Population Genetics Problem #1

Dan Schoen and Mike Clegg (Evolution 39:1242-1349; 1985) studied the influence of flower color on the outcrossing rate in the common morning glory, Ipomoea purpurea. Focusing just on results from the first experimental design and ignoring the color differences, these are the data they report:

<table>
<thead>
<tr>
<th>Maternal genotype</th>
<th>Offspring genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>Est(^F) Est(^F)</td>
<td>(267) (62) (0)</td>
</tr>
<tr>
<td>Est(^F) Est(^S)</td>
<td>(81) (120) (44)</td>
</tr>
<tr>
<td>Est(^S) Est(^S)</td>
<td>(0) (143) (170)</td>
</tr>
</tbody>
</table>

When plants reproduce by a mixture of self-fertilization and outcrossing the expected frequencies of getting a particular offspring genotype, given the mothers genotype can be written as:

\[
\begin{array}{c|ccc}
\text{Maternal genotype} & \text{Est}^F\text{Est}^F & \text{Est}^F\text{Est}^S & \text{Est}^S\text{Est}^S \\
\hline
\text{Est}^F\text{Est}^F & p_m\tau + (1 - \tau) & q_m\tau & 0 \\
\text{Est}^F\text{Est}^S & \frac{p_m\tau}{2} + (1 - \tau)/4 & \frac{1}{2} & \frac{q_m\tau}{2} + (1 - \tau)/4 \\
\text{Est}^S\text{Est}^S & 0 & p_m\tau & q_m\tau + (1 - \tau) \\
\end{array}
\]

where \(p_m\) is the frequency of the \text{Est}^F allele in successful male gametes and \(\tau\) is the fraction of offspring produced through outcrossing.

Using these data answer the following questions:

1. What is the outcrossing rate in this experimental population?
2. Is the allele frequency in maternal plants equal to the allele frequency in pollen that participates in fertilization?
3. What is the inbreeding coefficient in the maternal plants?
Hints

- Treat each maternal genotype separately, e.g., consider the numbers of $\text{Est}^F \text{Est}^F$ and $\text{Est}^F \text{Est}^S$ offspring derived from $\text{Est}^F \text{Est}^F$ mothers as a binomial sample.

  \[
  k_{\text{ff}} \sim \text{dbin}(ff, n_{\text{ff}}) \\
  ff \leftarrow \tau p_m + (1-\tau)
  \]

  where $k_{\text{ff}}$ is the number of $\text{Est}^F \text{Est}^F$ offspring from $\text{Est}^F \text{Est}^F$ mothers and $n_{\text{ff}}$ is the sample size of progeny from $\text{Est}^F \text{Est}^F$ mothers. Treat the offspring numbers from heterozygous mothers as a multinomial sample.

  \[
  k_{\text{fs}[1:3]} \sim \text{dmulti}(fs[], n_{\text{fs}}) \\
  fs[1] \leftarrow \tau p_m/2 + (1-\tau)/4 \\
  fs[2] \leftarrow 1/2 \\
  fs[3] \leftarrow \tau(1-p_m)/2 + (1-\tau)/4
  \]

  And treat the alleles in mothers as independent so that you can estimate $p_f$ as

  \[
  n_{\text{f}} \sim \text{dbin}(p_f, n) \\
  n_{\text{f}} \leftarrow 2n_{\text{ff}} + n_{\text{fs}} \\
  n \leftarrow 2(n_{\text{ff}} + n_{\text{fs}} + n_{\text{ss}})
  \]

- Use the following priors on the parameters.

  \[
  p_m \sim \text{dunif}(0,1) \\
  p_f \sim \text{dunif}(0,1) \\
  \tau \sim \text{dunif}(0,1) \\
  f \sim \text{dunif}(0,1)
  \]

- Input the data using this format.

  \[
  \text{list}(k_{\text{ff}}=267, n_{\text{ff}}=329, k_{\text{fs}}=c(81, 120, 44), n_{\text{fs}}=245, k_{\text{ss}}=143, n_{\text{ss}}=313)
  \]