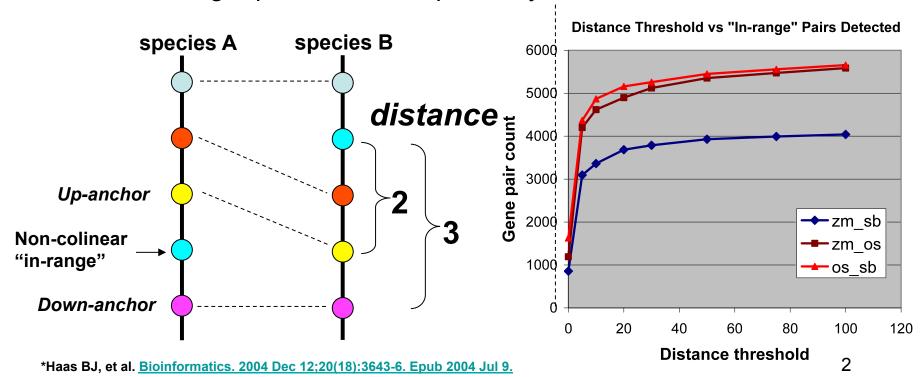
Aim1 Objectives

- Proposal: Evaluate WGA data in reference to gene-level synteny (based on colinear orthologs).
 - Find missing annotations, conserved noncoding, nature of rice "hypothetical" genes, signatures of moved genes.
- Curate incoming genomes with respect to annotation.
 - Develop generic attribute tags to describe low-confidence genes
 - E.g. MSU6 56.7 K loci, 16 K TE, 11 K "hypothetical"

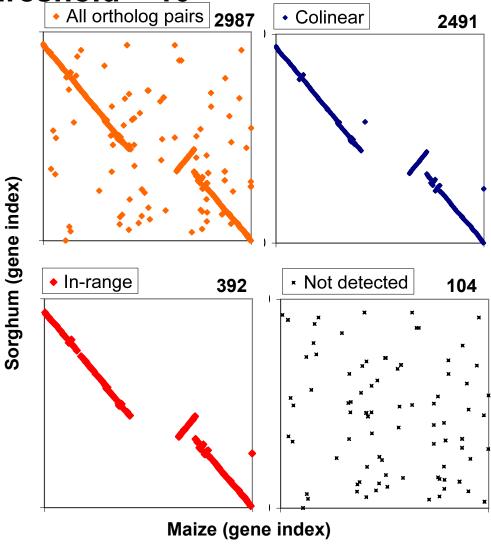
Prior year accomplishment: Synteny Detection Method

- Method developed for maize (Science paper).
- Reduced to practice as Gramene Runnables and DB by Zhenyuan (Jerry) Lu
- All ortholog pairs (from Compara) => assign numeric order
- DAGchainer* to find colinear chains (minimum length of 5 genes and no more than 10 genes intervening 2 neighbors)
- Add "in-range" pairs based on proximity to nearest colinear anchors

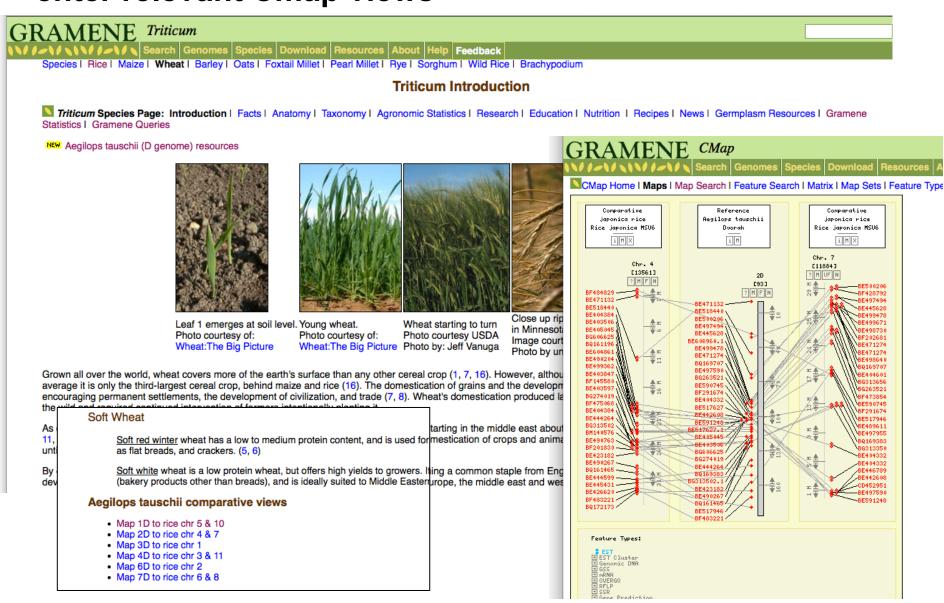


Example: Maize Chr. 1 vs Sorghum Chr. 1

Distance Threshold = 10



Preconfigured links added to Wheat species page to enter relevant Cmap views



Missing Links:

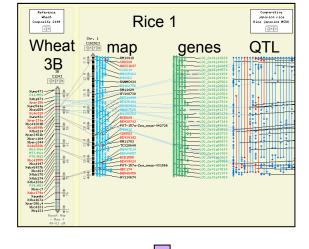
Find Genes and Variation Data for wheat Via Rice Synteny

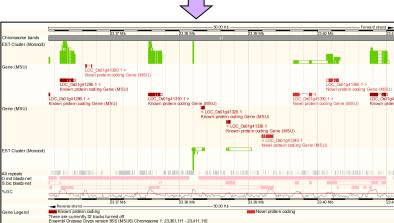
Genetic interval of interest

Need links to facilitate

SNP Markers







Rice Browser

- http://www.gramene.org/db/cmap/viewer?
 data_source=Build30;session_id=3c705f187ed4d10d254897703ea7463b;step=6;session_mod=start=1=grjp2009a-1=7000000;
- http://www.gramene.org/Oryza_sativa/Location/View?r=1:23361111-23411110;time=1262729945075.075
- http://www.gramene.org/db/diversity/diversity_view?
 action=show_allele_data&div_experiment_id=1&cdv_marker_id=24&db_name=diversity_wheat