

Students obtain two coins from the teacher. Each coin is marked with heads side and a tails side. Flip the two coins and record the genetic code on the data sheet by circling heads or tails. Then, circle the appropriate genetic code. For example, two heads for length would be TT and indicate a dominant or long physical trait. One head and one tail for length would be Tt and indicate a dominant or long physical trait. Two tails for length would be tt and indicate a recessive or short physical trait. Repeat for seed shape and pod color. Students can then cross their pea with another student's pea using the data obtained. To do this, students place the first allele (T or t) of their genotype (TT, Tt or tt) in the top center box and the second allele in the top right box. The other student places the first allele of their genotype in the left center box and the second allele in the left bottom box. Students then complete the remaining four boxes with two alleles, one from each student's pea, yielding the potential genotypes of an offspring. For example, the center box would include the allele from the top center box and the left center box, etc.