
Preface

Potato (*Solanum tuberosum* L.; $2n = 4x = 48$) is the fourth most important food crop of the world after rice, wheat and maize, with a worldwide production of 381.68 million tons in the year 2014 (FAO). This highly productive non-cereal food crop, domesticated in the highland tropics of the Andes mountains in South America, has been declared the 'Food for the Future' by the United Nation's Food and Agriculture Organization, who celebrated the year 2008 as the 'International Year of the Potato'. By 2020, it is estimated that more than two billion people worldwide will depend on the potato for food, feed, or income. Potato is a member of the asterid clade of eudicot that represents 25% of the flowering plant species and it belongs to the Solanaceae, a family of about 90 genera and 2800 species. The family Solanaceae contains several well-known cultivated crops such as tomato (*Lycopersicon esculentum*), eggplant (*Solanum melongena*), tobacco (*Nicotiana tabacum*), pepper (*Capsicum annuum*), petunia, and potato (*Solanum tuberosum*). The International Code of Nomenclature of Cultivated Plants (ICNCP 2009) recognized four species of cultivated potato, i.e. *Solanum tuberosum*, with two cultivar groups, *Andigenum* containing diploids, triploids and tetraploids, and the *Chilotanum*, from which our modern tetraploid cultivars arise; *Solanum ajanhuiri* (diploid); *Solanum juzepczukii* (triploid); and *Solanum curtilobum* (pentaploid).

Despite the importance of potato as a world food crop, the genetics and inheritance of many important qualitative and quantitative agronomic traits of this crop were poorly understood. The reasons for the scanty knowledge on genetics of this crop are attributed to tetraploidy, the high degree of heterozygosity and the absence of homozygous inbred lines or any collection of genetically well-defined marker stocks. In addition, the long generation time and the frequently observed distorted segregation ratios discouraged geneticists from choosing the potato as a model species for genetic research. However, for a critical investigation of complex biological processes like tuberization, yield, disease resistance, etc. and to enable rapid, genome-based breeding strategies, a comprehensive genetic analysis of the crop was a prerequisite. To resolve this problem the international community of potato researchers took on the task of deciphering the entire genetic code of potato by sequencing. Thus, the Potato Genome Sequencing Consortium (PGSC) was initiated in January 2006, consisting of 29 laboratories spread over 15 countries, i.e. Argentina, Brazil, China, Chile, Denmark, India, Ireland, Italy,

The Netherlands, New Zealand, Peru, Poland, Russia, the United Kingdom and the United States of America. The consortium deciphered 727 MB of 844 MB potato genome using a unique homozygous doubled-monoploid potato clone (DM) and a hybrid sequencing approach consisting of Illumina sequencing-by-synthesis, Roche/454 Pyrosequencing, and the classical Sanger sequencing platforms. The PGSC sequenced the potato genome as a public effort and made it freely available to all the researchers. Free access to the potato genome data triggered extensive post-genomic work on gene discovery, marker development, evolutionary and plant diversity studies, improved breeding, and engineering of new phenotypes in potato, etc. Other scientific communities also utilized the sequence data to understand basic plant biology, biochemistry, and comparative genomics. This is evident from >880 citations of the *Nature* article on the potato genome sequencing by May 2017.

The present compilation is an attempt to assess the post-genomic research on structural and functional genomics, transcriptomics, repetitive sequences and their application, resistance genes and their application, nutrient use efficiency, and abiotic stress management in potato, etc. We hope the information compiled in this book will be useful for students, researchers, teachers, industry personnel and all other people interested in potato improvement, production and protection. The primary users of this book will be universities, public sector institutes as well as government and industrial potato biologists/breeders who are involved in research to understand biological and agronomic processes in potato. It will be our privilege to receive any suggestion for future improvement. We are grateful to Series Editor Prof. Chittaranjan Kole for giving us opportunity to prepare this book. We are highly thankful to Springer team for their valuable inputs.

Shimla, India
Wuhan, China
Shimla, India

Swarup Kumar Chakrabarti
Conghua Xie
Jagesh Kumar Tiwari

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Kumar Chakrabarti, S.; Xie, C.; Tiwari, J. (Eds.)

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