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Titolo	The Pigeonpea Genome / / edited by Rajeev K. Varshney, Rachit K. Saxena, Scott A. Jackson
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Edizione	[1st ed. 2017.]
Descrizione fisica	1 online resource (XVII, 104 p. 17 illus. in color.)
Collana	Compendium of Plant Genomes, , 2199-479X
Disciplina	633.37
Soggetti	Plant genetics Plant biotechnology Agriculture Plant Genetics Plant Biotechnology
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Pigeonpea genome: An overview -- Key plant and grain characteristics and their importance in breeding and adaptation of pigeonpea cultivars -- Botanical description of pigeonpea [Cajanus cajan (L.)Millsp.] -- Wide crossing technology for pigeonpea improvement -- Modern genomic tools for pigeonpea improvement: Status and Prospects -- Molecular mapping of genes and QTLs in pigeonpea -- Germplasm characterization and trait discovery -- Whole-genome sequencing of pigeonpea: requirement, background history, current status and future prospects for crop improvement -- Sequencing pigeonpea genome -- Future prospects.
Sommario/riassunto	Pigeonpea (Cajanus cajan) is a crop of small land holding farmers in arid and semi-arid regions of the world. It has a number of usages starting from protein rich food to vegetarian families; fuel wood; nitrogen supplier to soil; recycling minerals in soil to animal feed etc. Pigeonpea has been considered to be originated and domesticated in central India from where it travelled to different parts of the world such as Africa and Latin America. In ongoing scenario of climate change, biotic and especially abiotic stresses will make the conditions more

challenging for entire agriculture. This volume focusing on the pigeonpea genome will collate the information on the genome sequencing and its utilization in genomics activities, with a focus on the current findings, advanced tools and strategies deployed in pigeonpea genome sequencing and analysis, and how this information is leading to direct outcomes for plant breeders and subsequently to farmers.