

CHAPTER IV CONCLUSIONS

In the current study, the nucleotide sequence homology among maize and a wide array of plant species was assessed using maize RFLP probes. Based on the results, it was possible to imply the genetic relatedness of maize to these plant species. The genetic relationships implied by this approach seem to be consistent with proposed phylogenetic relationships based on morphological and biochemical evidence. This indicates the feasibility of using this approach to study the genetic relatedness of wide arrays of plant species.

One of the objectives of this study was to compare the cDNA probes and random genomic probes for their ability to hybridize with the plant species analyzed. In general, cDNA probes hybridized with a wider array of plant species than the random genomic probes. Therefore cDNA probes seem to be more appropriate to be used in future studies of this kind.

The group of plant species analyzed in this study showed different levels of sequence homology to maize. Some of the species (such as *Z. mays* ssp. *mexicana*, *Z. mays* ssp. *parviglumis*, *Z. diploperrenis*, *Z. luxurians*, *Coix lacryma-jobi*) showed a very high degree of sequence homology to maize. Species such as *Sorghum sudanense*, *Sorghum bicolor*, *Tripsacum dactyloides*, *Saccharum officinarum*, *Sorghastrum nutans*, *Andropogon gerardii* and *Panicum miliaceum* also showed a fairly high degree of sequence

homology to maize. Therefore it would be possible to generate RFLP maps of these species using maize probes.