

Supplementary Table 6

Counts of responses to pre- and post- questions for University of Cincinnati students about annotation and

No.	Question
1	What are some major difficulties associated with genome sequencing and assembly?
	Correct answers included three or more of the following points:
	A. Obtaining research funds for sequencing
	B. Recovery of enough DNA for inbred lines or large individuals necessary for sequencing
	C. Proper sequencing depth for assembly
	D. Computing time and power for assembly
	E. Adequate assessment of genome assembly quality
	F. Sex-specific bias
	G. Assignment of genome scaffolds to chromosomes
	H. Accurate gene prediction.
	I. Removal of chimeras and/or microbial contamination
	difficulties associated with genome assembly
2	What information is utilized to predict genes in a newly assembled genome?
	Correct answers included three or more of the following points:
	A. Previously sequenced gene in NCBI
	B. RNA seq data
	C. <i>de novo</i> assemblies, such as those from Trinity or Oases
	D. Proteins/gene sequences in other organism
	E. Known characteristics of transcriptional start and stop sites.
	F. Known characteristics of splice sites
	G. ORF prediction software
	*Other answers are acceptable if these indicate the student understands the process of gene prediction
3	How does a sequenced genome increase tools available for research on an organism?
	Correct answers included two or more of the following points:
	A. Studies on transcriptional regulation through transcription factors is possible.
	B. DNA methylation studies can be conducted.
	C. Splice variants in genes can be examined.
	D. Development of transgenic lines can more accurate by reducing off-target effects.
	E. RNA interference can be developed to target specific splice variants
	F. Studies assessing the presence or absence of genes can be more accurate
	G. Potential interplay between hosts and symbionts can be examined by looking at the gene repertoire.
	*Other answers are acceptable if these indicate the student can justify why the genome will improve research.

could be assessed.