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Sarwar Azam

Current Designation and Organization

Scientist B

(from November, 2013 to till date)

*National Institute of Animal Biotechnology (NIAB),
Hyderabad*

Previous Organization and Designation

Special Project Scientist (Computational Genomics),

(from November, 2012 to November, 2013)

*International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru, Hyderabad, India*

Visiting Scientist (Bioinformatics),

(from November, 2010 to October, 2012)

*International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru, Hyderabad, India*

Senior Research Fellow (Bioinformatics),

(from March, 2010 to October, 2010)

National Institute of Plant Genome Research (NIPGR), New Delhi, India

Education

M.Tech. (Computational and Systems Biology)

2009 Jawaharlal Nehru University

New Delhi, India

M.Sc. (Biotechnology)

2006 Jamia Millia Islamia

New Delhi, India

B.Sc. (Bio-Sciences)

2004 Jamia Millia Islamia

New Delhi, India

Awards/Fellowship /Success achieved

- **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 VI, which was fully funded by MHRD, Govt. of India upto class XII.

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 and automate workflow of SNP discovery from next generation short sequences and also predict the best set of SNPs for further genotyping. Pipeline integrate various open source tool, offers a wide range of choice to user for predicting SNPs. Ultimately this pipeline predict the best parental combination for MABC and MARS. Pipeline is implemented in CGI-perl and shell script
- Developed a tool for quality preprocessing of Next-generation raw sequences

Publications:

Research Article

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. Kudapa*, H., **Azam***, S., Sharpe A.G, *et al.* (2013) Comprehensive transcriptome assembly of chickpea (*Cicer arietinum*) using Sanger and Next Generation Sequencing platforms: Development and applications. *PLoS ONE* (Accepted, In press)
9. Ruperao, P., Chan, C., **Azam, S.**, *et al.* (2013) Chromosomal genomics for genome assembly validation. *Plant Biotechnology Journal* (communicated)
10. **Azam, S.** , Rathore, A., Shah, T., *et al.* (2013) ISMU: Integrated SNP mining and utilization pipeline for accelerated breeding. *BMC Bioinformatics* (communicated)