TEACHING THE GENOME GENERATION™

The Jackson Laboratory

Leading the search for tomorrow's cures

CURRICULUM OVERVIEW

TEACHING THE GENOME GENERATION

This document will introduce you to *Teaching the Genome Generation*™ (*TtGG*) and help you determine which components best fit your curriculum needs. If you have any questions or wish to implement *TtGG*, contact *ttgg@jax.org*

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PROGRAM OVERVIEW AND LEARNING GOALS

Teaching the Genome Generation (*TtGG*) was designed to provide high school teachers the content knowledge, teaching strategies, and resources needed to enhance student learning in genomics and personalized medicine. This course will provide instruction in molecular genetics, use of bioinformatics tools, and discussion of the ethics of genetics research. Teachers will develop lessons designed for their unique school environment and resources. Through the *TtGG* community, teachers will have access to additional resources and expert assistance during the academic year.

The program is divided into three major branches, which should be taught in an integrated fashion, not as isolated units. These topics are: 1) the ethics involved in DNA testing (both in the classroom and in the community), 2) the methods involved in isolating, amplifying and detecting DNA, and 3) the bioinformatic methods utilized in analyzing DNA, RNA or amino acid sequences. An overview of each of these is provided in this handbook. Additionally, *TtGG* lab exercises utilize human genes, rather than bacteria or other animals, which connects students to the material presented and allows them take ownership of the results.

By providing laboratory, bioethics and bioinformatics professional development, participating teachers will increase their ability to teach complex concepts of genomics and bioethics to students. Consequently, students exposed to the *TtGG* content, will demonstrate an enhanced understanding of genomics content and will be more likely to have positive attitudes towards and participate in future STEM courses.

LEARNING GOALS

After teachers complete the *TtGG* program, they will be able to:

1. Perform modern laboratory techniques and properly use laboratory equipment.
2. Interpret DNA gels and sequence data to infer genotype for several common human variants.
3. Teach the ethical concerns surrounding personalized medicine, including informed consent.

Student learning goals are identified at the beginning of each Protocol.

Program Acknowledgments

This program was designed and is maintained by the *TtGG* Team at The Jackson Laboratory, including Dr. Charlie Wray, Michael McKernan, Dr. Kelly LaRue, Dr. Sarah Wojiski, and Alison Kieffer, MBA. These protocols were modified for classroom use by Barbara Farrell, formerly of North Yarmouth Academy.

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INTRODUCTION TO PERSONALIZED MEDICINE

Medicine as we know it is undergoing a drastic revolution due to the promise of the emerging field of genomics. Through analysis of large DNA sequence databases, scientists are realizing the extent of genetic variation among humans and how those variants can affect an individual's health and their response to treatment. Medicine is no longer one size fits all; it's personal. Patients and their doctors can elect to submit samples for genetic tests (which would return results based on a single gene) or genomic tests (in which a panel of genes or a whole genome can be sequenced). These results can help guide patient lifestyle for disease prevention or direct treatment for alleviation of disease.

One such gene of medical importance is CYP2C19, a gene involved in drug metabolism, and is available for study through *TtGG*. Variants in this gene can cause slow metabolism or accumulation of toxic metabolites. Armed with this kind of information, patients and their doctors are empowered to make informed decisions concerning pharmaceutical treatment. This could save valuable time in disease recovery and money, not only in the medical industry, but from the patient's pocket.

Through *TtGG*, teachers and their students will gain experience in the process of isolating DNA, amplification of gene regions and analysis of genotype through restriction enzyme digestion, gel electrophoresis and DNA sequence analysis.

ETHICAL CONSIDERATIONS

The use of humans or human samples in research has always been a point of debate and scientists have learned much about the ethical implications of doing so throughout the long history of biological research. Today, there are many regulations that researchers must follow, including protecting the privacy of the human subject. DNA sequence and genotype falls into that category since it inherently carries the information that describes who an individual is. No other human who has ever lived on the face of this earth carries the same DNA sequence as you (unless you have an identical twin). The unique genetic signature of the individual therefore must be protected from broad dissemination and misuse. Individuals can elect to have their genetic information distributed throughout the research community, but they must provide informed consent, a written document outlining all intended future use of the human sample. Through *TtGG*, teachers and students will explore ethical issues by engaging in classroom discussion (supplemented by pgED lesson plans) about the handling of their personal samples.

The *TtGG* PROTOCOL 1: DNA EXTRACTION uses saliva and cheek cells therein as a source for extracting purified human DNA. In order to maintain anonymity and protect the personal information of students providing a DNA sample, the donation must be voluntary.

STEPPING INTO BIOINFORMATICS

Advancement in DNA sequencing technologies has not only made the process faster, but has increased the number of samples that can be processed in a day. The volume of DNA sequences generated for even a single human genome would be impossible to organize, sort and annotate manually. Therefore, computational methods have been employed to do the hard labor.

TtGG provides two in-class bioinformatics exercises as a foundational experience in analyzing their sequence data. The first is designed to introduce students to the NCBI (National Center for Biotechnology Information) database by exploring example of known diseases. The second activity provides further experience in utilizing NCBI BLAST (Basic Local Alignment Search Tool) for sequence identification and comparison as well as inter-species comparisons of DNA and amino acids using EBI (European Bioinformatics Institute) ClustalW2.

INVALUABLE LABORATORY EXPERIENCE

The process of experimentation and performance of laboratory skills is vital for all students, whether they continue in the sciences or simply act as advocate for their own health. Knowledge and understanding of scientific practices grounds the discipline in reality rather than seeming like magic (as seen on many television programs). The following six protocols were designed as a series of experiments so students can follow the process from DNA collection to DNA sequencing.

Target gene options

TAS2R38	Three missense mutations in coding sequence
CYP2C19	Creation of aberrant splice site resulting in frameshift
ACTN3	Nonsense mutation, premature stop codon
ACE	Insertion mutation of Alu repeat within intron
OXTR	Silent mutation within intron

PROTOCOL 1: DNA EXTRACTION (all genes)

This experiment is designed to give students the opportunity to collect human samples and complete the steps needed to extract the DNA from the cells collected. Instead of this lengthy protocol you can opt for PROTOCOL 1b: QUICK DNA, a 20 minute heat-based DNA isolati. User beware the QUICK DNA sample is dirtier than the long method.

Skills learned: DNA collection and extraction, micropipetting and centrifugation.

Protocol Structure

STEP 1	8 minute video
	Break point if needed
STEPS 2-8	20 minutes
	Break point if needed
STEP 9	90 minutes minimum
	Incubation period
STEPS 10-30	60-70 minutes
	Break point if needed
STEPS 32-34	5 minutes

PROTOCOL 2a (ACE, ACTN3, TAS2R38 or OXTR) and 2b (CYP2C19): PCR

Protocols 2a and 2b are the same experiment; however, different PCR cocktails are needed to amplify the gene(s) of interest. Therefore, two separate Protocols were developed to avoid confusion. The experiment is designed to take DNA samples collected in PROTOCOL 1 and make enough copies to run future tests, including restriction digest, gel electrophoresis and ultimately DNA sequencing.

Skills learned: micropipetting, PCR cocktail preparation, use of thermal cycler, centrifugation.

Protocol Structure

STEPS 1-6	25 minutes
	Break point if needed
STEPS 8-12	25 minutes
	Break point if needed
STEP 13-18	Several hours
	Incubation period

PROTOCOL 3: RESTRICTION DIGEST (CYP2C19 or OXTR)

This experiment is designed to take DNA samples amplified in PROTOCOL 2 and perform a restriction enzyme digest. After the digest is complete, samples are subjected to gel electrophoresis (PROTOCOL 4) to determine if variants are present.

Skills learned: micropipetting and restriction enzyme digestion.

Protocol Structure

STEPS 1-6	15 minutes
	Break point if needed
STEPS 7-12	40 minutes

PROTOCOL 4: GEL ELECTROPHORESIS (all genes)

This experiment is designed to take DNA samples amplified in PROTOCOL 2 and perform gel electrophoresis to determine if samples are homozygous or heterozygous for gene variants. PROTOCOL 4 can also be completed with the products of PROTOCOL 3 to visualize restriction enzyme digestion of DNA.

Skills learned: micropipetting and agarose gel electrophoresis.

Protocol Structure

ALL STEPS	30 minutes

PROTOCOL 5: SEQUENCING PREP (ACTN3, TAS2R38 or CYP2C19)

This experiment is designed to take DNA samples amplified in PROTOCOL 2 and prepare them for sequencing. This protocol must be completed prior to sending DNA samples to The Jackson Laboratory for sequencing. DNA sequence analysis (PROTOCOL 6) should substantiate genotype of samples determined during gel electrophoresis (PROTOCOL 4).

Skills learned: micropipetting, enzyme digestion, sequencing preparation

Protocol Structure

STEPS 1-5	15 minutes
	Break point if needed
STEPS 6-11	20 minutes
	Incubation period
STEP 12-20	20 minutes

PROTOCOL 6: SEQUENCE ANALYSIS (ACTN3, TAS2R38 or CYP2C19)

This activity is designed to take the DNA sequence provided by The Jackson Laboratory and compare it to known sequences in databases, such as NCBI BLAST, to determine the gene identity and genotype of samples.

Skills learned: bioinformatics

Protocol Structure

STEPS 1-6 *or 1-14*	15 minutes
	Break point if needed
STEPS 7-9 *or 15-17*	35 minutes
	Break point if needed
STEP 10-13 *or 18-23*	30 minutes
	Break point if needed
STEP 14 *or 24*	35 minutes
	Break point if needed

INTEGRATING *TtGG* INTO YOUR CLASSROOM

The information presented in *TtGG* is critical for developing a scientifically literate population in the emerging genomics era. There are many ways in which this material can be disseminated to students including both science and non-science classes. The *TtGG* team is happy to help you modify the curriculum to fit your needs. Examples uses could include:

- Stand-alone Genomics course
- Parts of the protocols in advanced classes such as AP Biology

  NOTE: *TtGG* may be used to supplement or even replace *Investigation 3: Comparing DNA Sequences to Understand Evolutionary Relationships with BLAST* and *Investigation 9: Biotechnology: Restriction Enzyme Analysis of DNA* in the AP Biology curriculum. Many teachers may be reluctant to integrate the current genetics labs that they use with components of *TtGG*, however, the *TtGG* format establishes logical connections between biological methods rather than presenting them in discrete modules.
- Basic genetics/genomics content in introductory biology classes
- Ethics component in cross curricular classes:
  - Health class – personalized medicine
  - History – eugenics
  - Civics – politics, law, economics, voter information
  - DNA Forensics
- Bioinformatics in advanced classes with the help of:
  - Computer science teacher
  - Statistics or Mathematics teacher

TtGG Curriculum Alignment with High School Biology Standards

Lesson Plan	NGSS Alignment	AP Biology Alignment
Bioethics Lessons (pgEd)	Aligned to NGSS and Common Core within each lesson	3A3
Laboratory Protocol 1: DNA Extraction	HS-LS1-1, HS-LS3-1, HS-LS3-2	3A1, 3A3; SP 4.3
Laboratory Protocol 2: PCR amplification	HS-LS1-1, HS-LS3-1, HS-LS3-2	3A1, 3A3; SP 7.2
Laboratory Protocol 3: Restriction Digestion	HS-LS1-1, HS-LS3-1, HS-LS3-2	3A1; SP 7.2
Laboratory Protocol 4: Gel Electrophoresis	HS-LS1-1, HS-LS3-1, HS-LS3-2, HS-LS3-3	3A3, 3C1; SP 3.3, SP 5.1
Laboratory Protocol 5: Prep for Sequencing	HS-LS1-1, HS-LS3-1, HS-LS3-2	3A1; SP 7.2
Laboratory Protocol 6: Sequence Analysis	HS-LS1-1, HS-LS3-3, HS-LS4-1	3A1, 3A3, 3C1, 3C2; SP 3.3, SP 5.1
Bioinformatics Exercises	HS-LS1-1, HS-LS3-3, HS-LS4-1, HS-LS4-2	3A1, 3A3, 3C1, 3C2; SP 3.3, SP 5

EXTENSIONS TO LEARNING WITH *TtGG*

While this curriculum will satisfy the learning needs of many classrooms, perhaps you would like to make a curricular link to other subjects or maybe an introduction to genetic analysis will inspire some of your students to dig deeper. We recognize the need for continual innovation in our offerings. Therefore, we welcome the opportunity to aid you in the development of lesson plans for content and skills extension. Of course, lesson plans take time, so please contact us at *ttgg@jax.org* four weeks ahead of your intended date of execution.

If you buy your own molecular equipment, extension to the learning are endless! Several of our teachers have been able to purchase some or all of our suggested equipment through school budgets or grant opportunities.

You can utilize DNA amplification, gel electrophoresis, restriction digestion and sequencing to perform experiments in microbiology, antibiotic resistance, genetic engineering, population genetics, evolution, forensics and plant genetics, to name a few!

Finally, some advanced students may want to perform independent projects for the Maine State Science Fair, a graduation requirement or personal inquiry. Contact us at *ttgg@jax.org* to find out if we can support your budding scientists with projects related to the *TtGG* curriculum.

Human Genomics Topics

Unit 1: ACE (endurance) - IN/DEL
Essential Question: How do we determine the percentage of the class with each variant of the ACE (endurance) gene?

- Intro to genomics & bioinformatics
  - What is genomics and how is it different than genetics?
  - What are the fields of genomics research?
  - How do we access genomic information and models (bioinformatics)?
- Introduction to personalized genetics
  - How might new advances in personal genetics impact our lives, our medical decisions and society?
    - How would you decide whether or not to get your genome analyzed?
    - How might genome analysis change healthcare?
    - What are the benefits and concerns for you and other stakeholders?
- Ancestry tests
  - Are they accurate? What are the limitations?
  - What is admixture? How does this affect the accuracy of ancestry tests?
  - What are the ethical challenges? What are some solutions?
- Laboratory Techniques
  - Micropipetting
  - Crude DNA extraction
    - Benefits/drawbacks?
  - Polymerase Chain Reaction
    - Why do we need to use this technique? How do we carry out this technique?
  - Gel electrophoresis
    - How does this technique separate DNA fragments?

Unit 2: OXTR (the "love gene") - SNP with A variant restriction site for BamHI
Essential Question: How can more precise and technical methodologies be utilized to determine an accurate percentage of the class with each variant of OXTR ("love") gene if the two variants are the same number of base pairs in length?

- Genetic Variants
  - What are the different types of variants? How can each be tested for?
  - What factors affect the pathway from a gene to a disease?
  - If multiple gene variants can cause the same disorder, will treatments be the same? If not, how is the treatment determined?
- Bioinformatics
  - Utilizing case studies to become familiar with various gene databases and what each has to offer
  - What are the benefits & limitations of animal models & orthologues (comparable genes in other species)?
    - What are the ethical questions surrounding the use of animals for medical/genetic models?
- History of eugenics in the US

- How can we as a society avoid the mistakes of the past to take advantage of the promise of genetics
    - What is eugenics?
    - Why would improvements in healthcare that have the potential to save lives and reduce suffering through the use of genetic information cause people to worry about eugenics?
    - How did the eugenics movement in the United States impact people?
    - Why did some leaders think it would be beneficial to control who could have children and who could not?
        - Supreme Court case: Buck v. Bell
    - How can we avoid the mistakes of previous years so that society can benefit from advances in healthcare without the fear of unethical treatment?

- Reproductive Genetic Testing
    - How does genetic testing of embryos and fetuses offer hope to individuals wishing to have children, and what are some of the ethical implications of that testing?
        - Why have some people welcomed the option of genetic tests to learn about the genetic makeup of an embryo or fetus? What are the ethical issues surrounding the use of these tests?
        - What are the possibilities and limits of genetic testing to choose characteristics of offspring?
        - Are all of our traits determined by our genetic makeup?
        - What are potential barriers for accessing reproductive genetic technologies?
        - Do we need rules for the use of reproductive genetic technologies? If so, who should make the rules and how should they be enforced?
- Laboratory Techniques
    - Advanced DNA extraction
        - Benefits/drawbacks?
    - Polymerase Chain Reaction
    - Restriction Digestion
        - How do restriction enzymes work? How are they beneficial for genetic testing?
    - Gel Electrophoresis with Lonza Gels (most advanced/up to date way to carry out gel electrophoresis)

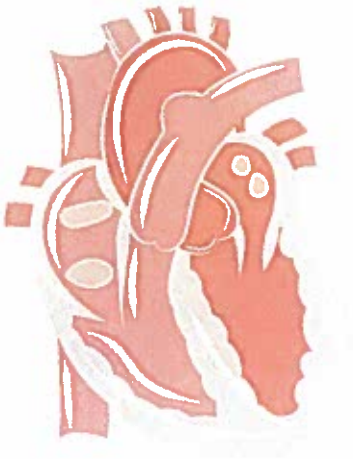
Unit 3: TAS2R38 (bitter taste gene) - SNP, needs to be sequenced by JAX
Essential Question: How can we determine the percentage of the class with each variant of TAS2R if the variants cannot be distinguished by one another via by gel electrophoresis? How can a full gene sequence be obtained and analyzed?

- Bioinformatics
    - How can we determine chromosomal loci?
    - How can we use genomic databases to give us information about evolution?
- Genome editing & CRISPR

- How might advances in our ability to change genomes impact individuals and society?
    - What is the difference between analyzing DNA and modifying DNA?
    - What are the newest techniques being developed? What is CRISPR?
    - How do we make decisions about whether or not and how to proceed with genome editing?
    - How can society ensure the promises of new genetic techniques are safe and equitably shared?
- DNA, Crime & Law Enforcement
    - How will advances in DNA technology impact individuals, law enforcement and society?
        - How is scientific progress affecting how DNA is used to solve crimes in the United States?
        - What are the benefits and dilemmas of collecting DNA from people when they are arrested, but before they have been charged with a crime?
        - As a society, how should we balance privacy rights with the rights of crime victims?
        - How can DNA evidence be used to free innocent people?
        - How are different communities (within and outside your own) affected by the policies and procedures around DNA collection and law enforcement?
- Laboratory Techniques
    - Advanced DNA extraction
    - Polymerase Chain Reaction
    - Gel Electrophoresis
        - What is the purpose of carrying out this step prior to sequencing if we know it will not distinguish between our variants?
    - Prep for Sequencing
    - Sequencing the gene (carried out by Jackson Labs, results sent to us)
    - Sequence Analysis via Chromas (PC) or 4Peaks (Mac)

ANGIOTENSIN I CONVERTING ENZYME (ACE)

ACE and Winning The Race



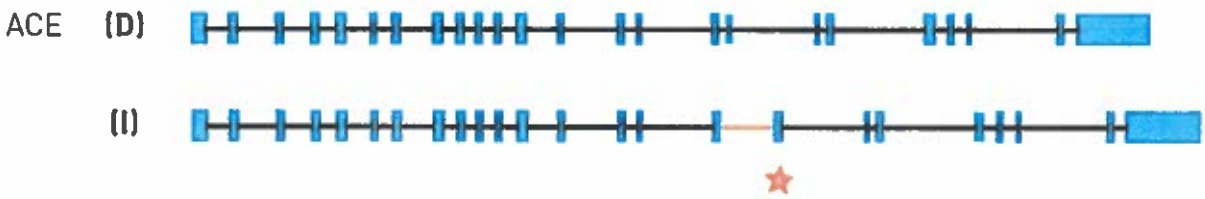
Blood Vessels

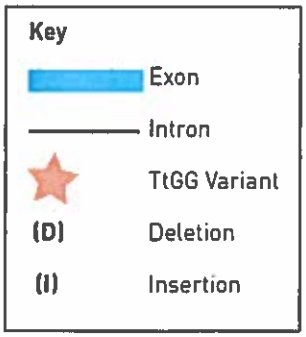
Biology Background

- The ACE gene produces the protein Angiotensin-converting enzyme (ACE), which functions as a protease that cuts other proteins.
- ACE plays a central role in the system that controls blood pressure by regulating the volume of fluids in the body.
- ACE is located within the cell membrane.
- ACE seems to be made in nearly all tissues of the human body, but appears to be most strongly expressed in capillaries (Human Protein Atlas).

Genomic Locus

The ACE gene is located on chromosome 17 of the human genome. The ACE gene is 21,310 base pairs in length and consists of 25 exons and 24 introns.

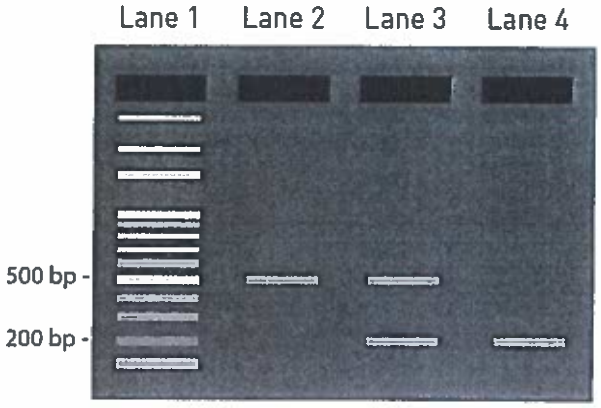




The TtGG Variant

- In this assay, you are studying one polymorphism, or variant in ACE called an INDEL (short for **In**sertion/**Del**etion) that is situated within intron 16 of the ACE gene.
- The common allele is considered the deletion (D), and the variant is an insertion of 287 base pair transposable element (I).
- Since this insertion is in the intron of the gene, it does not directly affect the amino acid sequence of the protein.

ACE Gel



Lane 1: DNA ladder
Lane 2: Homozygous I genotype, 500 bp
Lane 3: Heterozygous ID genotype, 200 bp, 500 bp
Lane 4: Homozygous G genotype, 200 bp

Population Genetics

- The insertion (I)/deletion (D) polymorphism located within intron 16 of the ACE gene (see star on page 1) has been studied for its contribution to physical endurance.
- This variant seems to reduce enzymatic activity, possibly due to a decrease in protein levels circulating in blood plasma.

Influence on Human Health

- The presence of the insertion allele has been associated with improved endurance performance in studies of mountaineers and soldiers.
- These effects are attributed to increased mechanical efficiency in muscles, possibly due to an increase in type 1 muscle fibers.
- Variants in ACE have also been associated with heart disease, but have not been proven to cause heart disease. Heart disease is a complex disorder that has many different genetic and environmental influences.
- Take this information with a grain of salt, as the presence of either ACE allele in no way causes the aforementioned physiological states.

Sources

-Online Mendelian Inheritance in Man (OMIM) http://www.omim.org/entry/106180#0001
-National Center for Biotechnology Information (NCBI) Gene http://www.ncbi.nlm.nih.gov/gene/1636
-Review on ACE and link to athletic performance: Puthucheary et al. The ACE Gene and Human Performance. Sports Medicine (2011)
-Human Protein Atlas
-UCSC Genome Browser

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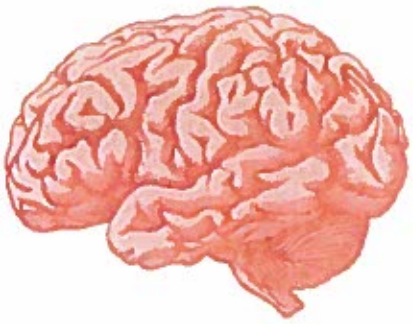
OXYTOCIN RECEPTOR (OXTR)

The Love Gene

Biology Background

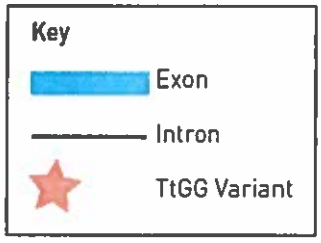
- The Oxytocin Receptor (OXTR) gene produces the OXTR protein, which functions as a receptor for the hormone and neurotransmitter oxytocin.
- The OXTR protein is an integral membrane protein of the family of G protein coupled receptors.
- OXTR has been demonstrated to exhibit its strongest effects in the brain (Human Protein Atlas).



Brain

Genomic Locus

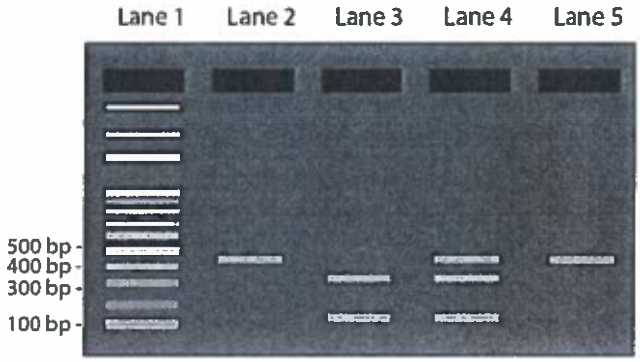
The OXTR gene is located on chromosome 3. It is 19,206 base pairs in length and consists of 4 exons and 3 introns.



The TtGG Variant

- In this assay you are examining a G>A polymorphism (SNP) in the third intron of the OXTR gene (see star).
- The A allele creates a site for the restriction enzyme BamHI to cut the DNA segment. Cut versus uncut DNA segments can be detected on a gel.

OXTR Gel



Lane 1: DNA ladder
Lane 2: Undigested sample, 435 bp
Lane 3: Homozygous A genotype, 120 bp, 310 bp
Lane 4: Heterozygous G/A genotype, 120 bp, 310 bp, 435 bp
Lane 5: Homozygous G genotype, 435 bp

Population Genetics

- The A allele has been associated with structural changes in the brain and was correlated with low scores in tests that measure social ability.
- In other studies, the G allele was linked to emotional sensitivity.
- Additionally, GG or GA genotypes were correlated with emotional support-seeking behaviors, whereas homozygous AA individuals had a tendency to become recluses during times of high emotional stress.

Influence on Human Health

- Variants such as these that are associated with complex, multifactorial traits such as behavior likely contribute only a small amount of effect, with many other genetic and environmental factors playing a significant role.
- Increased oxytocin levels (and its action through OXTR) are involved in many human behaviors including social bonding and fear reduction.
- Decreased levels of oxytocin or OTXR have been associated with disorders such as depression and autism.

Sources

-Online Mendelian Inheritance in Man (OMIM) http://www.omim.org/entry/167055
-National Center for Biotechnology Information (NCBI) Gene http://www.ncbi.nlm.nih.gov/gene/5021
-Review on OXTR and behavioral impacts see: Kumsta and Heinrichs Oxytocin, stress and social behavior: neurogenetics of the human oxytocin system. Current Opinion in Neurobiology. (2013)
-Human Protein Atlas

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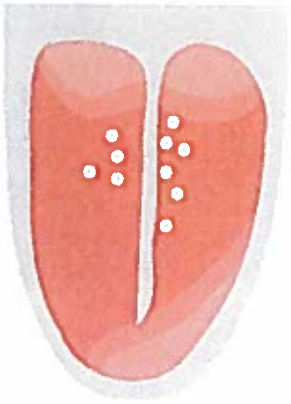
TASTE 2 RECEPTOR MEMBER 38(TAS2R38)

The Bitter Truth About Taste



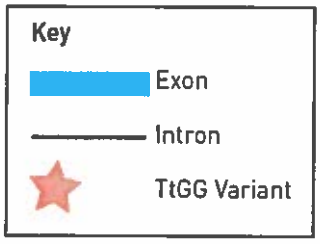
Tongue

Biology Background

- The Taste 2 Receptor Member 38 (TAS2R38) gene produces the TAS2R38 protein, which functions as a receptor to perceive a wide range of bitter compounds.
- Bitter taste receptors (TAS2Rs) are proteins found on taste cells (mucous epithelium cells) of the tongue (Human Protein Atlas).

Genomic Locus

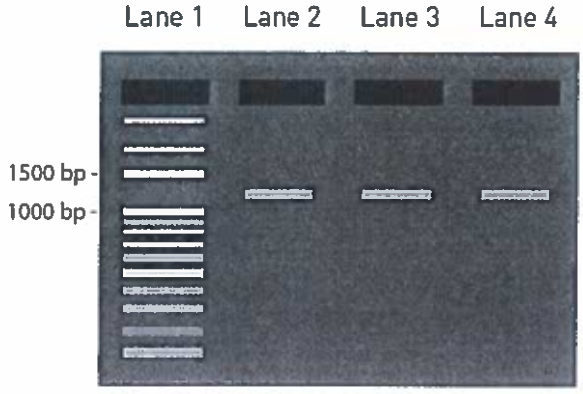
The TAS2R38 gene is located on chromosome 7. It is 1002 base pairs in length and consists of a single exon and no introns, encoding a 334 amino acid protein.



The TtGG Variants

- TAS2R38 is known to contain three non-synonymous single nucleotide polymorphisms (SNPs).
- The SNPs are located at base pairs 145, 785, and 886 (corresponding to amino acids 49, 262, and 296) and lead to eight possible genotypes in humans.

TAS2R38 Gel



Lane 1: DNA ladder
Lane 2: CCG genotype, 1200 bp
Lane 3: GTA genotype, 1200 bp
Lane 4: GCA genotype, 1200 bp

Please note that this variation can not be detected by size.

Population Genetics

- Current data suggest that the vast majority of the current human population is made up of two genotypes, CCG (which corresponds to the taster phenotype) or GTA (which corresponds to the non-taster phenotype).
- Different combinations of alleles can lead to other genotypes that correspond to intermediate-taster phenotypes.

Influence on Human Health

- The bitter taste receptor Taste 2 Receptor Member 38 (TAS2R38) is one of the most well studied taste receptors.
- It has been shown to be accountable for perception of compounds such as phenylthiocarbamide (PTC).

Sources

-Online Mendelian Inheritance in Man (OMIM) https://www.omim.org/entry/607751
-Review on TAS2R38 and its impacts on PTC receptivity see: Risso et al. Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. Nature Scientific Reports (2015)
-The Human Protein Atlas
-UCSC Genome Browser

Human Genomics at New Fairfield High School

Informed Consent for Sampling of Participant DNA

Purpose of the Procedure: The human genomics course demonstrates human genetic variation through molecular genetic laboratory experiments. All molecular genetics laboratory exercises are educational demonstrations and are not part of a current or future research project. These laboratory experiments are not diagnostic and are not performed in a clinical laboratory.

Risks and Discomforts: Genetic privacy and confidentiality are vitally important because of concerns over misuse of genetic information. Genetic information applies to more than one person. By revealing human DNA variants it is possible to learn presumptively about a person's parents, siblings, children, and others. The human DNA variants being tested are not associated with human disease susceptibility; however, it is possible that future discoveries could link tested variants to diseases. Risk is minimized because all participant samples are provided on an exclusively anonymous basis.

Methods: In human genomics laboratory demonstrations, buccal (cheek cell) samples are acquired by a non-invasive methods (swabbing the inner cheek or spitting into a tube).

Confidentiality of samples: Saliva samples are collected in identical tubes with no names, numbers, or identifying symbols. DNA samples and all laboratory results are anonymous. Use of anonymous, voluntary samples protects participants' privacy and confidentiality. The physical samples (original DNA and all laboratory-derived products) will be destroyed at the conclusion of the demonstration.

Voluntary participation: Provision of a buccal sample is completely voluntary. However, because samples are completely anonymous, it will be impossible to identify and remove a specific sample from the group if a participant decides to withdraw their participation after the sample has been collected.

Please check ONLY ONE of the following options:

I consent [myself or my child] to participate in the non-invasive collection of saliva and subsequent anonymous molecular genotyping. I understand that providing a cell sample for analysis is not a requirement.

I consent [myself or my child] to participate in the molecular genotyping, but do not wish to provide a cell sample.

_____

Student (print)

_____ _____

Student (sign) Date

_____

Parent (print)

_____ _____

Parent (sign) Date

Human Genomics at New Fairfield High School

Student Rights and Responsibilities in the Discussion and Study of Sensitive Topics

Some topics studied in the human genomics course may be distressing to some students. This may include, but is not limited to the studies of various genetic disorders, sex and gender, and genealogy. Studying these topics may prompt students to ask probing questions at home. If you are aware of particular course material that may be upsetting to you or your child, please bring these to the attention of the instructor prior to the start of the course or before it comes up in class. Additionally, if you ever wish to discuss your personal reactions to such material with the class or afterwards with the instructor, we welcome such discussion as an appropriate part of the coursework.

If you ever feel the need to step outside during one of these discussions, either for a short time or for the rest of the class session, you may always do so without academic penalty, but in order to ensure the safety of all students we ask that you proceed promptly to the school social worker or your guidance counselor who should inform the instructor of your whereabouts. You will be responsible for any material you miss. If you do leave the room for a significant time, please make arrangements to get notes from another student or see your instructor individually to discuss the situation.

By signing below, I am acknowledging that I understand the rights and responsibilities described above and consent [myself or my child] to participate in the discussion and study of sensitive topics within the Human Genomics course at New Fairfield High School. I understand that this course is a science elective and is not a required course.

_____

Student (print)

_____ _____

Student (sign) Date

_____

Parent (print)

_____ _____

Parent (sign) Date

QUANTITY	VENDOR	CATALOG #	ITEM	UNIT PRICE	TOTAL COST	
1	USA Scientific	2510-1101	Thermal-Lok 1-Position Dry Heat Bath	$418.95	$418.95	
1	USA Scientific	2520-0000	24-place 1.5/2.0 ml Thermal-Lok dry bath block	$95.75	$95.75	
1	USA Scientific	2621-0016	16-place microcentrifuge for 0.2 ml tubes	$208.95	$208.95	
1	USA Scientific	4062-0207	MiniSpin plus variable speed microcentrifuge	$1,687.20	$1,687.20	
1	USA Scientific	7404-5600	Vortex-Genie 2	$304.35	$304.35	
2	USA Scientific	2300-9602	Compact PCR tube rack, mixed neon colors	$28.35	$56.70	
1	USA Scientific	2380-1008	80-place tube rack, mixed standard colors	$44.00	$44.00	
8	MiniPCR	QP-1001-04	Set of three adjustable-volume micropipettes: 100-1000 µl, 20-200 µl, and 2-20 µl	$150.00	$1,200.00	
1	Biorad	1861096	T100 Thermal Cycler	$2,495.00	$2,495.00	*Only on special until 12/31/19 then $4,912
1	Amazon	Direct Link to Product	Cuisinart SCM-10 Snow Cone Maker, Red	$55.69	$55.69	
1	Wards	95045-604	Flash Gel Device Kit	$1,610.00	$1,610.00	
				SHIPPING	$817.66	
				TOTAL	$8,994.25	