

## **PLSC 731: Paper Review**

### **Whitkus et al – Comparative Genome Mapping of Sorghum and maize**

#### **Introduction**

1. Prior to mapping, what was the approach typically used to study chromosomal evolution? What new approach is the focus of this paper? What previous results suggest this approach would work for sorghum and maize?
2. Why compare sorghum and maize? What evidence exists that these species might contain duplicated loci? What are the research questions raised in this paper?

#### **Materials and Methods**

1. Describe the sorghum mapping population. Describe the probes used in this study. Was the final wash at high or low stringency? Were the survey restriction enzymes appropriate? Was sufficient information provided for you to assess the molecular map?
2. How was a duplicate locus recognized, and how were they designated?

#### **Results**

1. Describe in detail the sorghum linkage map.
2. What is the organization of the sorghum linkage groups relative to maize? Discuss duplicate loci within a species, conservation of gene order, and conservation of map distances.
3. Discuss the status of duplicate loci in maize and sorghum.

#### **Discussion**

1. Why were the authors concerned that they discovered 13 linkage groups? How did they account for this?
2. Discuss the length of the sorghum linkage map and why it might be an underestimate.
3. Provide compelling evidence that maize is a duplicated genome. What mechanism might account for this?
4. What chromosomal events distinguish sorghum and maize?
5. What issues are related to detecting duplicated loci?