1.	Name	Dr. Swarup Kumar Chakrabarti
2.	Date and place of Birth	5th March, 1958, Gopinathpur (West Bengal)
3.	Mailing address	Director, ICAR-Central Potato Research Institute, Shimla 171 001, H.P.
4.	Telephone/email	
	Office (Landline, mobile)	Tel: 0177-2625073, Fax: 0177-2624460 Mobile: 9400014400
	Email	director.cpri@icar.gov.in

5. Academic qualifications (Bachelor's Degree Onward)

S.No.	Degree	Institution	Year
1.	B. Sc. (Ag.) Hons.	Bidhan Chandra Krishi Viswavidyalaya, Kalyani, West Bengal	1980
2.	M. Sc.	ICAR-Indian Agricultural Research Institute, New Delhi	1983
3.	Ph. D.	ICAR-Indian Agricultural Research Institute, New Delhi	1987
4.	Post-Doc	Waksman Institute, Rutgers, USA	2002-03
5.	Post-Doc	CIRAD-AMIS, IGEPAM, France	1999
6.	Post-Doc	NRCPB, IARI, New Delhi.	1995-97

6. Employment record

S.No.	Important position held	Period (From-To)
1.	Director, ICAR-Central Potato Research Institute, Shimla, Himachal Pradesh	27.01.2016 to continuing
2.	Director, ICAR-Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala	02.04-2012 to 26.01.2016
3.	Head, Plant Protection, ICAR-Central Potato Research Institute (CPRI), Shimla, HP	31.03.2009 to 01.04.2012
4.	Principal Scientist (Biotechnology), ICAR-Central Potato Research Institute (CPRI), Shimla, HP	14.07.2006 to 30.03.2009
5.	Senior Scientist, ICAR-Central Potato Research Institute (CPRI), Shimla, HP	27.07.1998 to 13.07.2006
6.	Scientist (Sr. Scale), ICAR-Central Potato Research Institute (CPRI), Shimla, HP	29.12.1991 to 26.07.1998
7.	Scientist S1, ICAR-Central Potato Research Institute (CPRI), Shimla, HP	29.12.1986 to 28.12.1991

7. Significant contribution

Potato genome: Country Leader of the Potato Genome Sequencing Consortium comprising of 26 international institutes belonging to 14 countries. The consortium deciphered the complex genome of potato that has been published in the high impact journal "Nature". This is the first genome of a plant belonging to Asterid clade of eudicot that represents 25% of flowering plant species. A total of 39,031 protein-coding genes have been predicted in the sequence.

Publication

(i) Xun Xu, Shengkai Pan, Shifeng Cheng, Bo Zhang, Desheng Mu, Peixiang Ni, Gengyun Zhang, Shuang Yang, Ruiqiang Li, Jun Wang; Gisella Orjeda, Frank Guzman, Michael Torres, Roberto Lozano, Olga Ponce, Diana Martinez, German De la Cruz; **S. K. Chakrabarti,** Virupaksh U. Patil, *et al.* 2011. Genome sequence and analysis of the tuber crop potato. *Nature* **475**, 14 July, pp. 189-195.

(ii) Visser, R.G.F., Bachem, C.W.B., de Boer, J. M., & Bryan, G.J., **Chakrabati, S.K.**, Feingold, S., Gromadka, R., van Ham, R.C.H.J., Huang, S., Jacobs, J.M.E., Kuznetsov, B., de Melo, P.E., Milbourne, D., Orjeda, G., Sagredo, B., Tang, X. 2009. Sequencing the Potato Genome: Outline and First Results to Come from the Elucidation of the Sequence of the World's Third Most Important Food Crop. *Am. J. Pot Res*. 86: 417-429.

Functional genomics of late blight resistance: High throughput transcriptome analysis of the late blight resistant Indian potato cultivar Kufri Girdhari revealed up-regulation of 2,344 genes post-inoculation compared to pre-inoculation stage. Selected highly up-regulated genes were further validated for their expression in the cultivar by real-time (RT) PCR analysis. The data indicated that molecular chaperones played critical role in controlling resistance in Kufri Girdhari.

Publication

(i) Sundaresha, S., Tiwari, J. K., Sindhu, R., Sharma, S., Bhardwaj, V., **Chakrabarti, S.K.**, Singh B.P. 2014. *Phytophthora infestans* associated global gene expression profile in a late blight resistant Indian potato cv. Kufri Girdhari. *Australian J Crop Sci* **8**: 215-222.

Genome sequence of potato leaf roll virus (PLRV): The ssRNA genome sequences of five PLRV isolates were determined. The genome comprised of 5,883 nucleotides and deduced genome organization resembled other PLRV isolates. About 97.6-98.7% similarities was observed within the Indian isolates and were more close to European, Canadian, African, American and Czech isolates (95.8–98.6 %) than to an Australian isolate (92.9–93.4 %). These isolates were 43.7–53.1 % similar to other poleroviruses and 29.1–29.3 % to Barley yellow dwarf virus, a luteovirus. Out of five isolates, the isolate PBI-6 was recombinant one as detected by RDP3 software.

Publication

(i) Jeevalatha, A., Priyanka Kaundal, Shandil, R. K., Sharma, N. N., **Chakrabarti, S. K.**, and Singh. B. P. 2013. Complete genome sequence of potato leafroll virus isolates infecting potato in the different geographical areas of India shows low level genetic diversity. *Indian Journal of Virology* **24**: 199-204.

Molecular profiling of potato pathogens: Molecular marker analysis showed genome flexibility and population shift in *Ralstonia solanacearum* and population fixation of *Phytophthora infestans* in hills and plains. Very high level of diversity was observed among the isolates collected form a single field and also within clonal population of a single isolate of *R. solanacearum*. Molecular phylotyping of this bacterium revealed that the potato race (race 3/biovar 2), which was virtually absent in sub-tropical regions, is now establishing in Madhya Pradesh, West Bengal, and Karnataka. Similarly, molecular marker study revealed that *P. infestans* isolates collected from the hills were clustered together and was different from that of isolates from Indian plains. Diversity among the isolates from plains was more than that of hill isolates.

Publication

(i) Grover, A., Azmi, W., Gadewar, A.V., Pattanayak. D., Naik, P.S., Shekhawat, G.S., and **Chakrabarti, S.K**. 2006. Genotypic diversity in a localized population of Ralstonia solanacearum (Smith 1896) Yabuchi et al. (1996) as revealed by random amplified polymorphic DNA (RAPD) markers. *Journal of Applied Microbiology* **101**: 798-806.

(ii) Sagar, V., A.K. Somani, R.K. Arora, S. Sharma, **S.K. Chakrabarti**, S.K. Tiwari, R. Chaturvedi, B.P. Singh. 2013. Status of bacterial wilt of potato in the Malwa region of Madhya Pradesh in India. *Journal of Plant Pathology* 95: 321-328.

(iii) Athya, I., Singh, B.P., **Chakrabarti, S.K.** and Pattanayak, D. 2005. Genetic diversity and differentiation of Indian isolates of *Phytophthora infestans* as revealed by RAPD analysis. *Indian Journal of Experimental Biology* 43: 817-823.

QTL for late blight resistance: The diploid wild potato species *Solanum chacoense* possesses horizontal resistance to late blight. A molecular map of the species with 209 AFLP markers was developed using 126 F_1 population of *S. spegazzinii* (susceptible) × *S. chacoense* (resistant). QTL analysis identified two QTLs (LOD>2.5) located on linkage groups IX and X for late blight horizontal resistance.

Publication

(i) **Chakrabarti, S.K.**, Singh, B.P., Thakur, Garima, Tiwari, J.K., Kaushik, S.K., Sharma, S., Bhardwaj, V. 2014. QTL analysis of late blight resistance in a diploid potato family of Solanum spegazzinii × S. Chacoense. *Potato Research* **57**: 1-11.

Genetic variability during micropropagation: Considerable genetic variability may arise during *in vitro* micropropagation of vegetatively propagated fruit trees. Molecular analysis of micropropagated clones of the apple rootstock MM106 demonstrated appreciable genetic variability among the clones. It is necessary to ascertain genetic fidelity of micropropagated clones before taking them to field.

Publication

(i) Modgil, M., Mahajan, K., **Chakrabarti, S.K.**, Sharma, D.R. 2005. Molecular analysis of genetic diversity in micropropagated apple rootstock MM106. *Scientia Horticulturae* **104**: 151-160.

Bt-brinjal for management of fruit and stem borer: A synthetic *cry1Ab* gene of *Bacillus thuringiensis* was designed and transferred to brinjal by cocultivating cotyledonary explants with *Agrobacterium tumefaciens*. Hybridization experiments demonstrated gene integration and mRNA expression. Das-ELISA revealed toxin expression in the transgenic plants. The expression resulted in a significant insecticidal activity of transgenic brinjal fruits against the larvae of fruit borer.

Publication

(i) Kumar, P.A., Mandaokar, A.D., Sreenivasu, K., **Chakrabarti, S.K.**, Kaushik, S.C., Sharma, S.R., Bisaria, S., Kaur, S. and Sharma, R.P. 1998. Insect resistant transgenic brinjal plants. *Molecular Breeding* **4**:33-37.

Late blight resistant transgenic potato: The race non-specific resistance gene *RB* cloned from the sexually incompatible diploid species *Solanum bulbocastanum* was utilized to develop potato cultivars with durable late blight resistance. Five promising clones (KJ-16, KJ-21, KJ-65, KJ-66, and KJ-77) carrying the *RB* gene and showing very high level of late blight resistance along with good agronomic characters and yield have been identified and advanced to seventh clonal generation (F_1C_7). RCGM clearance is awaited for undertaking BRL 1 and 2 trials. Availability of RB transgenic potato varieties will be a boon for resource-poor small and marginal farmers.

Publication

(i) Shandil, R. K, Vasudha Bhardwaj, S. K. Kaushik, P.H Singh, B.P. Singh, K.V. Raman, S.K. Pandey, and **S.K. Chakrabarti**. 2008. Late blight resistance in RB-transgenic potato clones is dependent on their genotypic background. In "Abstracts-Global Potato Conference 2008: Opportunities and Challenges in the New Millennium" Indian Potato Association, Central Potato Research Institute, Shimla, pp. 292 (Abstract: **Best poster award**).

Transgenic potato with improved protein quality and quantity: The grain storage protein gene (*AmA1)* of *Amaranthus hypochondriacus* has been transferred into seven Indian potato cultivars. Yield of the transformed lines were at par control but protein content increased by 23-54%.

Publication

(i) Chakraborty, S., Chakraborty, N., Agrawal, L., Ghosh, S., Narula, K., Shekhar, S., Naik, P.S., Pande, P.C., **Chakrabarti, S.K**., and Datta, A. 2010. Next-generation protein-rich potato expressing the seed protein gene AmA1 is a result of proteome

rebalancing in transgenic tuber. *Proceedings of the National Academy of Sciences of the United States of America* **107**: 17533-17538.

Transgenic potato for tuber moth management: It was observed that expression of *cry1Ab* gene in potato through CaMV35S promoter failed to confer tuber resistance. Therefore, a new binary vector (pBinCG1) was designed and constructed for tuber specific expression of a synthetic *cry1Ab* gene in potato using the GBSSi promoter. This vector was used to develop Bt-transgenic lines of the Indian potato cultivar Kufri Badshah that showed very good control of tuber damage by potato tuber moth.

Publication

(i) **Chakrabarti, S.K.**, Mandaokar, A.D., Shukla, A., Pattanayak, D., Naik, P.S., Sharma, R.P. and Kumar, P.A. 2000. *Bacillus thuringiensis cry 1Ab* gene confers resistance to potato against *Helicoverpa armigera* (Hubner). *Potato Research* **43**: 143-152.

(ii) Kumar, M. Chimote, V., Singh, R., Mishra, G.P., Naik, P.S., Pandey, S.K., **Chakrabarti, S.K.** 2010. Development of Bt transgenic potatoes for effective control of potato tuber moth by using *cry1Ab* gene regulated by GBSS promoter. *Crop Protection* **29**: 121-127.

Chloroplast transformation for potato tuber moth management: Designed a new plastid transformation vector (pSKC21) for very high level (13% of total soluble protein) of *cry9Aa2* gene expression in plants through chloroplast transformation. Transplastomic tobacco lines expressing the native *cry9Aa2* gene showed very high-level of resistance towards potato tuber moth. This process will minimize environmental risk of transgenic crops by minimizing transgene escape through pollens.

Publication

(i) Chakrabarti, S.K., Lutzz, K.A., Lertwirijawonng, B., Svab, Z., and Maliga, P. 2006. Expression of the cry9Aa2 B.t. gene in tobacco chloroplasts confers extreme resistance to potato tuber moth. *Transgenic Research* **15**: 481-488.

Diagnostics for potato viruses: Developed dipstick kits for detection of PVY, PVX, PVA, PVS, and PVM; PCR/RT-PCR protocols for PALCV, PSTVd; qPCR protocols for PVY, PLRV, PALCV; NASH protocols for PVY and PLRV. Standardized a protocol to produce PVY coat protein in *Escherichia coli* BL21 cells that was successfully utilized for polyclonal antisera production and ELISA kit development.

Publication

(i) Jeevalatha A, Kaundal P, Venkatasalam EP, **Chakrabarti SK**, Singh BP. 2013. Uniplex and duplex PCR detection of geminivirus associated with potato apical leaf curl disease in India. *Journal of Virological Methods* **193**:62-67.

(ii) Mukherjee, K., Verma, Y., **Chakrabarti, S.K.**, Singh, M.N., and Khurana, S.M. Paul. 2004. Phylogenetic analysis of 5'-UTR and P1 protein of Indian common strain of potato virus Y reveals its possible introduction in India. *Virus Genes* **29**: 229-237.

(iii) Mukherjee, K., Verma, Y., **Chakrabarti, S.K.**, Singh, M.N., and Khurana, S.M. Paul. 2003. Cloning and sequencing of coat protein gene of an Indian potato leaf roll virus (PLRV) isolate and its similarity with other members of luteoviridae. *Virus Genes* **26**: 247-253.

(iv) Jeevalatha, A., P. Kaundal, N. N. Sharma, Priyanka Thakur, **S. K. Chakrabarti**, B. P. Singh. 2013. Expression of coat protein of an ordinary strain of *Potato virus Y* in *Escherichia coli* and production of polyclonal antibodies for diagnosis. *Journal of Phytopathology* **161**: 671–674.

8. Products, Technologies and Patents developed and their commercialization

SN	Product/Technology	Description/Commercialization
1.	Unique potato germplam	Developed and registered a unique tetraploid parental line YY 6/3 C11 possessing PVY extreme resistance gene (Ryadg) in triplex state (INGR

		10143). This clone is routinely being used as a parent in breeding programme for PVY resistance, since almost all the progeny derived from any cross with this parent will have at least one dominant Ry_{adg} allele conferring extreme resistance to PVY.
2.	Molecular markers for agronomic traits	A SCAR marker has been identified for differentiation of late blight resistant potato varieties from susceptible ones. Similarly, cytoplasmic markers associated with early bulking and processing characters have been identified.
3.	DNA fingerprints of potato varieties	Since RAPD failed to provide robust and reliable identification of potato varieties, semi-automated simple sequence repeat (SSR) based DNA fingerprints of all the potato varieties and advanced hybrids have been developed. This is being used for genetic fidelity study under NCS-TCP as well as variety identification on regular basis.
4.	Software for quick and authentic identification of potato varieties	A computer software (VarTRAC) was developed for speedy identification of a variety based on 50 different morphological attributes and DNA fingerprints based on 127 alleles from 4 SSR markers.
5.	Dipstick kits for on the spot virus detection	Developed dipstick kits for detection of five major potato viruses at field level using gold nanoparticles. These kits are portable and easy to use by any stakeholder including farmers. The kits have been validated by both public and private seed growers and commercialized by CPRI (http://cpri.ernet.in/?q=node/254).
6.	Diagnostic for defection of bacterial wilt pathogen	A protocol for *in vitro* genome enrichment of *Ralstonia solanacearum* by rolling circle amplification using ϕ29 DNA polymerase has been standardized. This enabled detection of even 1 cfu/ml of the pathogen.
7.	Diagnostics for detection of *Phytophthora infestans*	Seed tubers harbouring latent infection play a key role in perpetuation of late blight pathogen. Visual inspection of tubers often fails to detect the pathogen in seed tubers that often serve as infection foci in the field. A PCR based protocol has been developed and validated for rapid detection of *P. infestans* in apparently healthy seed tubers.
8.	Vector for RNAi mediated virus resistance	A binary plant transformation vector (pBinGTLC2) with haipin loop construct of the potato apical leaf curl virus AC2 gene has been developed. This construct was used to develop transgenic lines of the potato cultivars Kufri Pukhraj and Kufri Badshah and promising transgenic lines with very high level of virus resistance have been identified (Manuscript under preparation).
9.	Plasmid vector for *in vitro* transcription	A new *in vitro* transcription vector pUC-IVT has been designed and prepared specifically for studying cleavage of mRNA by ribonuclease P.
10.	Fusion gene for management of	Two truncated *Bacillus thuringiensis* endotoxin genes, belonging to the class *cry1Ab* and *cry1B*, and both

	diamondback moth	coding for N-terminal toxic fragments of the corresponding crystal proteins, were translationally fused. Expression of the fusion gene driven by the *cry1C* promoter in *Escherichia coli* at a very high level resulted in a protein with enhanced toxicity to the diamondback moth.
11.	Artificial diet for potato tuber moth	An artificial diet and rearing system was standardized and validated for potato tuber moth larvae [*Phthorimaea operculella* (Zeller)] under laboratory conditions. Potato tuber moth (PTM) completed its life cycle on this artificial diet and produced new generation. This diet facilitated identification of Cry9Aa2 as the most potent Bt toxin against *P. operculella*.
12.	Cry toxin for managing *Helicoverpa armigera*	Reported for the first time that the Cry1Ac toxin of *Bacillus thuringiensis* is the most potent Bt toxin against the pod borer. This result has been taken as a standard by the international scientific community (The *Bacillus thuringiensis* Toxin Specificity Database; http://cfs.nrcan.gc.ca/projects/119/2). A novel synergistic effect between Cry1Ac and Cry1F toxins has been reported against *H. armigera*. This concept is being used for delaying emergence of Bt-resistant insect population.

9. Awards/Honours Received

Award/Special Attainments	Year	Awarding Organization
Shri L.C. Sikka Endowment Award	2013-14	National Academy of Agricultural Sciences, New Delhi
S. Ramanajuam Award	2008-11	Central Potato Research Institute, Shimla
Dr. J.P. Verma Memorial Award	2010	Indian Phytopathological Society
Biotechnology Overseas Associateship	2002-03	Department of Biotechnology
Biotechnology National Associateship	1995-97	Department of Biotechnology
Recognition Award for potato genome sequencing	2011	Indian Potato Association
Councilor	2010	International Society for Plant Pathology
Councilor	2013	South Asia, International Society for Tropical Root Crops
Expert Member, Academic Council	2013	Tamil Nadu Agricultural University
Zonal President	2013	Indian Phytopathological Society
Secretary	2008-09	Indian Potato Association
Joint Secretary	1998-01	Indian Potato Association
Subject Editor	2006-09	Potato Journal published by

		Indian Potato Association
Member, Editorial Board	2010	Indian Phytopathology published by Indian Phytopathological Society
Convener, Satellite session on RB-transgenic potato	2008	Global Potato Conference, 2008
Best poster award	2008	Global Potato Conference, 2008
Best poster award	2006	National Seminar on Gene Constructs, Indian Institute of Horticultural Research, Bangalore
Best paper award	2005	Potato Journal, 32: 17-23
Best poster award	2003	Indian Potato Association
Member, Institute Management Committee	2004-07	IIVR, Varanasi, UP
Member, Institute Management Committee	2005-08	NRCM, Solan, HP

10. Fellowship in the National Societies and Academies

Fellow	2016	National Academy of Agricultural Sciences
Fellow	2008	Indian Potato Association
Fellow	2013	Indian Phytopathological Society
Fellow	2012	Confederation of Horticultural Associations of India

11. International and national research projects handled

Role	Title of Project	Year
Country Leader	Potato genome sequencing consortium- a multinational project involving 26 international institutes belonging to 14 countries.	2007- 2012
Principal Investigator	PotBio: Generating biomarkers for breeding healthy potatoes – a Indo-European collaborative project involving India, the Netherlands, Germany, Spain , and UK.	2010-2012
Principal Investigator	Engineering late blight resistance in susceptible commercial Indian potato cultivars -a multinational project involving USA, India, Bangladesh, Indonesia, Philippines, and Uganda.	2005-08
Principal Investigator	Molecular tagging of extreme resistance to potato Y potyvirus (PVY) and horizontal resistance to late blight in potato (ICAR Network project).	2005-08
Principal Investigator	Development of polymerase chain reaction based diagnostics for bacterial wilt pathogen *Ralstonia solanacearum.*	2001-04
Co-PI	Development of transgenic potato resistant to tuber moth, *Pthorimea operculella* and late blight, *Phytophthora infestans.*	2000-03
Co-PI	ICAR Network project “Development of transgenic potato with resistance to major viruses”.	1995 to continuing
Associate	Engineering viral gene derived resistance in Indian potato cultivars against viruses.	2004-07

Associate	Molecular characterization of temperate fruit germplasm under the programme "Improvement of the temperate fruit crops".	2004-08
Associate	Purification and characterization of an essential ribonucleoprotein complex-ribonuclease P from potato.	2005-08
Associate	Artificial microRNA and small interfering RNA-mediated silencing of UDP-glucose Pyrophosphorylase and vacuolar acid invertase gene for reduction of cold-induced sweetening in potato. (DBT project).	2007-10
Associate	Development of dwarf potato cultivars suitable for cultivation in hills and peninsular India through recombinant DNA technology.	2004-07
Associate	Biochemical and genetical evaluation of variability in Indian strains of *Pseudomonas solanacearum,* the causal agent of potato bacterial wilt.	1996-2000

12. International exposure

Country	Purpose / Subject title	Year
Waksman Institute, Rutgers, New Jersey, USA	Chloroplast transformation in plants.	2002-03
CIRAD-AMIS, IGEPAM, Montpellier, France	Recombinant DNA technology.	1999
Monash University, Victoria, Australia.	Master Class on Plant and Microbial Molecular Genetics.	1994
Bangladesh Agricultural Research Institute, Ghazipur, Joydebpur, Bangladesh	Interaction with the fellow scientists involved in development of late blight resistant transgenic potato under the ABSP II-sponsored global project involving USA, India, Indonesia and Bangladesh.	2006
Manila, Philippines	To attend the Board Meeting of Agricultural Biotechnology Support Project II.	2006
The Wisconsin University, Madison, The Michigan State University, East Lansing, and The Cornell University, Ithaca, USA	Finalization of a collaborative project on "Development of late blight resistant potato using the *RB* gene cloned from the wild potato species *Solanum bulbocastanum*.	2004
Laboratory of Plant Breeding Drevendaalsesteeg 1 NL-6708 PD Wageningen The Netherlands	Participation in the Potato Genome Sequencing Consortium (PGSC) Workshop.	2007
Washington, D.C.; Research Triangle Park, North Carolina; and Davis and Fresno, California, USA	Confined Field Trial Training Workshop.	2008
Ithaca, New York, USA	Agribusiness management programme course 2010.	2010
Dhaka, Bangladesh	Potato Partner Level Meeting under the	2010

	CPRI (ICAR) – ABSP II ongoing collaborative research project.	
Dhaka, Bangladesh	Annual board meeting of Agricultural Biotechnology Support Project II (ABSP-II).	2011
Bandung, Indonesia	ABSP II meeting on late blight disease resistance development.	2013
Cornell, Washington DC and New York, USA	Management and leadership development programme	2014
Nanning, China	World Congress on Root and Tuber Crops	1016

13. List of publication

(a) Research papers

1. Raju, S., Stephen, R., Ravi, V., Sheela, M. N., Jayantikumar, M., and **Chakrabarti, S.K.** 2015. Evaluation of postharvest physiological deterioration in storage roots of cassava (*Manihot esculenta*) genotypes. *Indian Journal of Agricultural Sciences* **85**: 1279–84.
2. Pradhan, D.M.P., Mukherjee, A., George, J., **Chakrabarti, S.K.**, Vimala, B., Naskar, S.K., Sahoo, B.K. and Samal, S. 2015. High starch, beta-carotene and anthocyanin rich sweet potato: ascent to future food and nutrition security in coastal and backward areas. *International Journal of Tropical Agriculture* **33**: 397-400.
3. Byju,G and **Chakrabarti, S.K.** 2015. Invasiveness of feral plants of tropical tuber crops and its implications on germplasm conservation. *Journal of Root Crops* **40**: 99-101.
4. Maniyam, N., Singh, H., **Chakrabarti, S. K.**, Mukherjee, A., Khurana, D. S. 2015. Performance of short duration cassava varieties in trans-gangetic plain region of Punjab in India. *Journal of Root Crops* **39**: 234-237.
5. Kamala, S., Makeshkumar, T., Sreekumar, J., **Chakrabarti, S.K.** 2014. Whole transcriptome sequencing of diseased elephant foot yam reveals complete genome sequence of Dasheen mosaic virus. *Virology Reports*, http://dx.doi.org/10.1016/ j.virep.2014.11.001.
6. Kumar, R., Jeevalatha, A., Sharma, N. N., Sharma, S., **Chakrabarti, S.K.**, Singh, B. P. 2014. Development of PCR based methods for detection of Potato Aucuba Mosaic Virus in India. *Potato Journal* **41**: 166-174.
7. **Chakrabarti, S.K**., Singh, B.P., Thakur, Garima, Tiwari, J.K., Kaushik, S.K., Sharma, S., Bhardwaj, V. 2014. QTL analysis of late blight resistance in a diploid potato family of Solanum spegazzinii × S. Chacoense. *Potato Research* **57**: 1-11.
8. Sundaresha S. Tiwari, J.K., Sindhu, R., Sharma, S., Bhardwaj, V., **Chakrabarti, S.K.**, Singh B.P. 2014. *Phytophthora infestans* associated global gene expression profile in a late blight resistant Indian potato cv. Kufri Girdhari. *Australian Journal of Crop Science* **8**: 215-222.
9. Sagar, V., Jeevalatha, A., Mian, S., **Chakrabarti, S.K.**, Gurjar, M.S., Arora, R.K., Sharma, S., Bakade, R.R., Singh, B.P. 2013. Potato bacterial wilt in India caused by strains of phylotype I, II and IV of *Ralstonia solanacearum. European Journal of Plant Pathology* **138**: 51-65.
10. Hussain, T., Sharma, S., Singh, B.P., Jeevalatha, A., Sagar, V., Sharma, N.N., Kaushik,

S.K., **Chakrabarti, S.K.**, Anwar, F. 2013. Detection of latent infection of Phytophthora infestans in potato seed tubers. *Potato Journal* **40**: 141-148.

11. Kaushik, S. K., Sharma, R., Garg, I.D., Singh, B.P., **Chakrabarti, S.K.**, Bhardwaj, V., and Pandey, S.K. 2013. Development of a triplex (YYYy) parental potato line with extreme resistance to potato virus Y using marker assisted selection. *Journal of Horticultural Science & Biotechnology* **88**: 580–584.

12. Tiwari, J.K., Poonam, **Chakrabarti, S.K**., Kumar, V., Gopal, J., Singh, B.P., Pandey, S.K., Pattanayak, D. 2013. Identification of host gene conferring resistance to Potato virus Y using Ry gene-based molecular markers. *Indian Journal of Horticulture* **70**: 373-377.

13. Sagar, V., A.K. Somani, R.K. Arora, S. Sharma, **S.K. Chakrabarti**, S.K. Tiwari, R. Chaturvedi, B.P. Singh. 2013. Status of bacterial wilt of potato in the Malwa region of Madhya Pradesh in India. *Journal of Plant Pathology* **95**: 321-328.

14. Jeevalatha, A., P. Kaundal, N. N. Sharma, Priyanka Thakur, **S. K. Chakrabarti**, B. P. Singh. 2013. Expression of coat protein of an ordinary strain of *Potato virus Y* in *Escherichia coli* and production of polyclonal antibodies for diagnosis. *Journal of Phytopathology* **161**: 671–674.

15. Jeevalatha, A., Kaundal, P., Venkatasalam, E.P., **Chakrabarti, S.K.**, Singh, .BP. 2013. Uniplex and duplex PCR detection of geminivirus associated with potato apical leaf curl disease in India. *Journal of Virological Methods* **193**:62-67.

16. Jeevalatha, A., Priyanka Kaundal, Shandil, R. K., Sharma, N. N., **Chakrabarti, S. K.**, and Singh. B. P. 2013. Complete genome sequence of potato leafroll virus isolates infecting potato in the different geographical areas of India shows low level genetic diversity. *Indian Journal of Virology* **24** (2): 199-204.

17. Vijesh, N., **Chakrabarti, S.K.**, Sreekumar, J. 2013. Modeling of gene regulatory networks: A review. *Journal of Biomedical Science and Engineering* **6**: 223-231.

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