

Sarwar Azam

Scientist B

National Institute of Animal Biotechnology, Hyderabad

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Academic qualifications

M. Tech. (Computational and Systems Biology)	Jawaharlal Nehru University, New Delhi, India	(2007-2009)
M. Sc. (Biotechnology)	Jamia Millia Islamia, New Delhi, India	(2004-2006)
B. Sc. (Biosciences)	Jamia Millia Islamia, New Delhi, India	(2001-2004)

Details of employment

Scientist B	<i>National Institute of Animal Biotechnology, Hyderabad, India</i>	November, 2013 to till date
Special Project Scientist (Computational genomics)	<i>International Crops research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India</i>	Nov., 2012 to Nov., 2013
Visiting Scientist (Bioinformatics)	<i>International Crops research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India</i>	Nov., 2010 to Oct., 2012
Senior Research Fellow (Bioinformatics)	<i>National Institute of Plant Genome Research (NIPGR), New Delhi, India</i>	March, 2010 to Oct., 2010

Awards & Fellowships

- **Certificate of Appreciation** for the outstanding contribution in the area of Functional Genomics and Bioinformatics for the year 2011 as part of **Bioclues Innovation, Research and Development (BIRD)** award
- **"Exceptional Scientific Article in a High Impact Journal Award"** from ICRISAT in 2011
- CSIR – UGC NET examination in Life sciences held in June 2008, December 2008 & June 2009
- DBT fellowship 2007-2009 for M.Tech. course
- BCIL Fellowship for BITP from DBT, Govt. of India, 2006
- Merit scholarship by central wakf board, MOMA, Govt. of India, 2004
- Merit scholarship by central wakf board, MOMA, Govt. of India, 2003
- Qualified for Jawahar Navodaya Vidyalaya entrance exam to get admission in class VIth, which was fully funded by MHRD, Govt. of India upto class XIIth.

Bioinformatics Software Developed

- **ccSAMFlex**: a tool to Predict the SNPs on basis of coverage base consensus calling (CbCC) method. Tool is written in perl and has been added in ISMU pipeline
- **ISMU** – Integrated SNP Mining and Utilization (ISMU) pipeline: The pipeline is user friendly with GUI and automated workflow for SNP discovery from next generation short sequences and also predict the best set of SNPs for further genotyping. Pipeline integrate various open source tools, offers a wide range of choice to user for alignment and SNP prediction.
- **BhainsBase**: A database for buffalo genomic research developed in Java environment using PostgreSQL database management system.
- **Genome comparison Tool (GCT)** : Tool can compare two genome sequences of prokaryote and display their syntenic regions as Circos output.

Extra-mural Project details

S. No.	Name of the project	Funding agency	Status	year	Role
1	Development of Integrated SNP mining and utilization pipeline	Generation Challenge programme (GCP)	Completed	2011	Co-Investigator
2	Genome wide association study for identification of novel loci associated with resistance to Theileriosis in India	Department of Biotechnology (DBT)	Ongoing	2015	Co-Principle Investigator

Association with scientific society

- ❖ Life time member of Association for the Promotion of DNA Fingerprinting – ADNAT
- ❖ Member of Bioclues

Publications (Cumulative Impact Factor= 142, Total Citations=995)

1. Varshney, R.K., Song, C., Saxena, R.K., **Azam, S.**, *et al.* (2013) Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nature Biotechnology* doi:10.1038/nbt.2491
2. Varshney, R.K., Chen, W., Li, Y., Bharti, A.K., Saxena, R.K., Schlueter, J.A., Donoghue, M.T.A., **Azam, S.**, *et al.* (2012) Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nature Biotechnology* 30:83–89
3. **Azam, S.**, Thakur, V., Pradeep, R., *et al.* (2012) Coverage based consensus calling (CbCC) of short sequence reads and comparison of CbCC-results for the identification of SNPs in chickpea, a crop species without the reference genome. *American journal of Botany* 99:186-192
4. Gaur, R., **Azam, S.**, Jeena, G., *et al.* (2012) High-throughput SNP discovery and genotyping for constructing a saturated linkage map of chickpea (*Cicer arietinum* L.). *DNA Research* doi:10.1093/dnares/dss018
5. Chen, X., Zhu, W., **Azam, S.**, *et al.* (2012) Deep sequencing analysis of the transcriptomes of peanut arial and subterranean young pods identifies potential genes related to early embryo abortion. *Plant Biotechnology Journal* doi: 10.1111/pbi.12018
6. Kim, D., Parupalli, S., **Azam, S.**, Lee, S. and Varshney, R.K. (2013) Comparative sequence analysis of nitrogen fixation-related genes in six legumes. *Frontiers in Plant Genomics and Genetics* doi: 10.3389/fpls.2013.00300
7. Ali, L., Madrid, E., Varshney, R.K., **Azam, S.**, *et al.* (2013) Mapping and identification of a *Cicer arietinum* NSP2 gene involved in nodulation pathway. *Theoretical and Applied Genetics* doi: 10.1007/s00122-013-2233-3
8. **Azam, S.**, Rathore, A., Shah, T., *et al.* (2013) ISMU: Integrated SNP mining and utilization pipeline for accelerated breeding. *PLoS One* doi: 10.1371/journal.pone.0101754
9. Kudapa*, H., **Azam***, S., Sharpe A.G, *et al.* (2014) Comprehensive transcriptome assembly of chickpea (*Cicer arietinum*) using Sanger and Next Generation Sequencing platforms: Development and applications. *PLoS One* doi: 10.1371/journal.pone.0086039
10. Ruperao, P., Chan, C., **Azam, S.**, *et al.* (2014) Chromosomal genomics for genome assembly validation. *Plant Biotechnology Journal* doi: 10.1111/pbi.12182
11. RK Varshney, RR Mir, S Bhatia, M Thudi, Y Hu, **S Azam**, *et al.* (2014) Integrated physical, genetic and genome map of chickpea (*Cicer arietinum* L.). *Functional & integrative genomics* 14 (1), 59-73
12. Jaganathan, D., Thudi, M., Kale, S., **Azam, S.**, *et al.* (2014). Genotyping-by-sequencing based intra-specific genetic map refines a “QTL-hotspot” region for drought tolerance in chickpea. *Molecular Genetics and Genomics*, 1-13.

13. Mir, R. R., Kudapa, H., Srikanth, S., Saxena, R. K., Sharma, A., **Azam, S.**, *et al.* (2014). Candidate gene analysis for determinacy in pigeonpea (*Cajanus* spp.). *Theoretical and Applied Genetics*, 127(12), 2663-2678.
14. Ali, L., **Azam, S.**, Rubio, J., *et al.* (2015) Detection of a new QTL/gene for growth habit in chickpea CaLG1 using wide and narrow crosses. *Euphytica*, 1-13.
15. Sinha, P., Pazhamala, LT., Singh, VK., Saxena, RK., Krishnamurthy, L., **Azam, S.**, *et al.* (2015) Identification and validation of selected universal stress protein domain containing drought-responsive genes in pigeonpea (*Cajanus cajan* L.). *Frontiers in plant science*, 6:1065.
16. Angela*, HW., Sharma*, M., Thatcher*, LF., **Azam***, S., Hane, JK., *et al.* (2016) Comparative genomics and prediction of conditionally dispensable sequences in legume–infecting *Fusarium oxysporum* formae speciales facilitates identification of candidate effectors. *BMC Genomics*, 17:191.
17. **Azam, S.**, Rao, S. B., Jakka, P., NarasimhaRao, V., Bhargavi, B., Gupta, V. K., & Radhakrishnan, G. (2016). Genetic characterization and comparative genome analysis of *Brucella melitensis* isolates from India. *International Journal of Genomics*, 2016.
18. Faisal, S. M., Varma, V. P., Subathra, M., **Azam, S.**, *et al.* (2016). Leptospira surface adhesin (Lsa21) induces Toll like receptor 2 and 4 mediated inflammatory responses in macrophages. *Scientific Reports*, 6.
19. Parthasarathy*, S., **Azam***, S., Lakshman Sagar, A., Narasimha Rao, *et al.* (2017). Genome-guided insights reveal organophosphate-degrading *Brevundimonas diminuta* as *Sphingopyxis wildii* and define its versatile metabolic capabilities and environmental adaptations. *Genome biology and evolution*, 9(1), 77-81.

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