Student writing reveals their heterogeneous thinking about the origin of genetic variation in populations

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Framework

- Constructed Response (CR) assessments allow students to represent their knowledge in their own language (Birenbaum and Tatsouka 1987; Martinez 1999; Kuechler and Simkin 2010)
- Novices focus on surface features of problems (Chi, Feltovich, & Glaser, 1981; Nehm & Ha, 2011; Heredia, Furtak, & Morrison, 2012)

 Can lexical analysis of student writing reveal their understanding of origins of genetic variation?

 Do surface features of the question influence student writing about origins of genetic variation? •Focus on major learning goals for introductory genetics (Smith et al 2008)

•751 students took the GCA at the University of Colorado, pre and post (2008-2010)

•Subset of GCA questions are particularly difficult on the post test (Smith and Knight, 2012)

•9 post test questions with a single incorrect answer selected by 20% or more of the students

Original GCA multiple-choice question

A population of buffalos is isolated such that no new buffalos can come into their territory.

Which of the following is primarily responsible for the appearance of new alleles in this population?

a) Reassortment of chromosomes during the process of creating sperm or eggs.

b) Mutations in cells that will become sperm or eggs.

c) Changes in the environment that favor some buffalo traits over others.

d) Random mating between the buffalos in the population.

Methods

Questions

1. Explain how new alleles (gene versions or variants) arise in populations of animals

2. Explain how new alleles (gene versions or variants) arise in a bacterial colony

Methods

Questions

1. Explain how new alleles (gene versions or variants) arise in populations of **animals**

2. Explain how new alleles (gene versions or variants) arise in a **bacterial** colony

- 348 responses
 - 233 from an Introductory genetics class at University 1
 - 115 from an Introductory biology class at University 2

Text Analysis

- Software
 - IBM SPSS Text Analysis for Surveys
 - IBM SPSS Modeler
- Procedure
 - Library Construction and Feature Extraction
 - Categorization

Custom Libraries -identify words and phrases relevant to the question

Response

1. New alleles could arise from mutation, recombination and gene flow.

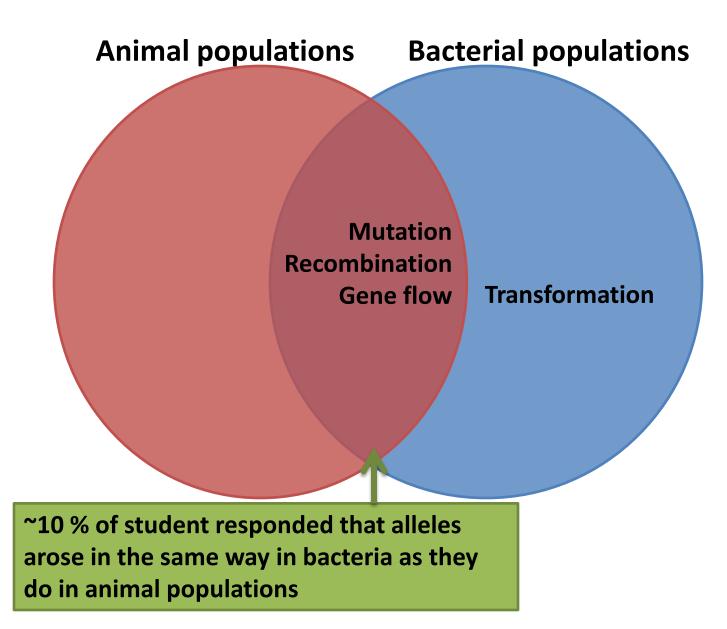
Categories can identify multiple representations of one idea

Response	Categories
 New alleles could arise from mutation, recombination and gene flow. 	Allele
 Selective pressure could naturally press for new variants in a population 	Allele

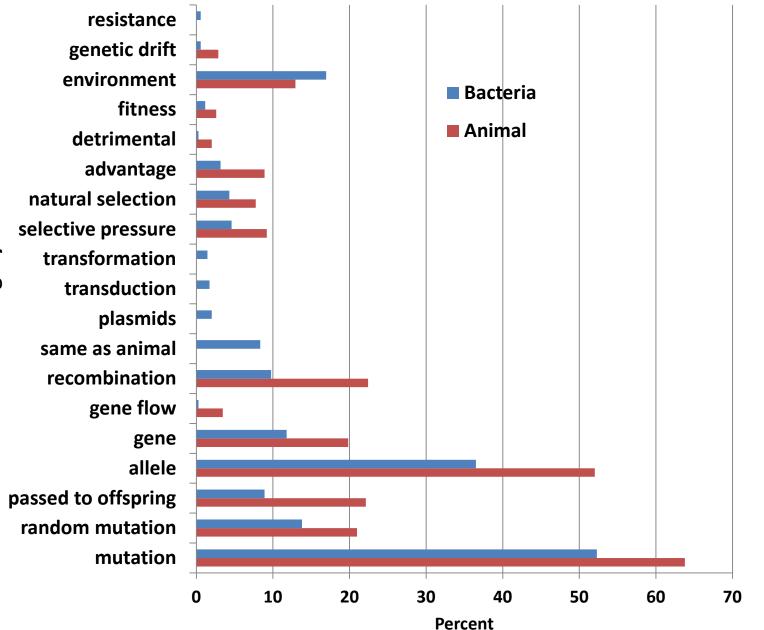
Each response assigned to one or more categories

	Response	Categories
1.	New alleles could arise from mutation, recombination and gene flow.	Allele Mutation Recombination Gene flow
2.	Selective pressure could naturally press for new variants in a population	Allele Selective pressure Population

Expected student responses

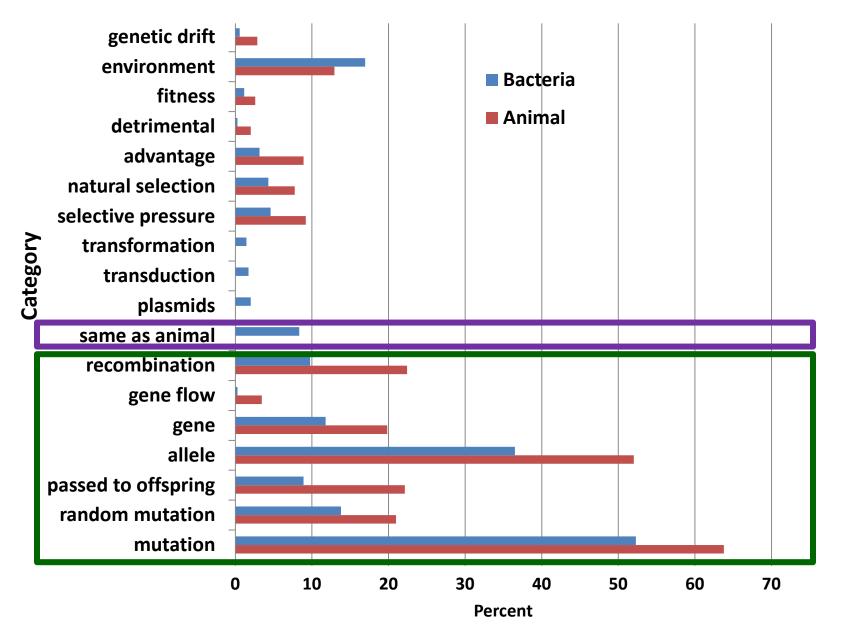


Category Frequencies

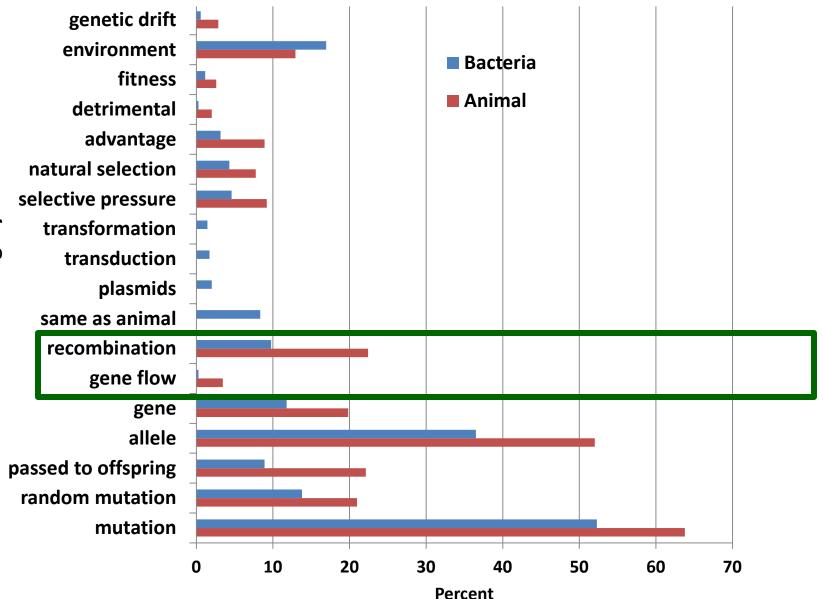


Category

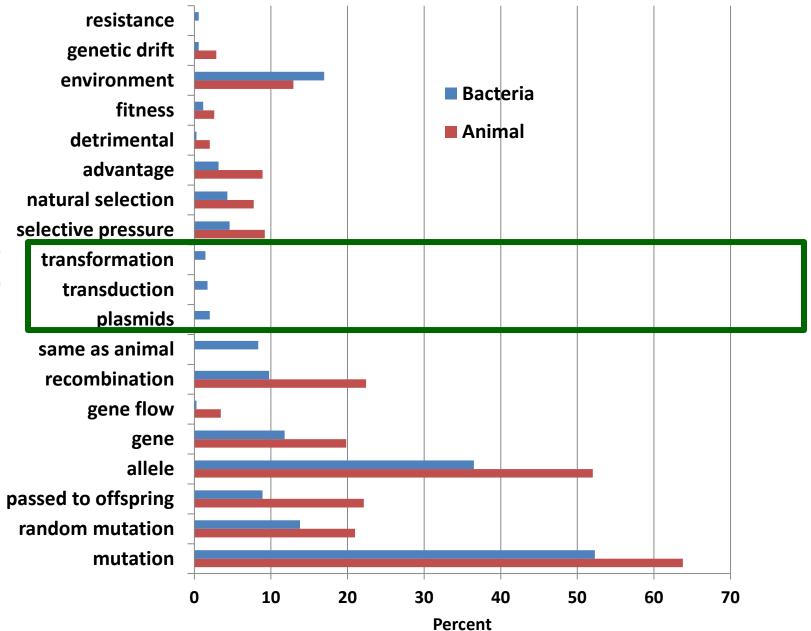
Students may not identify sources of new alleles common to both animal and bacterial populations



Few students identified some sources of new alleles

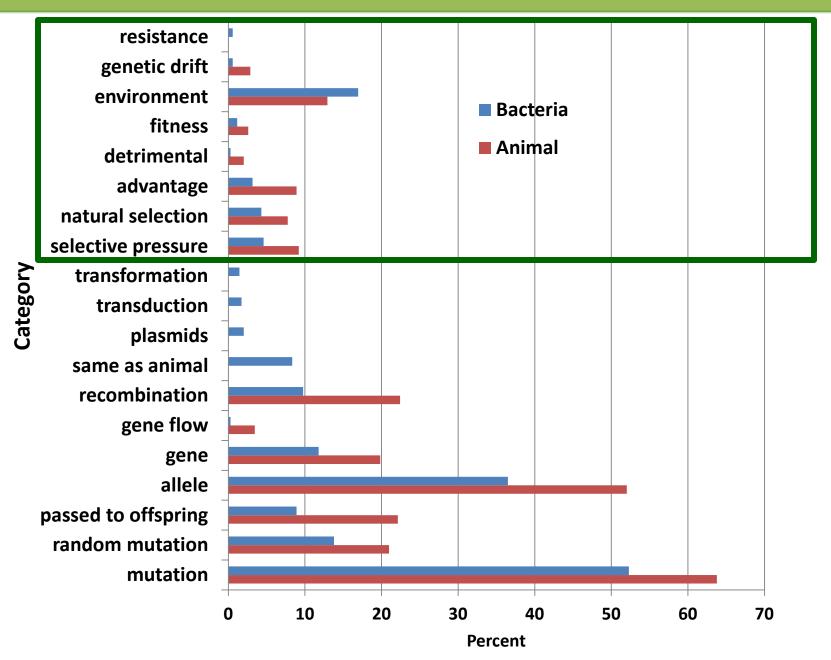


Few students identified mechanisms unique to bacteria



Category

Students focus on selection, not origin of variation



 Can lexical analysis of student writing reveal their understanding of origins of genetic variation?

Conclusion

- Lexical analysis uncovered ideas in student writing about allelic origins
 - Few students identified gene flow as a source of new alleles
 - Students focus on trait selection, rather than origin of alleles
 - Few students identified mechanisms unique to bacteria
- Surface features may influence students writing about allelic origins
 - Students may not identify sources of new alleles common to both animal and bacterial populations

Research Questions

 Do surface features of the question influence student writing about origins of genetic variation?

Conclusion

- Surface features may influence students writing about allelic origins
 - Students may not identify sources of new alleles common to both animal and bacterial populations

Acknowledgments

 Funding NSF DUE 1022653



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