11/1/22, 9:17 AM

Genetics PBL

	1						
Criteria		Rati	ings				Pts
Choose 1 of the following	5 pts Full Marks			0 pts No Marks			
Selects one of the following:	Clearly selects one of the following on parent fill out permission slip	options. If doing personal	trait, has	Does not sel fails to do pro	ect from one of the t oject.	hree options or	
1. A specific trait in your pet or theoretical pet							
2. Special populations: Blue People of Troublesome Creek,							5 pts
Queen Victoria, or Ellis-van Creveld syndrome in the Amish 3. A trait that you							
PARENTAL PERMISSION							
Trait/Gene Research Research the specific trait, gene	<b>30 to &gt;29.0 pts</b> <b>Above Standard</b> Meets ALL criteria listed below: 1.	29 to >27.0 pts Approaching Above Standard	27 to >24 At Standa Meets AL	ard	24 to >15.0 pts Approaching Standard	15 to >0 pts Below Standard	30 pts
location, and chromosome gene sequence (either full gene sequence or	Selects a complex trait (either codominant, X-linked, or polygenic). 2. Identifies the chromosome, location and name	Meets ALL criteria listed below: 1. Selects a complex trait (ex. polygenic, X-	listed belo Selects a follows sir dominanc	ow: 1. trait that mple æ/recessive	Missing 1 of the criteria listed in the AT STANDARD	Missing 2 or more from the AT STANDARD	
allele ex. Tt, TT, etc.)	of gene responsible for the trait. (ex. chromosome 15, OCA 2 gene, SNP rs12913832) 3. Finds	linked, codominant) 2. Identifies the chromosome, location	inheritanc widow's p Identifies	,	category	category OR Does not turn in	

Criteria		Rat	ings			Pts
	and lists the gene sequence responsible for the trait and what the non-trait sequence is (ex. OCA2 gene sequence: ACTTGACACTTA for blue eyes, ACTTGATACTTA for brown eyes) 4. Correctly identifies the type of mutation responsible for the gene/trait (ex. substitution, deletion, insertion)	and name of gene responsible for trait (ex. Chr. 15, OCA 2 gene) 3. Lists all allele combinations needed for trait to be present and absent (ex. GG for blue eyes, TT or TG for brown)	and gene responsible for trait 3. Lists all allele combinations needed for trait to be present and absent (ex. Ww or WW for widow's peak)		project/ project unrelated to the PBL	
odel ake a Hanging obile showing an	30 to >29.0 pts Above Standard	29 to >27.0 pts Approaching Above Standard	27 to >24.0 pts At Standard	24 to >15.0 pts Approaching Standard	15 to >0 pts Below Standard	30 p

Genetics PBL

inheritance pattern - Criteria in the following		Ra	tings			Pts
forms: Pedigree or Family Tree	Model CLEARLY Shows and Meets ALL criteria listed below: 1. Selects a complex trait (either codominant, X-linked, or polygenic). 2. Identifies the chromosome, location and name of gene responsible for the trait. (ex. chromosome 15, OCA 2 gene, SNP rs12913832) 3. Tracks trait through AT least 3 generations (ex: students> grandparents) 4. Shows all possible genetic sequence combinations for selected traits for all generations (ex. brown eyes can be heterozygous brown or homozygous brown) 5. Clearly identifies where the mutation occurs in order to produce said trait (see exemplar listed in assignment/in class)	Model CLEARLY Shows and Meets ALL criteria listed below: 1. Selects a complex trait (ex. polygenic, X- linked, codominant) 2. Identifies the chromosome, location and name of gene responsible for trait (ex. Chr. 15, OCA 2 gene) 3. Tracks trait through at least 3 generations (ex: students >grandparents) 4. Shows ALL possible allele combinations needed for trait to be present and absent (ex. GG for blue eyes, TT or TG for brown)	Model CLEARLY Shows and Meets ALL criteria listed below: 1. Selects a trait that follows simple dominance/recessive inheritance (ex. widow's peak) 2. Identifies chromosome and gene responsible for trait 3. Tracks trait through at least 3 generations (ex. students >grandparents) 4. Shows ALL allele combinations needed for trait to be present and absent (ex. Ww or WW for widow's peak)	Missing 1 of the criteria listed in the AT STANDARD category	Missing 2 or more from the AT STANDARD category OR Does not turn in project/ project unrelated to the PBL	

Criteria		Ra	tings			Pts
Live Presentation	30 to >29.0 pts	29 to >27.0 pts	27 to >24.0 pts	24 to >15.0 pts	15 to >0 pts	30 pts
Students presents	Above Standard	Approaching Above	At Standard	Approaching	Below	
model to class.	Student CLEARLY covers and	Standard	Student CLEARLY	Standard	Standard	
	EXPLAINS ALL criteria listed	Student CLEARLY	covers and EXPLAINS	Missing 1 of the	Missing 2 or	
	below: 1. Selects a complex	covers and EXPLAINS	ALL criteria listed below:	criteria listed in	more from	
	trait (either codominant, X-	ALL criteria listed	1. Selects a trait that	the AT	the AT	
	linked, or polygenic). 2.	below: 1. Selects a	follows simple	STANDARD	STANDARD	
	Identifies the chromosome,	complex trait (ex.	dominance/recessive	category	category OR	
	location and name of gene	polygenic, X-linked,	inheritance (ex. widow's		Does not	
	responsible for the trait. (ex.	codominant) 2.	peak) 2. Identifies		turn in	
	chromosome 15, OCA 2 gene,	Identifies the	chromosome and gene		project/	
	SNP rs12913832) 3. Tracks	chromosome, location	responsible for trait 3.		project	
	trait through AT least 3	and name of gene	Tracks trait through at		unrelated to	
	generations (ex: students>	responsible for trait (ex.	least 3 generations (ex.		the PBL	
	grandparents) 4. Shows all possible genetic sequence	Chr. 15, OCA 2 gene) 3. Tracks trait through	students			
	combinations for selected traits	at least 3 generations	>grandparents) 4. Shows ALL allele			
	for all generations (ex. brown	(ex: students	combinations needed			
	eyes can be heterozygous	>grandparents) 4.	for trait to be present			
	brown or homozygous brown)	Shows ALL possible				
		p				

Criteria		Ratings		
	5. Clearly identifies where the mutation occurs in order to produce said trait (see exemplar listed in assignment/in class)	allele combinations needed for trait to be present and absent (ex. GG for blue eyes, TT or TG for brown)	and absent (ex. Ww or WW for widow's peak)	