

## OB6. Sequence Comparison of Orthologous Regions in the Sorghum and Maize Genomes

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### Objectives

Comparative genome analysis of syntenic chromosomal regions has potential for the discovery of genes, genomic elements and evolutionary change. Also, by using comparative analysis, closely related small genome could be used as surrogate for map-based cloning of useful genes in the large genome species.

### Materials and Methods

- Target regions: colored aleurone(*cl/pl1*) and TATA-binding protein(*tbp*)
- Screening & physical mapping using the BACs of sorghum and maize with target genes, and constructing shotgun libraries with pCR4TOPO system(*Invitrogen*)
- Auto-sequencing(ABI3700), and assembling(phredPhrap/CONSED) of sorghum 2 BACs, Maize 4 BACs, and finishing with various sequencing chemistries including with/without thermofidase
- Putative gene-annotation:
  - a. Identifying various repetitive elements including transposable elements
  - b. Finding putative genic regions with different databases(TIGR, NCBI etc.) and gene prediction programs(GeneMark.hmm/FGENESH/Genescan etc.)

### Results and Discussion

We selected two regions(colored aleurone(*cl/pl1*) and TATA-binding protein(*tbp*)) of the sorghum and maize to accomplish analysis of micro-collinearity between the orthologous regions. Two sorghum BACs(*tbp* and *cl*) and four maize BACs(*tbp1/2* and *cl/pl1*) were identified, and total 975-kb was sequenced. The preliminary sequence analysis revealed conserved genes and their orders between sorghum and maize on two orthologous regions. The rearrangements were found from sorghum/maize and the homoeologous segments(paralogs) within maize since maize is potential tetraploidy. Analysis of other genomic elements including mobile elements is being conducted.

#### Sorghum-Maize Orthologous Region: *tbp*

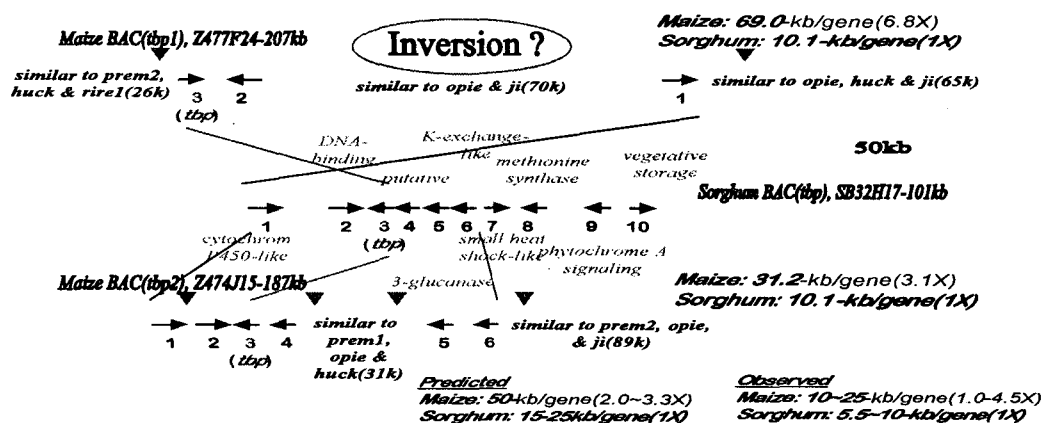


Fig 1. Example of sequence comparison on the genomic region of *tbp1* gene between sorghum & maize.

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