Subodh Verma

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Professional Experiences

2023 - To date	Postdoc Fellow at Institute of Plant Genetics, Polish Academy of Sciences, Poznan,
	Poland
2019 - 2023	Postdoc Fellow at Central European Institute of Technology, Brno, Czech Republic,
	Hormonal Crosstalk in Plant Development-Helene Robert Boisivon group
2021 - 2023	Worked as Marie Curie Postdoc Fellow

• Investigating the transcriptional regulation of auxin biosynthetic genes in Arabidopsis embryo

Education

2012-2019	 Ph.D. Plant Molecular Biology, Plant Genetics & Genomics National Institute of Plant Genome Research (NIPGR); Jawaharlal Nehru University (JNU), Delhi, India Thesis title: Identification and characterization of genes related to seed development in chickpea (<i>Cicer arietinum</i> L.); Supervisor: Dr. Sabhyata Bhatia
2009-2011	M.Sc. Biotechnology Bundelkhand University Jhansi (U.P.), India 6 months MSc project on "Screening and characterization of iron storage, ferritin gene in various wheat varieties" at National Agri-Food Biotechnology Institute (NABI) Mohali, Punjab, India

Awards/Honours/Fellowships

2021	Plantae fellow by ASPB society
2019	Marie Skłodowska-Curie- Individual Fellowship from European Union
2012-2017	Junior & Senior Research Fellowship awarded by Department of Biotechnology (DBT), Govt of India
2013	Qualified National Eligibility Test (NET) for Lecture Ship; Rank: 25 conducted by Council of Scientific and Industrial Research (CSIR), India
2012	Qualified Graduate Aptitude Test in Engineering in Biotechnology (GATE-BT); 98.76 percentile

Publications

Verma S, Robert HS The MADS-box protein SHATTERPROOF 2 regulates *TAA1* expression in the gynoecium valve margins. (Under review in Plant reproduction journal).

Verma S, Attuluri VPS, & Robert HS (2022) Transcriptional control of Arabidopsis seed development. *Planta*, 255(4), 1-19. <u>https://doi.org/10.1007/s00425-022-03870-x</u>

Verma S, Attuluri VPS, Robert HS (2021) An Essential Function for Auxin in Embryo Development. *Cold Spring Harbor perspectives in biology*, a039966. https://doi.org/10.1101/cshperspect.a039966

Verma S, Bhatia S (2019) A comprehensive analysis of the B3 superfamily identifies tissue specific and stress responsive genes in chickpea (*Cicer arietinum L.*). *3 Biotech* 9: 346. https://doi.org/10.1007/s13205-019-1875-5

Verma S, Bhatia S (**2019**) Analysis of genes encoding seed storage proteins (SSPs) in chickpea (*Cicer arietinum* L.) reveals co-expressing transcription factors and a seed-specific promoter. *Funct Integr Genomics* 19, 373–390 (2019). <u>https://doi.org/10.1007/s10142-018-0650-8</u>

Verma S, Gupta S, Bandhiwal N, Kumar T, Bharadwaj C, Bhatia S (**2015**) High-density linkage map construction and mapping of seed trait QTLs in chickpea (*Cicer arietinum L.*) using Genotyping-by-Sequencing (GBS). *Scientific Reports* 5, 17512. <u>https://doi.org/10.1038/srep17512</u>

Pradhan S, Verma S, Chakraborty A, Bhatia S (2021) Identification and molecular characterization of miRNAs and their target genes associated with seed development through small RNA sequencing in chickpea. *Funct Integr Genomics* 20, 763–773. <u>https://doi.org/10.1007/s10142-021-00777-w</u>

Gaur R, Verma S, Pradhan S, Ambreen H (2020) A high-density SNP-based linkage map using genotyping-by-sequencing and its utilization for improved genome assembly of chickpea (*Cicer arietinum* L.). *Funct Integr Genomics* 20, 763–773.

Pradhan S, Kant C, **Verma S**, Bhatia S (**2017**) Genome-wide analysis of the CCCH zinc finger family identifies tissue specific and stress responsive candidates in chickpea (*Cicer arietinum L.*). *PLoS one*, *12*(7), e0180469 <u>https://doi.org/10.1371/journal.pone.0180469</u>

Gupta S, Kumar T, **Verma S**, Bharadwaj C, Bhatia S (**2015**) Development of gene-based markers for use in construction of the chickpea (*Cicer arietinum L*.) genetic linkage map and identification of QTLs associated with seed weight and plant height. *Mol Biol Rep*, 1-10. <u>https://doi.org/10.1007/s11033-015-3925-3</u>

Verma S, Pandey V, Chakraborty S, Bhatia, S. ABI3 controls seed protein content in chickpea (Under communication)

Book Chapters

Kant C, Pandey V, **Verma S,** Tiwari M, Kumar S (2017) Transcriptome analysis in chickpea (*Cicer arietinum L*): Applications in study of gene expression, non-coding RNA prediction and molecular marker development" in: Priscila Cirillo (eds.) Transcriptome Analysis, INTECH Open Access Publishers, ISBN 978-953-51-5452-5.

Alok A, sharma S, Kumar J, Verma S, sood H (2017) Engineering in plant Genome Using Agrobacterium: Process and Future. In: V.C. Kalia, A.K. Saini (eds.), Metabolic Engineering for Bioactive Compounds, Springer.