

Preface

The angiosperm family Brassicaceae is commonly termed the mustard family or, because of their characteristic flowers consisting of four petals in the form of a Greek cross, the Cruciferae. It comprises 338 genera assigned to 25 tribes and includes the widely studied species *Arabidopsis thaliana* (L.) Heynh. (thale cress) of the Camelinae and a diverse array of cultivated types within the Brassiceae, including oilseed rape, mustards, leafy vegetables, root vegetables, and cole (stem vegetable) crops.

The initial focus for the application of genomic approaches in the Brassicaceae was *A. thaliana*, which had been selected by the late 1980s as a “model” species in which to study plant biology at the molecular level. This was the first plant species for which a genome sequencing program was launched in the mid-1990s by the *Arabidopsis* Genome Initiative, culminating in 2000 in the landmark publication of an analysis of its complete genome sequence. This resource has facilitated the unprecedented expansion in our understanding of plant biology over the last decade.

Genomic and comparative genomic analyses have been applied to a number of species within the Brassicaceae, revealing much about genome evolution in plants, particularly after the publication of *Arabidopsis* genome sequence. Such studies revealed, for example, that the ancestral karyotype for the Brassicaceae was probably $n=8$, and that numerous chromosomal rearrangements and a reduction in chromosome number shaped the genome of *A. thaliana*. Angiosperms have a propensity to undergo chromosome doubling, or polyploidization. Such events are followed by a process of “diploidization,” during which genomes stabilize and gene copy number is reduced. The Brassicaceae presents an excellent opportunity to study these processes. The genome sequence of *A. thaliana* provides evidence for as many as three polyploidization events, the last of which occurred near the origin of the Brassicaceae, and is anticipated to be present throughout the family. A distinctive feature of the tribe Brassiceae is extensive subsequent genome triplication, indicative of a hexaploidy event. In addition, several species, particularly within the Brassiceae, are recently formed allotetraploids, e.g., *Brassica napus* ($n=19$) was formed by hybridization of *Brassica rapa* ($n=10$) and *B. oleracea* ($n=9$). Our increasing understanding of these processes is crucial for the interpretation of data from comparative genomic analyses.

The most extensive genomic resources have been developed for the tribe Camelinae, principally, though not exclusively, for *A. thaliana*. These include 130 Mb genome sequence of *A. thaliana*, 1.5 m *A. thaliana* ESTs, multiple commercially available *A. thaliana* microarrays, publicly available gene knockout lines, resource centers for plant lines and DNA stocks, and public databases.

Genomic resources are rapidly developing for the tribe Brassiceae, mainly driven by the economic importance of the *Brassica* species crops. These include ongoing genome sequencing of the *B. rapa* genespace, 0.8 m ESTs from *Brassica* species, a commercially available *Brassica* microarray, many linkage maps (some being integrated), mutagenized populations, resource centers for distribution of BAC libraries, public databases, and a steering committee to coordinate research efforts.

Genomic resources are being developed for a few species from other tribes, which are being studied primarily because of particular attributes, e.g., *Thlaspi caerulescens* which is being studied for metal hyperaccumulation, *Arabis alpina* for perenniality, *Thellungiella halophila* for salt tolerance, and *Boechera* sp. for apomixis.

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