

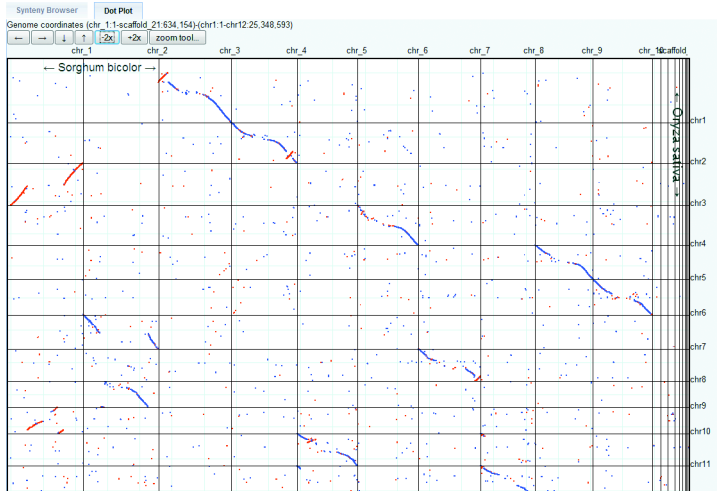
Visualizing genomes: techniques and challenges

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Supplementary figures and text:

Supplementary Figure 1	Global dot-plot of <i>Sorghum bicolor</i> and <i>Oryza sativa</i> assemblies displayed using VISTA-Dot.
Supplementary Figure 2	The VISTA Synteny Browser.

Supplementary Figure 1 Global dot-plot of *Sorghum bicolor* and *Oryza Sativa* assemblies displayed using VISTA-Dot.



Supplementary Figure 1. Axis scales are the lengths of concatenated *S. bicolor* and *O. Sativa* chromosomes (430 MB and 730 Mb, respectively). Red lines show alignments on different strands (i.e. inversions between genomes). Blue lines show alignments on the same strand. This plot highlights several large conserved regions between chromosomes of these two genomes. For example, there is extensive similarity between chromosome 2 of *O. sativa* and chromosome 4 on *S. bicolor* (blue) with a relatively large inversion (red).

Supplementary Figure 2 The VISTA Synteny Browser.



Supplementary Figure 2. An alignment of a *Mycosphaerella fijiensis* assembly and the *Mycosphaerella graminicola* finished genome is displayed at three levels of resolution. **(a)** An ideogram represents the whole-genome alignment. **(b)** Conservation within scaffold_7 of *M. fijiensis* is displayed. Syntenic regions are colored according to the chromosome to which they align on *M. graminicola*. **(c)** A “linked tracks” view is shown of *M. fijiensis* scaffold_7 versus *M. graminicola* chromosome 5. Regions in *M. fijiensis* (dark gray) are connected with lines to regions in *M. graminicola* (green) to indicate conservation. A gene model track is displayed as a line with hollow blocks immediately inside of the position scale for each organism. Both chromosome/scaffold can be zoomed and panned independently.