

Jim Myers - Linkage in common bean

P gene controls color expression. Plants with *pp* have white seeds, white flowers and no pigment in vegetative parts. Plants with *P-* have colored seeds, purple flowers and may have varying degrees of pigment on stems and leaves.

A gene for white mold resistance has been found and we want to determine its inheritance and whether it is linked to *P*. For the purposes of this exercise, we will assume that resistance is controlled by a single major gene *WM* where *WM-* gives resistance and *wmwm* produces susceptibility.

The population used for this is a recombinant inbred population that has been inbred to the F_6 by single seed descent. A black seeded resistant parent was crossed to a white seeded susceptible parent to create the F_1 , which was self-pollinated to produce the F_2 . From the F_2 , 96 individuals were allowed to self again to produce F_3 families. In the F_3 and in each subsequent generation, a single seed from each family was used to plant the next generation. There are 96 families in the population, each represented by a single seed in the materials provided to you. You have two seed packets per population – one containing seed of resistant individuals, the other containing seed of susceptible individuals.

Questions before conducting exercise:

1. What are the parental classes? (from description above)
2. What is the expected individual segregation ratios for *P* and *WM*? (Remember this is an F_6 population)
3. What is the expected joint segregation?

Parts to the exercise:

1. Count the number of black and white seeds in each resistance class.
2. Test the null hypothesis that the two traits are controlled by single genes.
3. Test the null hypothesis that the two traits segregate independently. (What is the alternate hypothesis?)
4. Calculate recombination fraction to estimate linkage.

Post-exercise questions:

1. Do the individual traits fit the expected segregation ratio?
2. Are the traits linked and if so, how tight is the linkage?