PLSC 731: Paper Review

Vallejos et al – A molecular marker-based linkage map of *Phaseolus vulgaris* L. (reference pages in parentheses)

1. What was the status of the genetic map of *Phaseolus vulgaris* (common bean) prior to the publication of this paper? (733)
2. How can you overcome low levels of restriction fragment lengths polymorphisms (RFLP) in a species? (733)
3. What mapping population was used? (733)
4. Why were the phenotypic differences among the parents of the mapping population mentioned? (734)
5. Describe the nature of the probe library and why it was appropriate for this study? (734)
6. Given the methylation state of plants, were the enzymes used in the population screen appropriate? (734)
6. Why were probes pooled for the hybridizations? What permitted this technique? (734)
7. Explain Figure 1. (735)
8. Why did the authors mention that different restriction enzymes where able to detect more polymorphism? (735)
9. What is expected ratio of a single monogenic RFLP locus in a backcross population? (735)
10. Why should a person developing a molecular marker map be concerned about segregation distortion? (735)
11. How many loci were defined for this map? Why do more than one probe map to the same locus? (737)
12. How many duplicate loci were detected? How might duplicate loci occur genetically? (737)
13. Was the cloning of *Pst*I fragments a useful method of obtaining low copy number probes? (738)
14. Provide an explanation for the observation that clusters of markers were observed in this population. (738)