### GENIQUEST Advisory Board Meeting



### GENIQUEST Project Goals

- Develop and test a tool enabling students to import, manipulate and analyze genomics data
- Increase secondary students' knowledge and skills at data analysis and scientific research
- Improve secondary school teachers' and students' access to cutting-edge STEM data sets
- Determine the viability of online data as a tool for engaging secondary school teachers and students in scientific inquiry

#### GENIQUEST Revised Timeline – June 2008

					Year	1											Year	2					
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Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	Sept.	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	.Sept.

Communication and Planning PI Meeting Programmer/Jackson/MMS	Lommunication and Planning I Meeting Programmer/Jackson/MMSA Teleconferences Programmer/Jackson/MMSA Teleconferences Programmer/Jackson/MMSA Teleconferences Advisory Board Mtg. Advisory Board Mtg. Advisory Board Mtg. Advisory Board Mtg.														
Piloting and Field Testing	Call for piloting teachers	Summe student testing	r Teacher training	Classroom pilots	Field Test teacher recruitment	Field-test teacher training	Classroom field-testing								
Instructional FlowLearning about QTL processTranslating QTL process to student termsDeter- mining curricular scope	Developing initial instructional sequences	Section 1 pilot authoring	Section 2 pilot authoring	Sections 1 and 2 revision	Section 3 Authoring		Revisions based on field testing								
	MMSA/C authoring meeting	oncord g	MMSA/Concord authoring meeting	MMS/ autho meeti	A/Concord pring ing		MMSA/Concord authoring meeting								
Software Design Determining user interface require- ments Inventorying abilities of existing software	Developing authoring environment		Determining student logging desires	Initial st logging	udent Deterr work studer collabo possib	nine t Stude pration collab ilities	ent logging and poration								
Science Content/Jackson Labs Creating Program- dragon ming DNA genome structure browser	Initial QTL Ir testing d ir	ncorporating ragon genome nto Biologica	QTL incorpo- ration	Genome browser and RQTL integration	Mouse genome data preparation	Integration of mouse genome and existing research data									
Funding Funding	Year 1				NSF DR-K-12 Full Project Proposals Due	Fur	nding Year 2								

### GENIQUEST Instructional Flow









#### Mouse Data



#### Open Level



### The Intro level familiarizes students with the dragons and reviews basic genetics



### Initial investigations introduce dragons, heredity rules and chromosomes/genes.



### Meiosis view introduces details of reproduction and DNA view links chromosomes to alleles



### Recombination introduced into meiosis and students learn to breed genetic strains





### Students discover genetic markers and uncover their usefulness





### Students discover genetic markers and uncover their usefulness





# Once genetic details are established, students build up to basic QTL analysis







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### Students breed two strains of dragons with a distinct, varying trait to create offspring pool



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1.8 m 🕈	
4.9 m	
3.2 m 🕈	
3.0 m 🕈	
4.6 m	
1.7 m 🕈	
5.2 m	

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2.8 m	
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1.8 m 🕈	
4.9 m	
3.2 m 🕈	
3.0 m 🕈	
4.6 m	
1.7 m 🕈	
5.2 m	

# Students characterize individuals as high, low or mixed according to the selected trait



# Markers on each individual are characterized according to corresponding phenotypes













### Students quantify this relationship by averaging phenotype values for each marker position



### Students quantify this relationship by averaging phenotype values for each marker position



M <sub>AA</sub>	M <sub>AB</sub>	M <sub>BB</sub>	M <sub>AA</sub>	M <sub>AB</sub>	M <sub>BB</sub>
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# The candidate marker position connects to two genes, one of which research shows as likely



### Level I introduces a disease and opens student experimentation on a model species



### Students learn about disease and model species, and identify need for QTL analysis



### Students breed affected and unaffected strains of model species and run QTL analysis





#### QTL scans result in two peaks, one narrow and one broad



### Investigating genes near peaks eliminates one and leaves second ambiguous

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### Investigating genes near peaks eliminates one and leaves second ambiguous

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#### Investigating genes near peaks eliminates one and leaves second ambiguous

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### Combining information from two separate QTL scans of this chromosome yields gene





### Combining information from two separate QTL scans of this chromosome yields gene





### Level 2 transfers students' learning about QTL analysis to problems involving mice



### Students learn about mouse genome and initial scenario

#### Showing 100 kbp from 11, positions 59,160,000 to 59,260,000

#### Instructions

Search using a sequence name, gene name, locus, or other landmark. The wildcard character \* is allowed. To center on a location, click the ruler. Use the Scroll/Zoom buttons to change magnification and position.

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# Students led through initial QTL scan to identify gene and reproduce research results

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### Students encounter new scenario and analyze one of multiple research datasets

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### Scans yield interesting, but ambiguous results for individual datasets



### Scans yield interesting, but ambiguous results for individual datasets



### Students collaborate on problem, combining datasets across class to narrow QTL peak



## Students collaborate on problem, combining datasets across class to narrow QTL peak



# Students investigate new peak area to identify candidate gene, reproducing research



### Level 3 frees students to explore data sets further and investigate new problems



### Students investigate previous datasets for new questions or scan new, unanalyzed datasets



#### GENIQUEST Revised Timeline – June 2008

					Year	1											Year	2					
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Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	Sept.	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	.Sept.

Communication and Planning         PI Meeting       Programmer/Jackson/MMSA Teleconferences       Programmer/Jackson/MMSA Teleconferences       Programmer/Jackson/MMSA Teleconferences         Advisory Board Mtg.       Advisory Board Mtg.       Advisory Board Mtg.       Advisory Board Mtg.							
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Software Design Determining user interface require- ments Inventorying abilities of existing software	Developing authoring environment		Determining student logging desires	Initial st logging	udent Deterr work studer collabo possib	nine nt Stude oration collat ilities	ent logging and poration
Science Content/Jackson Labs Creating Program- dragon ming DNA genome structure browser	Initial QTL Ir testing d ir	ncorporating ragon genome nto Biologica	QTL incorpo- ration	Genome browser and RQTL integration	Mouse genome data preparation	Integration of mouse genome and existing research data	
Funding Funding	Year 1				NSF DR-K-12 Full Project Proposals Due	2 Fur	nding Year 2