after viewing the video and the initial discussion. Part II will take another class period or more depending on the amount of discussion.

In Part II students will examine some recent data displayed as a graph, analyze the graph, and then discuss the pros and cons of developing drugs based on racial background.

Procedure:

1. If sufficient computers are available, students should work in pairs. If computer access is limited, students can work in groups of 3 – 4.
2. Distribute printed copies of the Student Handout to each student.
3. Examining the two sequences for SNP's could be done as a demonstration with the whole class on an overhead projector or with a computer and a projection system.
4. If you wish, discuss Part 1 before students begin Part 2 to ensure that they understand what they have learned thus far.
5. Emphasize that the BLAST search is an exciting opportunity for students to follow the exact same steps that scientists use in order to expand the results of their research on nucleotides.
6. Provide students with a digital version of the Student Handout so they can easily copy and paste the sequences into the BLAST search. They can, of course, type the sequences into the search box, but errors will result in delay and frustration.
7. Keep in mind that BLAST is a tool that is used daily by scientists all over the world. When students 'BLAST' their sequences, they will be put in a queue. It may take seconds to several minutes for their results to appear, depending on how busy the site is at the time.
8. Have students answer the questions in Part II with their lab partner or in small groups, or use the questions as the basis for a whole class discussion.

Question Answer Key

Part 1:

Student will examine these sequences and locate the SNP.

Sequence A: GGGGAGCGCCCAAGCAGCTCCGGCGCTTCTCCATCGCCACCCTGCGG

Sequence B: GGGGAGCGCCCAAGCAGCTCCAGCGCTTCTCCATCGCCACCCTGCGG

(Note: Do not use these sequences to copy and paste into BLAST; use the sequences in the student handout that do not have bolded and underlined letters)

At what number nucleotide of the sequence is the SNP located? _____22_____

After conducting a BLAST search and reading a suggested abstract, students are asked: What is the name of the gene associated with these sequences? _____

Homo sapiens cytochrome P450 or CYP2A6

Question Answer Key

Part 2:

1. Which ethnic groups have the gene for the highest levels of enzyme activity that break down nicotine? *Approximately 80% of African-Americans and Caucasians have normal CYP2A6 activity. Between 15 and 20% of both populations have 75% enzyme activity; 5% of each has 50% enzyme activity. Neither population shows members with no activity.*

2. Which ethnic group has genes for lowest levels of enzyme activity resulting in the need to smoke less in order to maintain higher nicotine levels in the blood? *Asians have the lowest levels of CYP2A6 activity. Chinese and Koreans have lower levels than Japanese.*
3. Which ethnic groups are at greatest risk of smoking more and becoming addicted? *African-Americans and Caucasians are at greatest risk for becoming addicted.*
4. If a drug could be developed that would reduce CYP2A6 enzyme activity, which ethnic groups would benefit most? *African-Americans and Caucasians would benefit the most because they have the highest frequency of normal activity. However, there are some Asians who also have normal activity.*
5. Your company thinks it can develop a drug that will inactivate CYP2A6 enzyme activity. The company hopes this medication can help certain groups of people stop smoking and lower their risk for developing lung cancer.
 - Is it right to develop drugs that would be useful to some ethnic groups and not others?
Answers will vary
 - What are the pros and cons of developing drugs based on racial background?
Answers will vary but may include:
 Pros: *The drug would be targeted to those it would benefit most. It would save time and money in medical costs.*
 Cons: *It could be a public relations nightmare for the company. There are still members of the Asian population that the drug would benefit, and there are some members of the African American and Caucasian populations that would not benefit.*

Some background for the BLAST search

Sequence A is CYP2A6*1, which is the wild-type.

Sequence B is CYP2A6*6, which shows decreased activity. The base change from C to A in Sequence B causes a change in the 128th amino acid in the protein from arginine to glutamine. The sequences that are given are shortened, and do not represent the entire gene sequence. (After all there is only a one letter change and the mRNA sequence that is listed in GenBank is 1751 bases long!)

There are numerous alleles of CYP2A6 and most cause decreased or no enzyme activity, but a few are the result of duplications and therefore these people would have increased enzyme activity.

Many of these alleles show markedly decreased activity in Asian populations. Persons with these alleles are referred to as PM, or poor metabolizers. Asians with these alleles either do not smoke, or if they do, they seem to need to smoke fewer cigarettes per day, resulting in a lower incidence of lung cancer in Asian populations. (See Additional Resources.)

In Part 2 of the Student Handout the graph shows that Asians have lowered CYP2A6 activity in comparison to both African Americans and Caucasians. The bars on the graph represent the percent of enzyme activity versus whether the individual is homozygous "normal" (white bars), heterozygous normal/reduced activity, heterozygous normal/no activity, and homozygous no activity. Notice that 80% of African Americans are homozygous normal for enzyme activity, which means that they may need to smoke more to keep their nicotine levels high. Also, notice that Asians are much more polymorphic in enzyme activity, and exhibit variety even within their 'race'. You might want to ask students if viewing all Asians as one ethnic group is therefore justified.

The discussion section in Part 2 could be optional, but the activity lets students answer for themselves whether they feel that 'racially profiling' in medicine is justified or not.

Further Exploration

1. Students who are interested in both biology and computers might be interested in learning more about bioinformatics, an emerging field of biological study. One resource is <http://www.vcu.edu/csbc/bioinformatics/index.html>
2. Depending on your students' interest and ability, you may wish to have them read one or both of the following articles to learn more about the opportunities and controversies associated with race-influenced medicine. If they have computer access at home, they could read them for homework and be prepared for a class discussion the next day.

"I Am a Racially Profiling Doctor", by Sally Satel,

<http://www.sallysatelmd.com/html/a-nytimes3.html>

"Why Do We Still Believe in Race?" by Kenan Malik,

http://www.kenanmalik.com/lectures/race_cheltenham.html

3. Assessment: After the class discussion, have the students write an essay defending their position on the topic. You could also include this as an essay question on a test.

Student Handout: SNP's - Race and Smoking

Name _____

Introduction

As a result of the Human Genome Project, we have learned that the human DNA sequence is 99.9% the same and that our genome contains an estimated 3 billion nucleotides. The 0.1% difference in 3 billion is 3 million, thus on average there is a nucleotide difference every 1000 bases between any two people. Most of these differences are in areas of the DNA that do not code for proteins, but some differences are found in coding sequences. Single-nucleotide substitutions of one base for another that are found in at least 1% of the general population are called SNP's. SNP is an acronym for Single Nucleotide Polymorphism. Each SNP location in the genome can have up to four versions - one for each nucleotide, A, C, G, and T. Changes found in less than 1% of the population are referred to as mutations.

We inherit our DNA from our parents, and they inherited theirs from their ancestors, and so on. Mutations are considered rare events, so the SNP's that are found tend to be inherited. Because populations of people traditionally lived and married within ethnic groups, particular SNP's became concentrated in those ethnic groups. Examples already referred to in the lesson are Sickle cell anemia, Tay-Sach's, and Cystic Fibrosis. However, not all SNP's cause overt genetic diseases. Some affect our biochemistry in more subtle ways and this activity will address an SNP that affects the way in which an individual responds to nicotine in cigarettes.

Procedure:

You and a partner will take on the roles of two pharmacogenomics researchers looking for SNP's in populations. You also want to know if an SNP might be associated with differences in biochemical responses to any of the drugs your company is developing.

In Part I you will first examine two sequences to see if there is a Single Nucleotide Polymorphism (SNP).

Then you will use an online bioinformatics tool called BLAST to determine if the SNP you found is part of a known gene and what that gene may be. BLAST is a database used daily by scientists to expand the results of their study. You will have the opportunity to do exactly what scientists do when they use the BLAST database to search the human genome.

In Part II you will examine some recent data, analyze a graph, and then discuss the pros and cons of developing drugs based on racial background.

Part 1

1. Look at the following 2 sequences:

Sequence A:

GGGGAGCGCCCAAGCAGCTCCGGCGCTTCTCCATCGCCACCCTGCGG

Sequence B:

GGGGAGCGCCCAAGCAGCTCCAGCGCTTCTCCATCGCCACCCTGCGG

2. Locate the Single Nucleotide Polymorphism (SNP) in each of the sequences and underline them.
3. At what number nucleotide of the sequence is the SNP located? _____

In order to determine if these sequences are associated with a known gene, you will use an online bioinformatics tool, called BLAST.

Background on BLAST: In 1988, the US government established the National Center for Biotechnology Information (NCBI) to be a national resource for molecular biology information. NCBI creates public databases of information, develops software for data analysis, and conducts research in computational biology. NCBI shares data with other international resources, updating its databases daily. The development of new computer programs to handle and compare all of this data became necessary and also a new field of biology called bioinformatics was created. One of the programs developed is called BLAST, or *Basic Local Alignment Sequence Tool*. The data you will be searching were entered into this online database by the scientists who collected it.

Follow the steps below to do the BLAST search just as a scientist would. **Please note that the Website layout will probably change over time and these specific directions may be different.**

1. Go to the NCBI home page at <http://www.ncbi.nlm.nih.gov/BLAST>. Click on the third option under Nucleotide in the upper part of the screen: *Nucleotide/nucleotide BLAST [blastn]* search. By choosing this option you will be comparing your nucleotide sequence to all the other nucleotide sequences in the database.
2. In the top portion of the new page is a box labeled 'Search'. Copy and paste Sequence A from your Word document into the Search box. Click on the BLAST! button.
3. The next screen should display, "*Your request has been successfully submitted and put into the Blast Queue*". This screen will also tell you approximately how much time it will take for your results to be ready.
4. Click on the 'Format' button for your results. You may have to wait a short while longer. Be patient! You are waiting your turn with every other scientist who is using the database service throughout the world!
5. When your results are ready, the 'results of BLAST' screen will appear. The screen presents reference information and then the results in graphical form with a series of horizontal colored bars. The color of the bar corresponds to the 'alignment score'. The alignment score is influenced by the length of the query sequence; the longer the query sequence, the higher the score can be. (You actually used a fairly short sequence). The color groups show the quality of the match in descending order, with the best-match group first.
6. Scroll down below the series of colored bars to see a list of the match sequences corresponding to the bars. You can see that the sequence you entered resulted in many matches. The first entry in the list corresponds to the first bar, and so on. At the right of each entry is an E value. This is the number of matches of this quality that could be expected by chance in a database the size of the one that was searched. They are ordered according to the best match. A score of 0.0 means that it matches exactly. The smaller the E score, the less likely it is that the match is a coincidence.
7. To learn more about how this sequence is related to nicotine, click on the entry coded as: **gi|20522239|ref|NM_000762.4** HINT: To find it quickly, scan the list looking for 'ref' in the middle of the entries. (It was a few down the list in August 2005.)

On this page next to the word, DEFINITION, the name of this gene is given. What is the name of this gene? _____

8. Scroll down a little further to see a list of publications associated with this gene. Each one begins with 'REFERENCE'. For each reference there is a brief 'REMARK' that provides a very brief summary of the study. If you scan these remarks, you will see several that deal with nicotine and smoking. Find the one with the number **15225612** next to 'PubMed'. Click on the number to see a more detailed abstract of a study dealing with nicotine levels. (This was reference # 8 in August 2005.)
9. The abstract of this paper begins by stating, "Cytochrome P450 (CYP) 2A6 metabolizes a number of drugs and a variety of procarcinogens." You will find reading this abstract very challenging because it was written for other scientists who are familiar with the terminology used.

Think of the abstract as a 'coded puzzle' and see how much of it you can understand. The abstract is easier to understand if you remember that CYP2A6 is 'the name' of the gene sequence you entered in the BLAST database. What are some things you 'decoded' from reading this abstract?

If you want more of a reading challenge, click on the Box labeled 'Full Text Article' to see the whole article. The box is located just above the abstract title.

10. If you repeat Steps 2 through 8 for Sequence B, find the reference with the number **15475735** next to 'PubMed'. Click on the number to see an abstract of a study of rate of nicotine metabolism. (This was reference # 7 in August 2005.)

From reading this abstract, what was this study about? Was this abstract a little easier to understand than the previous one (15225612)?

Part II

If you read the brief descriptions or read one or two of abstracts of the studies you found with your BLAST search, you know that your SNP is indeed associated with a gene that produces an enzyme that helps break down nicotine in the liver so that it can be eliminated in the urine. You may also have seen that there are many different versions of this gene and that some versions affect the rate at which nicotine is broken down. Nicotine binds to receptors in the brain and eventually causes the release of dopamine, a neurotransmitter that creates a sensation of pleasure. People who make less of this enzyme process nicotine at a slower rate. Therefore, they do not appear to need to smoke as much in order to keep the level of nicotine high in their blood. Here is some data that has been collected recently by researchers at the University of Toronto:

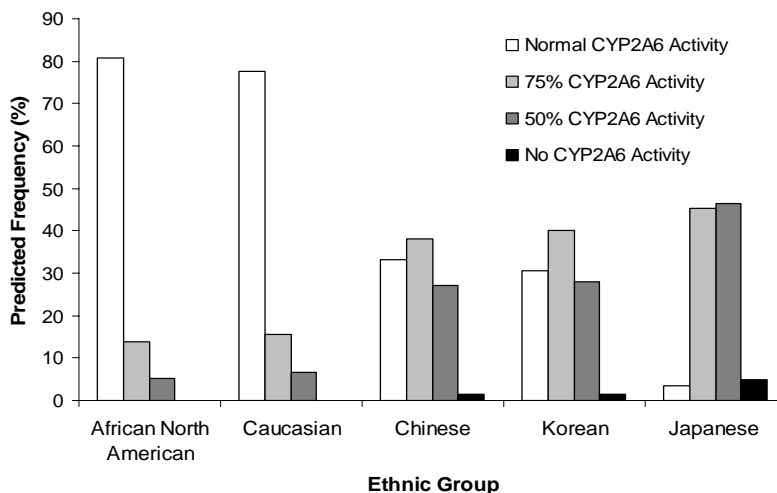


Figure 1. Frequencies are reported in percentage by predicted activity. Genotype frequencies are calculated based on average allele frequencies and Hardy-Weinberg estimations of homozygotes and heterozygotes. No CYP2A6 activity: homozygous for *CYP2A6**2, *CYP2A6**4 and *CYP2A6**5 inactive alleles. 50% CYP2A6 activity: heterozygous for inactive alleles and homozygous for any combination of reduced activity alleles *CYP2A6**6, *CYP2A6**7, *CYP2A6**9, *CYP2A6**10 and *CYP2A6**12. 75% CYP2A6 activity: heterozygous for reduced activity alleles. Normal CYP2A6 activity: remaining percentage of those not included in any other group. The African North American ethnic group includes both African-Americans and African-Canadians. (Unpublished data: **Implications of *CYP2A6* Genetic Variation for Smoking Behaviours and Nicotine Dependence**, Viba Malaiyandi, BSc,¹ Edward M. Sellers, M.D., Ph.D,^{1,2} and Rachel F. Tyndale, PhD,^{1,3}. In Press. Used with permission.)

Examine the graph and answer the following:

1. Which ethnic groups have the gene for the highest levels of enzyme activity that break down nicotine?
2. Which ethnic group has genes for lowest levels of enzyme activity resulting in the need to smoke less in order to maintain higher nicotine levels in the blood?
3. Which ethnic groups are at greatest risk of smoking more and becoming addicted?
4. If a drug could be developed that would reduce CYP2A6 enzyme activity, which ethnic groups would benefit most?
5. Your company thinks it can develop a drug that will inactivate CYP2A6 enzyme activity. The company hopes this medication can help certain groups of people stop smoking and lower their risk for developing lung cancer.
 - Is it right to develop drugs that would be useful to some ethnic groups and not others?

- What are the pros and cons of developing drugs based on racial background?

Further Exploration

If you are interested in both biology and computers, you might be interested in learning more about bioinformatics, an emerging field of biological study. One resource is

<http://www.vcu.edu/csbc/bioinformatics/index.html>

To learn more about the opportunities and controversies associated with race-influenced medicine, read the following online articles:

I Am a Racially Profiling Doctor, by Sally Satel, <http://www.sallysatelmd.com/html/a-nytimes3.html>

Why Do We Still Believe in Race? by Kenan Malik,

http://www.kenanmalik.com/lectures/race_cheltenham.html

Additional Resources

Because Web sites frequently change, some of these resources may no longer be available. Use a search engine and related key words to generate new Web sites.

CYP2A6 and Smoking Behavior

Nicotine metabolism shows ethnic bias <http://www.sciencenews.org/articles/20020119/fob6.asp>

Race and the Clinic: Good Science? <http://www.annieappleseedproject.org/racclingoods.html>

Genetic Polymorphisms in the Cytochrome P450 2A6 (CYP2A6) Gene: Implications for Interindividual Differences in Nicotine Metabolism <http://dmd.aspetjournals.org/cgi/content/full/29/2/91>

CYP2A6 Allele Nomenclature <http://www.imm.ki.se/CYPalleles/cyp2a6.htm>

Decreasing smoking behaviour and risk through CYP2A6 inhibition.

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=pubmed&dopt=Abstract&list_uids=12818518

CDC Genomics and Disease Prevention Search engine (search under CYP2A6-many hits!)

<http://www2a.cdc.gov/genomics/GDPQueryTool/>

Blood Pressure and African Americans

Nitromed website: <http://www.nitromed.com/BiDil.shtml>

Pharmacogenomics

<http://science.bio.org/>

<http://www.wellcome.ac.uk/en/genome/index.html>

Articles

Bamshad, Michael and Olson, Steve. The Genetics of Race. Scientific American, November 2003, p. 81-85.

Genomic Revolution

The website to the governmentally-funded Human Genome Project, with links about genomics, the history of the project, and more:

http://www.ornl.gov/sci/techresources/Human_Genome/education/education.shtml

Secrets of the Sequence Videos and Lessons

This video and 49 others with their accompanying lessons are available *at no charge* from

www.vcu.edu/lifesci/sosg

