



# Genetic Detection of Stress Syndrome in Pigs

## Genetics Unit

<p><b>Grade Level</b> 9-12</p> <p><b>Lesson Length</b> 2 periods x 55 minutes</p> <p><b>STEM Careers</b></p> <ul style="list-style-type: none"><li>Quantitative Geneticist</li><li>Molecular Geneticist</li><li>Clinical Geneticist</li><li>Immunologist</li><li>Pharmacologist</li><li>Computational Biologist</li></ul> <p><b>Next Generation Science Standards</b></p> <ul style="list-style-type: none"><li>MS-LS3-1</li><li>MS-LS4-5</li><li>HS-LS1-1</li><li>HS-LS3-1</li><li>HS-LS3-2</li></ul> <p><b>Inquiry-Learning Activity &amp; Lesson Plan Authors (2022)</b></p> <ul style="list-style-type: none"><li>Daniel Ciobanu*</li><li>Bryan A. Reiling*</li><li>Nathan Conner*</li><li>Taylor Ruth*</li><li>Christopher Stripling**</li></ul> <p>*University of Nebraska-Lincoln **University of Tennessee</p> <p>Funded by a USDA-NIFA-PDAL grant, Award Number 2021-67037-34298, Program A7501.</p>	<p><i>These lessons aim to bring the science, skills of inquiry, critical thinking, and problem solving to life through an agricultural context.</i></p>  <p><b>Learning Objectives</b></p> <p>By the end of this unit, students should be able to:</p> <ul style="list-style-type: none"><li>Use genetic testing for detecting the cause of stress susceptibility in swine.</li><li>Analyze results and identify genetic solutions to limit the effects of stress susceptibility in a swine herd.</li></ul> <p><b>Materials List</b></p> <ul style="list-style-type: none"><li>Computer with internet access</li><li>Web sites to be accessed as part of this activity<ul style="list-style-type: none"><li>➤ University of California – Santa Cruz, Genomics Browser: <a href="http://www.genome.ucsc.edu/">http://www.genome.ucsc.edu/</a></li><li>➤ European Bioinformatics Institute (EMBL-EBI) maintains the world's most comprehensive range of freely available and up-to-date molecular data resources.<ul style="list-style-type: none"><li>▪ Clustal Omega: <a href="https://www.ebi.ac.uk/Tools/msa/clustalo/">https://www.ebi.ac.uk/Tools/msa/clustalo/</a></li></ul></li></ul></li></ul>
---	---



## ***Introduction (Interest Approach that aligns with the Investigation)***

To introduce students to the structure and function of DNA ...

Facilitate a 1-2 minute discussion with students over their current knowledge of the structure and function of DNA, then show the following video entitled "What is DNA and How Does it Work?" (5:23).

- <https://www.youtube.com/watch?v=zwibqNGe4aY>

How did students' perceived knowledge of DNA structure and function compare to what was presented in the video?

Facilitate a 2<sup>nd</sup> brief discussion (1-2 minutes): If we could read the DNA, what would it tell us, and how could we use that knowledge to improve human welfare?

Teachers may also wish to show the following video titled "Genomics Sequencing: Fighting Disease with Artificial Intelligence" (4:03) as an example of how genomics can help us fight Cancer.

- <https://www.youtube.com/watch?v=YSyRzJVd364>

## ***Essential Question***

- Using Porcine Stress Syndrome (PSS) as a model of a homozygous detrimental recessive trait, how can an understanding of genomics function to prevent the occurrence of such traits in a population?

## ***Learning Activity 1: [PowerPoint Discussion]***

Please use the provided information and/or PowerPoint to review basic DNA structure & function, and basic mendelian genetics. In addition, you will introduce students to the concept of molecular genetics and bioinformatics through the model of porcine stress syndrome (PSS). If teachers prefer to show a recording, that is available at ... <https://use.vg/H34KCx>.

### **Basic Genetic Definitions.**

- Deoxyribonucleic Acid (DNA): Genetic material within a cell.
- Nucleotide: The basic building block of DNA. A nucleotide consists of a sugar molecule (deoxyribose, for DNA), a phosphate group, and a nitrogen-containing base. The four bases used in DNA are adenine (A), cytosine (C), guanine (G), and thymine (T).
- Gene: A DNA fragment that codes for a specific trait. At the molecular level, a gene may consist of hundreds or even thousands of base pairs within the genome.
- DNA sequence: The order of base pairs (A, C, G, or T) within a genetic fragment.
- Allele: Alternative forms of a gene. More specifically, the sequence (order) of base pairs differs.
- DNA polymorphism: A variation in the DNA sequence.

**Basic Principles of Mendelian Genetics.** Although we can now “pinpoint” differences in base pair sequences of genes (or fragments of genes) and target those at the molecular level to facilitate genetic change, the basic principles of Mendelian genetics still determine the potential effects of different matings.

- Homozygous – Like alleles (i.e., BB or bb).
- Heterozygous – Unlike alleles (i.e., Bb).
- Review usage of the Punnett Square.

### **Principal Concepts – Genomics.**

- The genomes of humans and several livestock and plant species have been sequenced improving our ability to understand genetic factors that influence variation between individuals. For humans, why are some individuals more predisposed to diabetes, or heart disease, or cancer? For animals, why do some grow faster than others, or why is the steak from one beef animal more tender than that from another?
- DNA sequencing is an important component of modern animal and plant genetic improvement methods, but it also facilitates targeted interventions to prevent and treat human disease based on an individual’s genomic profile.
- Today, because of genomics, accurate genetic predictions of farm animals are available at or shortly after birth. Because the need for progeny testing is reduced, younger breeding stock can be used confidently to enhance genetic progress. In 2017, a genomic tested 2-month-old Holstein heifer named “Jedi Gigi” sold for \$251,000!

### **Background Information – Porcine Stress Syndrome.**

- What is Porcine Stress Syndrome (PSS)? During a stressful event such as transport, crowding, heat, rough handling, etc., pigs who are stress susceptible may exhibit hyperthermia, open mouth breathing, skin blotching, muscle rigidity, loss of mobility, and even death. In addition, pigs with PSS often produce a less desirable meat product that is pale, soft, and exudative (PSE).
- How did PSS originate? Ideally, we want fast-growing, heavy-muscled, lean market hogs. At some point in time (possibly in the mid- to late-1980s), there was a single-point mutation (i.e., at a specific location on the gene, one nucleotide or base pair was exchanged for another) and the resulting recessive allele provided for even more growth and muscle, 😊. As selection emphasis on lean growth continued, the newly mutated allele became more prevalent. Unbeknownst to researchers at the time, however, was that this recessive allele had a sinister downside … it also functioned to make pigs very susceptible to stress and generated PSE pork, 😞.
- What is the connection between PSS and molecular genetics? The introduction of molecular genetics to swine improvement was initiated by discovery of a recessive allele in the Ryanodine receptor 1 (*RYR1*) gene that is responsible for PSS (Fujii et al., 1991). This is more commonly referred to as the “stress gene”.
- Let’s get into the details of that mutation. The PSS allele is the result of a single-point mutation. Effectively, at a single location on the gene (loci), one base replaced another. In the case of PSS, it was a thymine (T) replacing a cytosine (C). At this location, the cytosine (C) codes for stress resistance which is dominant. The thymine (T), however, codes for stress susceptibility which is recessive.

- Thus, CC = stress resistant, CT or TC = stress resistant carrier, and TT = stress susceptible.
- What's the good news? Through genomics and associated planned breeding programs, like what your students will do as part of this inquiry-based learning activity, the PSS allele has effectively been removed from most modern genetic lines of pigs.

## ***Learning Activity 2: Use of Genomics within Animal Breeding***

While this activity could be done individually, it is recommended that students work in pairs or small groups of 3 to conduct this exercise to facilitate discussion & interaction. The instructor should explain each portion of the exercise, particularly those segments that engage external internet resources. Each group will use the provided lab report to document their findings and to record their hypothesis.

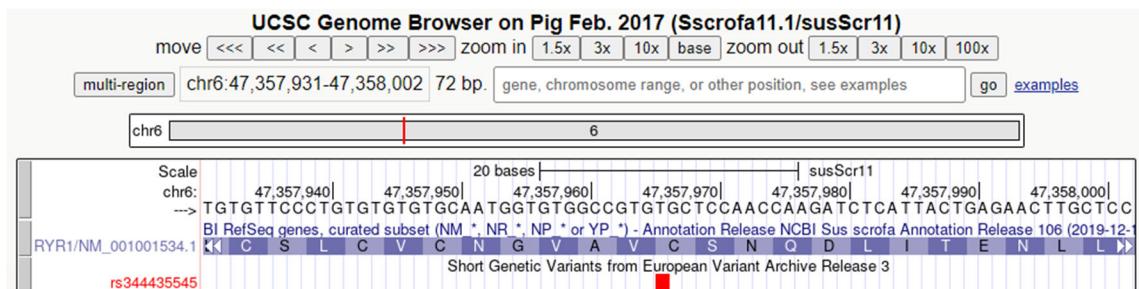
### **Part 1 – Assign the PSS RYR1 genotype to T. J. Tabasco**

1. Google It – Who is T.J. Tabasco?
  - a. T.J. Tabasco was a female (gilt or sow) Duroc (red breed of swine) born in 2001 in Illinois. Using skin from the ear, she was the first pig whose genome was fully sequenced, and that is considered the reference pig genome. Genetic fragments collected from all other pigs are compared to her.
2. Log into the UCSC Genome Browser ([www.genome.ucsc.edu](http://www.genome.ucsc.edu)).
  - a. Using an analogy, the Genome Browser is an online tool designed to quickly find a single sentence (i.e., a short DNA fragment) within a large book (i.e., the genome).
  - b. Select “Genome Browser”
    - i. Will “browse” reference swine genome (T. J. Tabasco) to determine her genotype for the “stress gene” (more accurately, RYR1 PSS).
  - c. Under “Pig Assembly”, select “Feb. 2017 (Sscrofa11.1/susScr11) from dropdown menu.
    - i. This represents the latest information available in the genome database.
  - d. Under “Position/Search Term”, enter
    - i. Chr6:47,357,934-47,358,000
  - e. Click “Go”. Results should be returned within seconds.

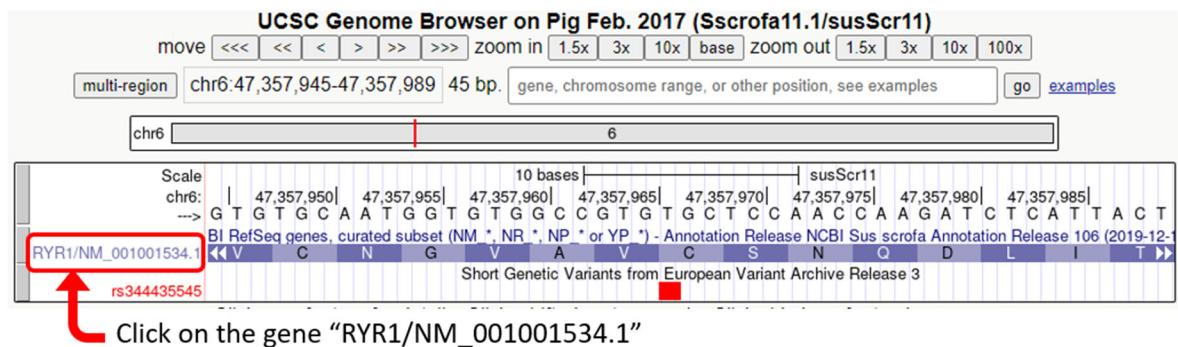
- f. To clear some of the clutter from the results display screen, adjust display to match the following screen shot. Once done, click “refresh” at the bottom of the screen.

### 3. Results, Questions, and Discussion.

- Did T. J. Tabasco possess the DNA polymorphism (rs344435545)? Yes
- What nucleotide is associated with this DNA polymorphism? T or thymine
- Was T. J. Tabasco a carrier for stress susceptibility? Yes



- d. Click on the gene (RYR1/NM ...) associated with this part of the swine genome.



- e. From the resulting page (shown below for instructors), at what position is this gene located, and how many base pairs are associated with this single gene?

Chromosome 6, 47339759-47458457.

Genomic size = 118,699 (may also subtract start number from end number).

### RefSeq Gene RYR1

RefSeq: NM\_001001534.1 Status: Provisional  
 Description: ryanodine receptor 1  
 Molecule type: mRNA  
 Source: BestRefSeq  
 Biotype: protein\_coding  
 Synonyms: CRC, RYR  
 Other notes: The RefSeq transcript has 27 substitutions, 4 frameshifts, 2 non-frameshifting indels compared to this genomic sequence  
 Protein: NP\_001001534.1  
 Entrez Gene: 396718

#### mRNA/Genomic Alignments (NM\_001001534.1)

BROWSER	SIZE	IDENTITY	CHROMOSOME	STRAND	START	END	QUERY	START	END	TOTAL
browser	15372	99.8%	6	+	47339759	47458457	NM_001001534.1	1	15378	15378

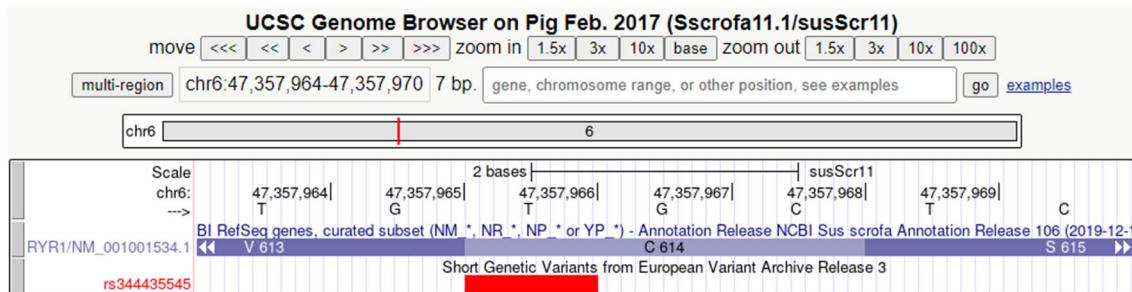
[View details of parts of alignment within browser window.](#)

Position: chr6:47339759-47458457  
 Genomic Size: 118699  
 Strand: +  
 Gene Symbol: RYR1  
 CDS Start: complete  
 CDS End: complete

Shows exact position of this gene and size in terms of number of gene pairs

To return to previous page, simply click the "back arrow"

- f. Zoom-in on the display 10X, by clicking the 10X button. From this display, what is the exact location of this DNA polymorphism on the swine genome that causes stress susceptibility, PSS, and PSE? [Chromosome 6, @ base pair 47,357,966.](#)



- g. Google It – How many chromosomes are associated with the swine genome? [38](#)
- h. In general terms, describe the overall enormity and complexity of the genome. [Nearly everything that characterizes an animal \(e.g. pig\) including hair color and eye color, erect vs. floppy ears, overall size, growth rates, reproductive performance, milking ability, carcass traits, etc., are controlled by genes.](#) We showed a single gene to have ~ 120,000 gene pairs, and yet, the change in a single nucleotide at a specific location on the genome causes a pig to show PSS or not! A single chromosome has millions of gene pairs and there are 38 chromosomes ... literally billions of genotypic combinations!

## **Part 2 – An Animal Breeding Problem.**

A farmer noticed that some of the pigs in the herd developed symptoms associated with Porcine Stress Syndrome (PSS) when transported between farm sites. On this farm, there are 2 boars (male) and 8 sows (female). Tissue samples from these 10 pigs were sent for DNA sequencing to assess the role of the RYR1 DNA polymorphism (i.e., stress gene) on this farm. The following DNA sequences surrounding the known location of the RYR1 DNA polymorphism were received.

```
>boar_1
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>boar_2
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_1
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_2
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_3
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_4
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_5
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_6
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_7
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_8
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
```

## **Part 2 Instructions**

1. Students should access Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).
2. Clustal Omega set-up and submission of data
  - a. On the Clustal Omega website, find where it says “Enter or paste a set of ...”
    - i. Select DNA from the drop-down menu.
  - b. From INSIDE the text box above (do NOT include box), copy everything, and paste into the box on the Clustal Omega website where it says, “sequences in any supported format”.
  - c. On the Clustal Omega website, find where it says “Output Format”
    - i. Select “ClustalW with character counts” from the dropdown menu (this should be the default selection).
  - d. Click “Submit”. Results should be electronically returned within 5-20 seconds.

3. What does the resulting output tell us?
  - a. At the bottom, the presence of an asterisk (\*) indicates that all pigs in the query are genetically the same at that location on their genome. Students may disregard any data associated with an asterisk (\*).
  - b. If an asterisk (\*) is not present, there are genetic differences between pigs.
    - i. The presence of a "C" indicates that the pig is homozygous for cytosine (the nucleotide that will code for stress resistance at that location on the genome).
    - ii. The presence of a "T" indicates that the pig is homozygous for thymine (the nucleotide that will code for stress susceptibility at that location on the genome).
    - iii. The presence of a "Y" indicates that the pig is heterozygous containing both cytosine and thymine (CT) at that location.
      1. Because cytosine, coding for stress resistance at this loci, is dominant, these animals will be phenotypically normal, but are carriers for stress susceptibility (PSS).

## Part 2 – Questions & Discussion

1. Based on the output provided, assign individual pig “stress” (RYR1) genotypes for each pig.

Boar 1 = CC

Boar 2 = CT (carrier)

Sow 1 = CC

Sow 2 = CC

Sow 3 = CT (carrier)

Sow 4 = CC

Sow 5 = CT (carrier)

Sow 6 = CC

Sow 7 = CC

Sow 8 = CC

2. Given specific genotypes for the “stress gene” (RYR1), develop mating strategies to limit the negative impact of PSS on the farm.

Mating of Boar 1 to Sows 1,2,4,6,7,8 → all offspring will be CC (resistant)

Mating of Boar 1 to Sows 3,5 → 50% CC (resistant), 50% CT (carriers)

Mating of Boar 2 to Sows 1,2,4,6,7,8 → 50% CC (resistant), 50% CT (carriers)

~~Mating of Boar 2 to Sows 3,5 → 25% CC, 50% CT, 25% TT (stress susceptible)~~

## Learning Activity 3: Industry and Career Video – Genetics

Show the industry and career video that discusses “real world” application of these basic scientific concepts, while also introducing students to career possibilities that function to bridge science and agriculture.



# Reflection

Using the prompts below to facilitate reflection, allow each student to respond in writing to the prompts and then facilitate a whole class discussion.

1. In general terms, describe overall “size” of the swine genome (as a model, for this lesson)?
  - a. The swine genome consists of 38 pairs of chromosomes, and on each chromosome are millions, if not billions, of nucleotides that represent the genetic code for an animal.
2. What is the general purpose of the genomic browser, and how does it help geneticists?
  - a. Using an analogy, the genomic browser is an online tool designed to quickly locate a sentence (i.e., a short DNA fragment) within a very large book (i.e., the genome).
3. Associated with the activity problem, why should Boar 2 not be mated to Sows 3 or 5?
  - a. Both the male and female are carriers (CT) for stress susceptibility. Using a Punnett Square, one can decipher that 25% of their offspring will show porcine stress syndrome.
4. Associated with the activity problem, what arguments can you provide for keeping the carrier animals (Boar 2 and Sows 3 & 5)?
  - a. Primary argument for keeping. Stress resistance is only 1 trait among many that are economically important. These individuals may excel in some of those other economically important traits (e.g. daily gain, feed efficiency, carcass merit, reproductive performance, etc), and it may take significant time to generate individuals with those same genetic advantages. Provided carriers are not bred to carriers, offspring will be stress resistant.
5. Associated with the activity problem, what arguments can you provide for culling and replacing the carrier animals (Boar 2 and Sows 3 & 5)?
  - a. Primary argument for culling and replacing. If the industry really wants to eliminate the stress gene, all individuals who carry the stress allele (T) should not be used for mating because at least half of a carrier boar’s offspring will also be carriers.



# Apply

Use the prompts below to facilitate small group and whole class discussion.

1. In general terms, describe the structure and make-up of DNA.
2. In general, describe the rules of dominance vs. recessiveness.
3. How does the technology of genomics facilitate genetic progress?

## References:

- Fujii J, Otsu K, Zorzato F, de Leon S, Khanna VK, Weiler JE, O'Brien PJ, MacLennan DH. Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia. *Science*. 1991 Jul 26;253(5018):448-51. doi: 10.1126/science.1862346. PMID: 1862346.
- *Genomics Sequencing: Fighting Disease with Artificial Intelligence*  
<https://www.youtube.com/watch?v=YSyRzJd364>
- *What is DNA and How Does it Work?* <https://www.youtube.com/watch?v=zwibgNGe4aY>

Extension is a Division of the Institute of Agriculture and Natural Resources at the University of Nebraska-Lincoln cooperating with the Counties and the United States Department of Agriculture.

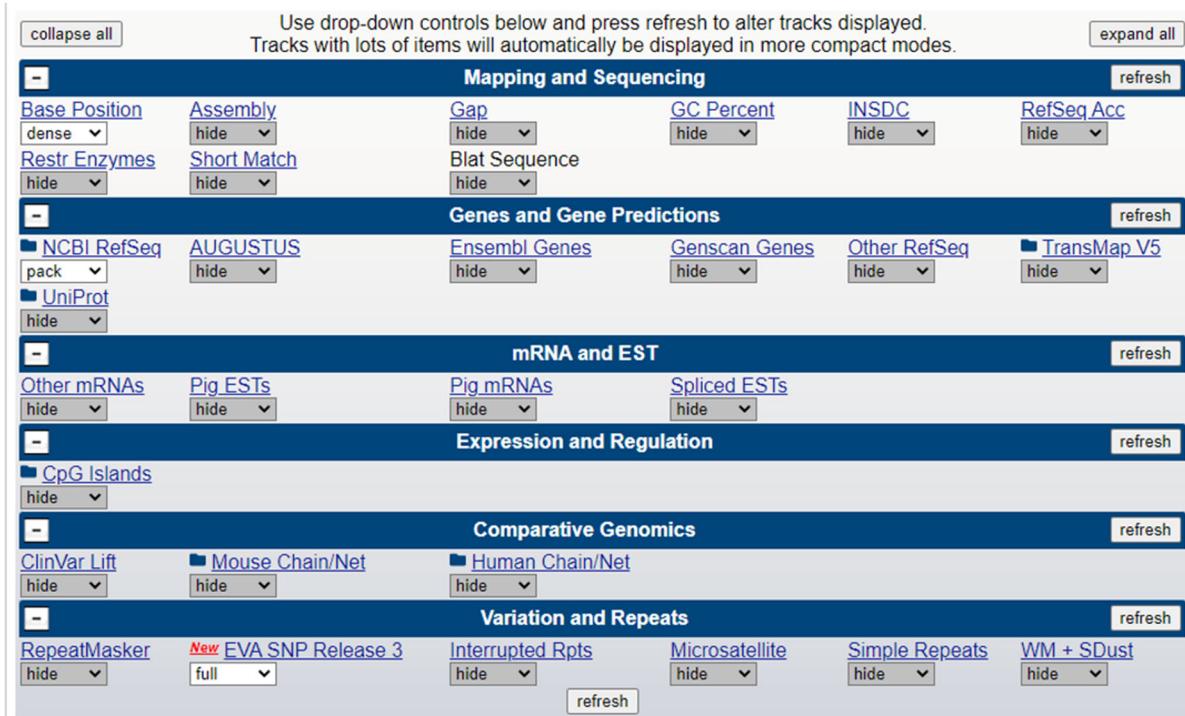


# **Use of Genomics within Animal Breeding**

## **(Student Instructions)**

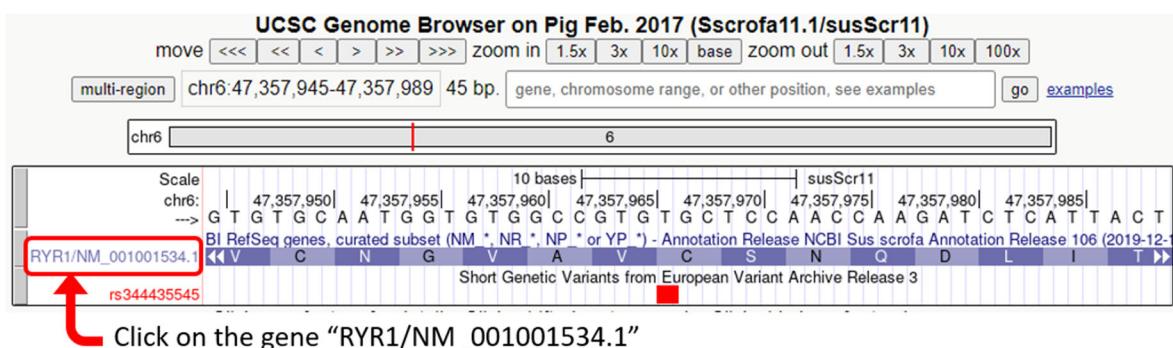
### **Part 1 – Assign the PSS RYR1 genotype to T. J. Tabasco**

1. Google It – Who is T.J. Tabasco?
2. Log into the UCSC Genome Browser ([www.genome.ucsc.edu](http://www.genome.ucsc.edu)).
  - a. Using an analogy, the Genome Browser is an online tool designed to quickly find a single sentence (i.e., a short DNA fragment) within a large book (i.e., the genome).
  - b. Select “Genome Browser”
    - i. Will “browse” reference swine genome (T. J. Tabasco) to determine her genotype for the “stress gene” (more accurately, RYR1 PSS).
  - c. Under “Pig Assembly”, select “Feb. 2017 (Sscrofa11.1/susScr11) from dropdown menu.
    - i. This represents the latest information available in the genome database.
  - d. Under “Position/Search Term”, enter
    - i. Chr6:47,357,934-47,358,000
  - e. Click “Go”. Results should be returned within seconds.
  - f. To clear some of the clutter from the results display screen, adjust display to match the following screen shot. Once done, click “refresh” at the bottom of the screen.



3. Results, Questions, and Discussion (a separate sheet is available for you to write your answers)

- a. Did T. J. Tabasco possess the DNA polymorphism (rs344435545)?
- b. What nucleotide is associated with this DNA polymorphism?
- c. Was T. J. Tabasco a carrier for stress susceptibility?
- d. Where is the RYR1 gene located, and how many base pairs are associated with this single gene? Clue -- Click on the gene (RYR1/N) associated with this part of the swine genome as shown below.



- e. Return to the previous page (click the “back arrow”) and zoom-in by clicking the 10X button. From this display, what is the exact location of this DNA polymorphism on the swine genome that causes stress susceptibility, PSS, and PSE?
- f. Google It – How many chromosomes are associated with the swine genome?
- g. In general terms, describe the overall enormity and complexity of the genome.

## Part 2 – An Animal Breeding Problem.

A farmer noticed that some of the pigs in the herd developed symptoms associated with Porcine Stress Syndrome (PSS) when transported between farm sites. On this farm, there are 2 boars (male) and 8 sows (female). Tissue samples from these 10 pigs were sent for DNA sequencing to assess the role of the RYR1 DNA polymorphism (i.e., stress gene) on this farm. The following DNA sequences surrounding the known location of the RYR1 DNA polymorphism were received.

```
>boar_1
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>boar_2
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_1
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_2
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_3
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_4
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_5
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGYGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_6
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_7
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
>sow_8
CTGACCTTGACCCCTAGGTGCTGGATGTCCGTGTTCCCTGTGTGCAATGGTGTGCCGTGCGCTCCAACCAAGATCTCATTACTGAGAACATTGCT
```

## **Part 2 Instructions**

1. Students should access Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).
2. Clustal Omega set-up and submission of data
  - a. On the Clustal Omega website, find where it says “Enter or paste a set of ...”
    - i. Select DNA from the drop-down menu.
  - b. From INSIDE the text box above (do NOT include box), copy everything, and paste into the box on the Clustal Omega website where it says, “sequences in any supported format”.
  - c. On the Clustal Omega website, find where it says “Output Format”
    - i. Select “ClustalW with character counts” from the dropdown menu (this should be the default selection).
  - d. Click “Submit”. Results should be electronically returned within 5-20 seconds.

3. What does the resulting output tell us?

- a. At the bottom, the presence of an asterisk (\*) indicates that all pigs in the query are genetically the same at that location on their genome. Students may disregard any data associated with an asterisk (\*).
- b. If an asterisk (\*) is not present, there are genetic differences between pigs.
  - i. The presence of a "C" indicates that the pig is homozygous for cytosine (the nucleotide that will code for stress resistance at that location on the genome).
  - ii. The presence of a "T" indicates that the pig is homozygous for thymine (the nucleotide that will code for stress susceptibility at that location on the genome).
  - iii. The presence of a "Y" indicates that the pig is heterozygous containing both cytosine and thymine (CT) at that location.
    1. Because cytosine, coding for stress resistance at this loci, is dominant, these animals will be phenotypically normal, but are carriers for stress susceptibility (PSS).

**Part 2 – Questions & Discussion** (a separate sheet is available for you to write your answers)

1. Based on the output provided, assign individual pig “stress” (RYR1) genotypes for each pig.
2. Given specific genotypes for the “stress gene” (RYR1), develop mating strategies to limit the negative impact of PSS on the farm (clue – this is where you get to generate Punnett Squares).

Name:

# ***Use of Genomics within Animal Breeding (Student Answers)***

## **Part 1 Questions**

1. Google It – Who is T.J. Tabasco?
  
  
  
  
  
2. Using Results from the Genome Browser, answer the following questions:
  - a. Did T. J. Tabasco possess the DNA polymorphism (rs344435545)?
  
  
  
  
  
  - b. What nucleotide is associated with this DNA polymorphism?
  
  
  
  
  
  - c. Was T. J. Tabasco a carrier for stress susceptibility?
  
  
  
  
  
  - d. Where is the RYR1 gene located, and how many base pairs are associated with this single gene?
  
  
  
  
  
  - e. What is the exact location of this DNA polymorphism on the swine genome that causes stress susceptibility, PSS, and PSE?
  
  
  
  
  
  - f. Google It – How many chromosomes are associated with the swine genome?
  
  
  
  
  
  - g. In general terms, describe the overall enormity and complexity of the genome.

## **Part 2 Questions**

1. Based on the output provided, assign individual pig "stress" (RYR1) genotypes for each pig.

Boar 1 = Sow 1 =

Boar 2 = Sow 2 =

Sow 3 =

Sow 4 =

Sow 5 =

Sow 6 =

Sow 7 =

Sow 8 =

2. Given specific genotypes for the “stress gene” (RYR1), develop mating strategies to limit the negative impact of PSS on the farm (clue – this is where you get to generate Punnett Squares).

Name:

# ***Lab Report***

**Please complete the following report during the design and implementation of your experiment.**

## **Research Problem**

- Describe what you are investigating and justify why you are investigating the problem.

## **Hypothesis**

- Formulate one or more hypotheses for your experiment.

## **Procedures**

- Create the steps you will follow for your experiment.

## **Data Collection**

- Describe the data that you will collect during your experiment.
- Provide graphs, tables, charts, and raw data as necessary.

## **Results**

- Explain your results.

## **Conclusion**

- Based on your data:
  - What can you conclude?
  - Were your hypotheses supported?
  - Were there limitations to your experiment?
  - What are new research questions that derived from this study?