data:
$$n_i = 854$$
, $n_2 = 249$, $n = 1103$
 $m_j = h T_{jo}$,
 $m_i = 827.25$, $m_2 = 275.75$

(a)
$$\chi^2 = \frac{(n_j - m_j)^2}{m_j} = 3.46$$
, (b) $\chi^2_{.10}(1) = 2.7$

- (c) The genetic model is not compatible with the observed data
- (d) A dichotomous measure of evidence does not provide as much information as a more quantitative evidence measure, nor does the dichotomous measure provide information about effect the

(2) (a)
$$90\%$$
 CE for $\pi_{1} = \hat{\pi}_{1} \pm 1.645 \sqrt{\frac{\hat{\pi}_{1}(1-\hat{\pi}_{1})}{n}}$
($\hat{\pi}_{1} = .7743$) = [.7535,.7950]

(b) Based on the observed data, we estimate that the prob. of a green seedling is between .7535 and .7950

```
> obs = c(854,249)
> n = sum(obs)

> pi.0 = c(.75,.25)
> m = n*pi.0

> c = length(obs)
> comp.level = .90
> cutoff = qchisq(comp.level,c-1)

> X2 = sum((obs-m)^2/m)
> G2 = 2*sum(obs*log(obs/m))
> print(c(X2,G2,cutoff))
[1] 3.459958 3.539017 2.705543

> pi.hat = obs[1]/n
> lower = pi.hat - qnorm(.95)*sqrt(pi.hat*(1-pi.hat)/n)
> upper = pi.hat + qnorm(.95)*sqrt(pi.hat*(1-pi.hat)/n)
> print(pi.hat,digits = 4)
[1] 0.7743
> print(c(lower,upper),digits = 4)
[1] 0.7535 0.7950
```