We have been developing a novel multiple-genome alignment software toolkit, and using programs developed so far, we comparatively studied the genome structures of grass and Arabidopsis plants. Whole-genome duplication, or polyploidization, typically doubles chromosome numbers in one generation. After that, chromosome numbers usually decline, sometimes eventually restoring the pre-polyploidy number. Chromosome number reduction has largely resulted from chromosome fusion, and biological mechanisms by which this occurs have been discussed. However, previous inference about the proposed mechanisms is still coarse and incompletely explains this complex dynamic process. Our recent study let us show how chromosome numbers reduced after recursively doubling or tripling in polyploidization. With other lines of evidence from human and yeast, we propose a new theory, emphasizing upon telomere-centric mechanism, to explain chromosome number reduction during the evolution of eukaryotes, which have linear chromosomes.

**RESULTS**

- With the support of this project, we have developed multiple software elements to align and graphically show genome alignment from global to local levels.
- Based on gene colinearity, we have developed software to align cotton, cacao and grape genomes, which helps understand the genome formation of cotton: it has a decaploid ancestor after splitting from cacao and other eudicots.

---

**PRODUCTS**

- Talks at conference
  - Wang X, Li XQ (2016). A brief introduction to the workshopGenomic features and chromosome functionality. Plant and Animal Genome Conference. (Workshop organizer)

**Publications**

- Wang X, ... Paterson AH. Multiple genome alignment spanning major Poaceae lineages reveals heterogeneous evolutionary rates and alters inferred dates for key events in grass evolution. Molecular Plant. 2013.

Contact: wang.xiyin@gmail.com