

## Plant phylogenetics and molecular genetics in the new era of genomics (*Turkish Journal of Botany*, Vol: 38, Iss: 6, 2014)

Although our knowledge of plants has grown enormously in recent decades, accurate identification and deep molecular analyses are still well below the level of understanding that we need for the efficient utilisation of the vast amount of genetic diversity that they represent in the environment.

Systematic studies of plants have been experiencing revolutionary advances since the 1980s as novel genomic and cytogenetic techniques have been combined with sophisticated phylogenetic and statistical methods. These modern approaches have allowed taxonomists to investigate the foundations of plant diversity, dissecting the origins and the evolutionary relationships of lineages. New phylogenies serve as frameworks for classification and realignment of plant taxa, resulting in new systematic treatments of different plant groups (e.g., APG, APG II, APG III) and contributing to a new vision of the green clade of the tree of life. Nevertheless, in spite of these many advances, our knowledge is still far from complete. Poorly known groups require more intensive taxon sampling and/or more exhaustive gene sampling.

The deep power of next-generation sequencing (NGS) methodologies and their associated techniques has been used to characterise some of the 'omic' features of plants and to disentangle the causes and tempo of plant speciation processes as well as evolutionary relationships. While model plant species, like *Arabidopsis* for dicots, *Brachypodium* for monocots, *Trithuria* for basal angiosperms, and *Physcomitrella* for bryophytes, together with several main cultivars, are among the plant species with the largest data sets of genomic and functional information, NGS methods are adding a wide number of plant lineages to a deeper analysis of species evolution. Concomitantly with these technical advances, new bioinformatic tools have been developed and are continuously being improved to process and analyse large amounts of raw data to make them manageable and useful for comparative studies (e.g., colinearity, structure, and function), phylogenetic inference, and population-genomics and individual-level studies.

This first special issue of the *Turkish Journal of Botany* commemorates the botanical background of the journal, of almost 4 decades, and its evolution towards a modern forum for advanced papers on biological, systematic, molecular genetic, and phylogenetic studies of plants. *Turkish Journal of Botany* papers cover a broad taxonomic spectrum of plant organisms along with their genetics, including representatives of algae, bryophytes, ferns, conifers, and angiosperms, which are focused on studies in the Mediterranean and Eurasian regions but also include other parts of the world.

In this issue, a collection of novel contributions on modern studies of genome size evolution, biogeography, phylogeography, molecular and morphological systematics, molecular genetics, and population conservation of plants is presented.

In the plant phylogenetics part of the special issue, Pellicer and coworkers investigate the evolution of genome size and rDNA karyotype in annual versus perennial species of the large world genus *Artemisia* (Asteraceae), confirming that downsizing has been a main trend in the annual taxa, phylogenetically confined to the basal lineages of the *Artemisia* tree. In their multidisciplinary phylotaxonomic and geographic study of the Mediterranean *Crocus* series *Reticulati*, Harke and coworkers identify 2 geographically isolated groups, low-latitude Turkish and high-latitude Italian-Black Sea-Caucasus lineages, providing new descriptions for 3 species and a reassessment of the core group. Another taxonomic reassessment is reported by Kazemi and coworkers on *Tanacetum aureum* (Lam.) Greuter, M.V. Agab. & Wagenitz in Iran. The systematic and phylogenetic revision of the moss genus *Bucklandiella* (Grimmiaceae) conducted by Bednarek-Ochyra and coworkers identifies a new Australasian species and shows its taxonomic closeness and relationships with other New Zealand and South American taxa. In their reproductive and genetic study of *Salix lapponum*, Pogorzaletc and coworkers detect high levels of pollen viability but low levels of recruitment and genetic diversity in populations from Poland, addressing conservation strategies for this endangered species. Another endangered endemic plant, *Barbarea integrifolia* DC. from Turkey, is documented by Filiz and coworkers, while the plastid and nuclear genomes of the relict and endangered *Chamaedaphne calyculata* (L.) Moench from Poland are analysed through genomics approaches by Szczecinska and coworkers. Patterns of phylogeography and vicariance of *Chamaerops humilis* L. (Palmae) are documented by Garcia-Castano and coworkers, who recommend conservation of at least some populations in each region studied. Elçi and coworkers report genetic diversity of Turkish commercial cotton varieties using fibre quality traits in addition to molecular markers and provide a potential guide for selecting specific germplasms with distinct genetic backgrounds in cotton breeding programs. Another diversity study is reported by Ijbari and coworkers, who study *Tamarix* L. accessions through K-means clustering analyses.

Grimm and Denk report cryptic speciation in field maples; they conclude that the Colchic genotype represents a survivor of the initial radiation within the section *Platanoidea*, predating the formation of modern species. Four North African *Astragalus* taxa are studied through multiple approaches including karyotype analysis, physical rDNA mapping, and genome size determination by Baziz and coworkers, who suggest that genome comparisons are on the way to becoming routine analyses for plant molecular systematics and phylogenetics.

In the molecular genetics part of this special issue, Paczos-Grzeda and Bednarek report the comparative analysis of hexaploid *Avena* species using multiple approaches and suggest that *A. sterilis* could be the progenitor of *A. sativa* and *A. fatua*. *DREB1A* from rice is explored by Nawaz and coworkers as a potential candidate for production of abiotic stress-tolerant crop(s) in the future, through homology modelling and molecular docking. Öztürk and coworkers present work that documents subcellular localisation and developmental regulation of 6 soluble pyrophosphatase isoforms from *Arabidopsis thaliana*. Sun and coworkers study a novel zeaxanthin epoxidase (*EsABA1*) in tobacco and conclude that the elevated expression of *EsABA1* enhances the tolerance of transgenic tobacco plants to high salinity stress. Watermelon ethylene receptor genes by Karakurt and coworkers, grapevine dehydrin by Hanana and coworkers, and winter wheat *sucrose synthase 1* by Armoniene and Brazauskas are described with respect to molecular, physiological, and functional details. Conserved microRNAs and their target transcripts are identified by Din and coworkers as potential markers for better food content and higher nutritional value as well as biotic and abiotic stress resistance in potato. The review article by Raina and coworkers reports on medicinal plants as potential sources of anticancer agents.

We hope that this issue will encourage the publication of new studies on the phylogenetics and molecular genetics of plants in the focal area and in other regions of the world. The Mediterranean basin and its close biogeographic territories, from SW Asia to Macaronesia, constitutes the cradle of speciation of many plant lineages, which shared a common palaeogeographic and palaeoclimatic history. The region was also an important bridge for dispersal of Irano-Turanian-Himalayan, eastern Asian, European, and other Holarctic floras, and some African floras, at different geological ages. It also harboured several Pleistocene glacial refugia, which provided recent postglacial colonisation founders from these geographical settings to the neighbouring regions that contributed to the current distribution of plant species in this part of the northern hemisphere. Despite its importance, many of its plant groups are still in need of thorough genomic and evolutionary investigations to better understand the evolution of the enormous genetic diversity found in this region.

#### Guest Editors

##### Associate Prof Dr Ekrem DÜNDAR

Department of Biology, Faculty of Arts and Sciences,  
Balıkesir University, Balıkesir, Turkey

##### Prof Dr Daniel R. BUSH

Department of Biology, College of Natural Sciences,  
Colorado State University, Fort Collins, CO, USA

##### Prof Dr Pilar CATALAN

Department of Agricultural and Environmental Sciences,  
University of Zaragoza, Huesca, Spain

Department of Botany, Institute of Biology,  
Tomsk State University, Tomsk, Russia