
Curriculum-vitae

Sandeep Kumar Kushwaha,

Scientist-E

National Institute of Animal Biotechnology (NIAB)

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Scientist-E (Nov 2019- Present), National Institute of Animal Biotechnology, Hyderabad, India

Researcher (March 2019- Sept 2019), Department of Biology, Lund University, Sweden

Job profile: Development of method to evaluate soil health and climate change indicators to facilitate agricultural management practices

Researcher (April 2018- Feb 2018), Department of Plant Breeding, SLU Alnarp, Sweden

Job profile: Development of method for the screening of resistant germplasm for resistant breeding

Postdoc (Aug 2015- March 2018), Plant breeding platform, Plant Breeding, SLU Alnarp, Sweden

Job profile: Bioinformatics data analysis and support for running collaborative projects between departments and SLU campuses, bioinformatics services and training courses.

Supervisor: Rodomiro Octavio Ortiz Rios

Research Engineer (July 2014 - July 2015), PlantLink, Plant Protection, SLU Alnarp, Sweden

Job profile: Bioinformatics data analysis and support for running collaborative projects between SLU Alnarp and Lund University, bioinformatics services and training courses.

Research Coordinator: Erik Alexandersson

Postdoc (Jan 2012-June 2014), Department of Biology, Lund University, Lund Sweden

Project: Functional and Structural diversity of microbes for carbon recycling in agricultural soils.

Supervisor: Katarina Hedlund, Dag Åhren

Ph.D.(2011), MANIT, Bhopal, M.P., India

Thesis: Computational Approach to Study Nucleotide and Peptide Sequences of *Mycobacterium tuberculosis*.

Advisor: Dr. Madhvi Shakya

M.Phil. (2007), APS University, M.P., India

Thesis: Tertiary Structure Prediction of Protein using Neural Network Techniques

Advisor: Prof. Vijay K. Agrawal

Post-Graduation (M.Sc. Bioinformatics, 2005), University of Allahabad, U.P. India

Thesis: Comparative Protein Modelling and Structural Analysis of Calmodulin Protein

Advisor: Prof. Dwijendra K. Gupta

Graduation (B.Sc., 2002), University of Allahabad University, U.P., India.

Professional Skills

- Track record of scientific publication and method development
- Proven success in the design, development, and deployment of data analysis pipelines
- Manage bioinformatics pipelines on shared computing infrastructure
- Next generation sequence data analysis expertise
- Genome assembly, gene prediction and annotation: identification, characterization and analysis and hand on genome assembly software.
- System biology- Gene and protein interaction, network analysis, function prediction, network reconstruction, multi-omics data integration and analysis
- Strong background in algorithms, data mining/machine learning and statistics for the development of analysis applications.
- Language: Perl, R, PHP
- Reproducible research tools: github, Rmarkdown
- Web database design and implementation.
- Experienced in Linux based server management, maintenance and services

Teaching Experience

- One and half year teaching experience as Associate lecturer at undergraduate and postgraduate level at JayPee University of Information Technology, India.

Developed Tool and Software

- **PINAT1.0:** protein interaction network analysis tool
- **MetCap:** a bioinformatics probe design pipeline for large-scale targeted metagenomics
- **NBSPred:** a support vector machine-based high-throughput pipeline for plant resistance protein NBSLRR prediction.
- **RGCap:** Resistance gene prediction and resistance gene sequence capture probe generation pipeline (manuscript writing)

Public Outreach Experience

- Contributed as volunteer in organizing 7th conference of International academy of Physical Sciences, 2004 at University of Allahabad.
- Manuscript reviewed (since 2010)
International Journal of Integrative Biology, Journal of Applied Life Sciences, The Open Bioinformatics Journal, Bentham Science Publisher, International Journal of Biological Macromolecules, Interdisciplinary Sciences: Computational Life Sciences, Science Asia journal, Cell Biochemistry and Biophysics, Network Modeling Analysis in Health Informatics and Bioinformatics, Springer, Bioinformatics, Oxford journals, Bioinformatics briefings, Molecular genetics and genomics, Journal of Experimental & Theoretical Artificial Intelligence, Journal of Biosciences, BioMed Research International

Membership of Professional Societies

- Indian Society of Technical Education (ISTE)
- Computer Society of India (CSI)
- Gwalior Academy of Mathematical Sciences (GAMS)
- Society of Applied Life Sciences (SALS)

Training in higher education teaching, research supervision and course design: Pedagogy courses

- Course in doctoral supervision (3 weeks), SLU, Sweden
- Teaching in Higher Education, basic course (3 weeks), SLU, Sweden

- Teaching in higher education, step two (2 weeks), SLU, Sweden
- Active e-learning course: course design and development (2 weeks), SLU, Sweden

Organized courses/Participated as resource person in bioinformatics training courses

- National Workshop on BIOINFORMATICS, 2007, at MANIT, Bhopal, M.P., India
- Introduction using databases for data mining and storage, (3-7 November 2015), Lund University, Sweden
- High Throughput Sequencing DNA and RNA-Seq Analysis for Plant Breeding (12-23 March 2018), SLU, Sweden.
- Short term course organised on "Next Generation Sequencing Data Analysis" at the Department of Biotechnology, MNNIT, India, December 17-23, 2018.

Research projects

- **2016-2017:** Computational Infrastructure: To drive the plant breeding education and research front at SLU, Kungliga Fysiografiska Sällskapet.
- **2016-2018:** The microbiome of the invasive pest *Drosophila suzukii* and its impact on the fly's sexual communication, behavior and reproduction, Crafoord foundation.
- **2016-2018:** Transcriptional regulation of oil in wheat, Crafoord foundation.
- **2017-2018:** Molecular Biology to Support Oat Breeding for Seed Development and Oil Storage, Kungliga Fysiografiska Sällskapet.
- **2018-2020:** Resistance Gene Array" a targeted approach for capturing of plant resistance genes, FORMAS.
- **2018-2019:** Targeted transcriptomics approach for the capturing of plant resistance genes at large scale Kungliga Fysiografiska Sällskapet.
- **2019-2020:** Promotion of Decoko (*Pisum sativum* ssp. *Abyssinicum*) for a food security in Ethiopia, VR network grant.

Workshop/Courses attended

- GENeco Summar meeting 2014, Kiplan, Skane Sweden.
- Attended GENeco Workshop on Genomic , 12-25 January, 2014, Cesky Krumlov, Czech Republic
- Attended course "DNA Amplification Technology", 21-25 October, 2013, Applied Microbiology, Lund University, Lund, Sweden.
- Attended four weeks course "Large scale genome analysis", 2013, Lund University, Lund, Sweden.
- Attended one week course "Transcriptome analysis", 2013, Lund University, Lund, Sweden.
- Attended one week course "Amplicon sequencing analysis", 2013, Lund University, Lund, Sweden.
- Attended course on "Statistics for Biologists" in 2012, Lund University, Lund, Sweden.
- Attended course on "Unix for Biologists" in 2012, Lund University, Lund, Sweden.
- Attended ISTE Workshop "Entrepreneurship Awareness Camp 2010", MANIT, Bhopal, India

Publications

Peer-reviewed original articles

- Desta ZA, Kolano B, Shamim Z, Armstrong SJ, Rewers M, Sliwinska E, Kushwaha SK, Parkin IA, Ortiz R, de Koning D-J: **field cress genome mapping: integrating linkage and comparative maps with cytogenetic analysis for rDNA carrying chromosomes.** *Sci Rep* 2019, **9**(1):1-14.
- Kushwaha SK, Grimberg Å, Carlsson AS, Hofvander P: **Charting oat (*Avena sativa*) embryo and endosperm transcription factor expression reveals differential expression**

- of potential importance for seed development.** *Molecular Genetics and Genomics* 2019:1-15.
- Kalyandurg PB, Tahmasebi A, Vetukuri RR, Kushwaha SK, Lezzhov AA, Solovyev AG, Grenville-Briggs LJ, Savenkov EI: **Efficient RNA silencing suppression activity of Potato Mop-Top Virus 8K protein is driven by variability and positive selection.** *Virology* 2019, **535**:111-121.
 - Vetukuri RR, Tripathy S, Malar C M, Panda A, Kushwaha SK, Chawade A, Andreasson E, Grenville-Briggs LJ, Whisson SC: **Draft genome sequence for the tree pathogen *Phytophthora plurivora*.** *Genome biology and evolution* 2018, **10**(9):2432-2442.
 - Vetukuri RR, Kushwaha SK, Sen D, Whisson SC, Lamour KH, Grenville-Briggs LJ: **Genome Sequence Resource for the Oomycete Taro Pathogen *Phytophthora colocasiae*.** *Molecular plant-microbe interactions* 2018, **31**(9):903-905.
 - Manoharan L, Kushwaha SK, Ahren D, Hedlund K: **Agricultural land use determines functional genetic diversity of soil microbial communities.** *Soil Biology & Biochemistry* 2017, **115**(December 2017):423-432.
 - Grenville-Briggs LJ, Kushwaha SK, Cleary MR, Witzell J, Savenkov EI, Whisson SC, Chawade A, Vetukuri RR: **Draft genome of the oomycete pathogen *Phytophthora cactorum* strain LV007 isolated from European beech (*Fagus sylvatica*).** *Genomics data* 2017, **12**:155-156.
 - Kushwaha SK, Vetukuri RR, Grenville-Briggs LJ: **Draft genome sequence of the mycoparasitic oomycete *Pythium oligandrum* Strain CBS 530.74.** *Genome Announc* 2017, **5**(21):e00346-00317.
 - Kushwaha SK, Vetukuri RR, Grenville-Briggs LJ: **Draft genome sequence of the mycoparasitic oomycete *Pythium periplocum* strain CBS 532.74.** *Genome Announc* 2017, **5**(12):e00057-00017.
 - Roy A, Walker III WB, Vogel H, Kushwaha S, Chattington S, Larsson M, Anderson P, Heckel DG, Schlyter F: **Data set for diet specific differential gene expression analysis in three *Spodoptera* moths.** *Data in brief* 2016, **8**:448-455.
 - Hofvander P, Ischebeck T, Turesson H, Kushwaha SK, Feussner I, Carlsson AS, Andersson M: **Potato tuber expression of *Arabidopsis* WRINKLED1 increase triacylglycerol and membrane lipids while affecting central carbohydrate metabolism.** *Plant biotechnology journal* 2016, **14**(9):1883-1898.
 - Manoharan L, Kushwaha SK, Hedlund K, Ahrén D: **Captured metagenomics: large-scale targeting of genes based on ‘sequence capture’ reveals functional diversity in soils.** *DNA Research* 2015, **22**(6):451-460.
 - Kushwaha SK, Manoharan L, Meerupati T, Hedlund K, Ahrén D: **MetCap: a bioinformatics probe design pipeline for large-scale targeted metagenomics.** *BMC Bioinformatics* 2015, **16**(1):65.
 - Kushwaha SK, Chauhan P, Hedlund K, Ahrén D: **NBSPred: a support vector machine-based high-throughput pipeline for plant resistance protein NBSLRR prediction.** *Bioinformatics* 2015, **32**(8):1223-1225.
 - Sagarika Biswas SKK, Rahul S. Mandal, Saugata Roy, Das HR: **Structural Model Based Designing of Inhibitors for Glial Fibrillary Acidic Protein.** *Annals of Biological Research* 2011, **2**(1):40-50.
 - Kushwaha SK, Shakya M: **Protein interaction network analysis—Approach for potential drug target identification in *Mycobacterium tuberculosis*.** *Journal of theoretical biology* 2010, **262**(2):284-294.
 - Mehta N, Raikwar A, Chauhan P, Kushwaha S, Pardasani K: **Identification of *Klebsiella granulomatis* strain K22-14 16S rRNA gene and its primer design.** *Journal of Pharmaceutical Sciences and Research* 2010, **2**(10):628.

- Sharma N, Kushwaha SK, Chauhan P, Shakya M: **Development of Efficient Drug Analogs for Dutasteride through Insilico Modeling**. *Internet Journal of Medical Informatics* 2009, 5(Issue 1):p2.
- S K Kushwaha NS, M Jha, K Menaria: **Molecular Dynamics Assessment of Modelled IgG Binding Receptor Protein (1PGB)**. *The Internet Journal of Bioengineering* 2008, 4(1):1-5.
- Kushwaha SK, Shakya M: **Molecular modelling and dynamics studies of Mycobacterium tuberculosis protein RelA (Rv2583c)**. *International Journal of Integrative Biology* 2009, 7(3):135.
- Kushwaha SK, Shakya M: **PINAT1. 0: protein interaction network analysis tool**. *Bioinformatics* 2009, 3(10):419.
- Kushwaha S, Shakya M: **Protocol of Rice Genome Annotation through Comparative Functional Genomics Approach**. *Internet Journal of Genomics & Proteomics;2009* 2009, 4(Issue 1):p4.
- Kushwaha S, Chauhan P, Jha M, Shrivastava S: **Rational drug designing for drug target alanine racemase (Alr) of mycobacterium tuberculosis**. *The Internet Journal of Laboratory Medicine* 2009, 3(2).
- Kushwaha S, Chauhan P, Shakya M: **Comparative Phylogenetics Approach for Discovering Alternative Source of Taxol**. *The Internet Journal of Bioengineering* 2008, 3(2).

Peer-reviewed review paper

- Paritosh K, Kushwaha SK, Yadav M, Pareek N, Chawade A, Vivekanand V: **Food waste to energy: an overview of sustainable approaches for food waste management and nutrient recycling**. *BioMed research international* 2017, 2017.
- Maurya NS, Kushwaha S, Mani A: **Recent Advances and Computational Approaches in Peptide Drug Discovery**. *Current pharmaceutical design* 2019, 25(31):3358-3366.

Peer-reviewed original articles (submitted)

- Erik Alexandersson, Sandeep Kushwaha, Aastha Subedi, Deborah Weighill, Sharlee Climer, Daniel Jacobson, Erik Andreasson: **Linking crop traits to transcriptome differences in a progeny population of tetraploid potato**, BMC Plant Biology (revised)
- Sandeep Kumar Kushwaha, Ramesh R. Vetukuri, Firuz Odilbekov, Nidhi Pareek, Tina Henriksson, Aakash Chawade : **Differential gene expression analysis of wheat breeding lines reveal molecular insights in yellow rust resistance under field condition**, Scientific report (revised)
- Shumei Wang, Ramesh R Vetukuri, Sandeep K Kushwaha, Pete Hedley, Jenny Morris, David J Studholme, Petra C Boevink, Paul RJ Birch1, Stephen C Whisson; **Infection of the model host plant *Nicotiana benthamiana* by *Phytophthora kernoviae* as a system to study tree pathogens**; Journal of experimental botany, Oxford.

Peer-reviewed conference papers

- Kushwaha SK, Shakya M: **Neural Network: A Machine Learning Technique for Tertiary Structure Prediction of Proteins from Peptide Sequences**. In: *2009 International Conference on Advances in Computing, Control, and Telecommunication Technologies: 2009*. IEEE: 98-101.
- Kushwaha SK, Shakya M: **Multi-layer perceptron architecture for tertiary structure prediction of helical content of proteins from peptide sequences**. In: *2009 International*

Conference on Advances in Recent Technologies in Communication and Computing: 2009. IEEE: 465-467.

- Rathore B, Kushwaha SK, Shakya M: **Identification of Melanoma (Skin Cancer) Proteins through Support Vector Machine.** In: *International Conference on Advances in Information and Communication Technologies: 2010.* Springer, Berlin, Heidelberg: 571-575.

Book Chapter

- Yadav BS, Chauhan P, Kushwaha S: **Bioinformatics Resources for Microbial Research in Biological Systems.** In: *Microbial Genomics in Sustainable Agroecosystems.* Springer, Singapore; 2019: 45-60.
- Yadav BS, Singh AK, Kushwaha SK: **Systems-Based Approach to the Analyses of Plant Functions: Conceptual Understanding, Implementation, and Analysis.** In: *Plant Bioinformatics.* Springer, Cham; 2017: 107-133.

Poster

- Vetukuri RR, Kalyandurg PB, Sen D, Kushwaha S, Brus-Szkalej M, Boevink P, Whisson SC, Savenkov EI, Grenville-Briggs LJ: **The role of viral and oomycete suppressors of silencing in modulating plant defense.** In: *2019 IS-MPMI XVIII Congress: 2019.* ISMPMI.
- Sen D, Kushwaha S, Lamour K, Tripathy S, Grenville-Briggs L, Vetukuri R: **New insights into pathogenicity of the emerging tropical pathogen: Phytophthora colocasiae on taro,** molecular plant-microbe interactions: 2019
- Kushwaha SK, Manoharan L, Hedlund K, Ahren D, **Protein interaction analysis approach for the investigation of lignin degradation pathways,** Lund University, May 2015, Sweden, London

Conferences attended/presented in Abroad

- Kushwaha SK, Manoharan L, Hedlund K, Ahren D, **Protein interaction analysis approach for the investigation of lignin degradation pathways,** Bioinformatics, Computational Biology and Biomedical Engineering, April 2013, UK, London
- Kushwaha SK, Participated in the 14th International Symposium on Microbial Ecology, Aug 2012, Copenhagen, Denmark

Conferences attended/presented in India

- Kushwaha SK, Shakya M: Multi-layer perceptron architecture for tertiary structure prediction of helical content of proteins from peptide sequences. In: *Advances in Recent Technologies in Communication and Computing, 2009 ARTCom'09 International Conference on: 2009: IEEE; 2009: 465-467, Kottayam, Kerala*
- Kushwaha SK, Shakya M: Neural Network: A Machine Learning Technique for Tertiary Structure Prediction of Proteins from Peptide Sequences. In: *Advances in Computing, Control, & Telecommunication Technologies, 2009 ACT'09 International Conference on: 2009: IEEE; 2009: 98-101, Thiruvananthapuram, Kerala.*
- Kushwaha SK, Shakya M., Multi-Layer Perceptron Architecture for Prediction of the Tertiary structure of Proteins from Peptide Sequence, Thirteenth Annual Conference & First International conference of GAMS on Mathematical Modelling in Engineering and Biosciences, Dec. 2008, Agra, U.P., India.

- Kushwaha SK, Shakya M: Protein interaction network analysis approach for potential drug target identification in Mycobacterium tuberculosis, 24th M.P. Young Scientist Congress, MPCST- 2009, Bhopal, M.P., India
- Kushwaha SKK, Simulation of a Soft Object Approach in Life Science, Presented Paper in National Seminar on Biotechnology and its Role in Facilitation of Green Revolution, 2006, Bhopal M.P., India
- Kushwaha SK, Structure Prediction and Analysis of Calmodulin Protein, presented Paper in National Symposium on Recent Trends on Molecular biology, 2006, Cancer Research Institute Gwalior, M.P., India
- Kushwaha SK, Homology Approach of Active Site Prediction of DBAT of Taxol Biosynthetic Pathway, Presented Paper in 12th Annual Conference of Gwalior Academics and Mathematical Sciences, 2007, Bhopal, M.P., India
- Kushwaha SK. Protocol of Sequence Search and Analysis, 7th Conference of International Academy of Physical Sciences, CONIAPS-VII 2004, at University of Allahabad, U.P., India