Dr. Sukumar Saha has a total of thirty five years of professional research experience. After working as a Research Assistant Professor for five years at Alabama A&M University the incumbent assumed the present position with USDA/ARS in 1997. He demonstrated outstanding stature and received significant recognition as an international authority in cotton genomics and cytogenetics for the development of genetic and cytogenetic resources that are being used by the scientists in the USA and around the world. He also received 2010 Outstanding Research Award in Cotton Genetics at the Beltwide Cotton Improvement Conference, Atlanta, January 4-7, 2011.

He made a major contribution in developing PCR-based SSR markers, a critical first step for the use of PCR-based marker technologies in the cotton breeding program. In collaboration with colleagues, the nominee discovered 306 PCR based SSR markers (JSPER) in Upland cotton from SSR enriched genomic DNA libraries. The nominee in collaboration with colleagues was also first to identify 133 PCR-based EST-SSR markers (MGHES), icons of functional genes, by using a cost effective data mining strategy from the publicly available cotton fiber EST database. JSPER and MGHES markers were first publicly available SSR and EST-SSR markers for use as a tool for marker assisted selection program (MAS) and molecular mapping in cotton.

He also made a significant contribution in the discovery of molecular markers associated with important traits in cotton. The nominee in collaboration with the scientists in Uzbekistan reported the first report on the use of association mapping strategy in cotton to the discoveries of: 1) genetic diversity in about 300 lines from Uzbekistan based on large number of molecular markers, fiber and agronomic traits, 2) the genome wide linkage disequilibrium (LD) value in cotton genome, and 3) association of several DNA markers with important fiber and agronomic traits and their chromosomal locations.

Discovery of the SNP, the next generation of DNA marker and icon of functional gene, is very difficult in a polyploid species like cotton. It is like solving two jigsaw puzzles at the same time, because cotton has two duplicated sets of chromosomes. In a collaborative project t he discovered a strategy for SNP marker identification in tetraploid cotton. This strategy was applied for SNP identification, phylo-genomic characterization, chromosome localization and linkage mapping of several candidate genes including *Expansin, R2R3-MYB* transcription factors associated with fiber development and *MIC-3* gene family, a gene family associated with root-knot nematode resistance response. This research opens up a new paradigm in SNP marker discovery especially cconsidering publicly available of many gene sequences now in GenBank.

He was one of the two lead scientists providing leadership in the release of 17 interspecific chromosome substitution lines in cotton. In a collaborative project, he developed and evaluated and these stable backcrossed *Gossypium barbadense* (Pima 3-79) chromosome substitution (CS-B) lines in a *G. hirsutum* (TM-1) background. These lines are near-isogenic with the exception of different substituted chromosomes or chromosome segments from Pima 3-79. This research also detected the chromosomal association of many important agronomic and fiber traits. Chromosome substitution line is one of the most powerful means of targeted interspecific introgression and steps toward novel quantitative trait locus identification. This research opens new paradigms in cotton breeding and genetics studies providing a tool to overcome the problems of interspecific introgression and in the discovery of some novel genes or traits whose effects could not be detected in the donor Pima 3-79 line. Dr. Saha in collaboration with other scientists developed for the first time 45 interspecific F1 monosomic and monotelodisomic plants for different chromosome or chromosome arm of *G. tomentosum* in Upland background. These lines were the primary foundation for the first time in the development of chromosome substitution lines from *G. tomentosum* (CS-T) species. Currently these CS-T lines are in different field trials for mapping of important QTLs. This research is a stepping-stone for the first time to provide a breeding tool towards chromosome specific introgression of valuable traits from *G. tomentosum* into Upland cotton.

He has also made a significant contribution in providing leadership in cotton research in other countries than USA. Dr. Saha has been awarded for funding in three different collaborating cotton research projects from 2002-present, with the scientists at The Institute of Genetics and Plant Experimental Biology, Tashkent, Uzbekistan under the program of Former Soviet Union (FSU) of International Program, USDA/ARS. The accomplishments of FSU projects are well documented in 15 publications in referred journals. These FSU projects have helped to establish one of the most advanced molecular biology lab in the Central Asia with state of the art technologies. This research provided an opportunity to train the next generation of public and private Uzbek cotton breeders and young scientists. Four young Uzbek scientists completed their Ph.D. and several young students finished their M.S. degrees in the advanced field of plant molecular biology through the FSU projects. Also an young scientist completed D.Sc. degree at the Academy of Sciences, Uzbekistan and received an International Best Scientist award from the Academy of Sciences of Third World Countries (TWAS) in the field of Agriculture from these collaborative research projects. Several Uzbek scientist visited USDA/ARS for long term period for advanced hands on training in molecular biology. The FSU research projects provided an opportunity for the first time to exchange over 1000 Uzbek cotton germplasm with USA and created for the first time of a germplasm passport database system in Uzbekistan Cotton Germplasm Center based on molecular and phenotypic data. Such database system can be used as a model to categorize the collection in other Germplasm Centers around the world. Uzbekistan scientists also received an unique set of interspecific chromosome substitution lines from USDA/ARS collaborators through this project. Currently they are utilizing these lines in their breeding program to improve Uzbek cotton cultivars.

He was one of eight founding scientists who initiated International Cotton Genome Initiative organization (ICGI) to facilitate collaborative research work on cotton genomics at the global level about eight years ago. Dr. Saha was elected in every election since its inception to be the steering committee member and chair/co-chair of the ICGI Germplasm Work Group. He, as the chairman of the Germplasm Work Group, provided leadership for the first time to document the current status of world cotton collection in collaboration with the curators from the major cotton growing countries and this report has recently been published in Crop Science as the cover page paper (2010. 50:1161-1179).

He provides leadership to several collaborative research agreements with universities. He received funding of over several million dollars as principal investigator in several competitive grant programs from USDA, USAID, NSF and Cotton Incorporated. He was also instrumental in providing support and developing collaborative research programs between USDA/ARS and 1890 schools. He also works as a USDA/ARS liaison officer with Alabama A&M University and Tennessee State University in several Capacity Building Research Projects. He is also appointed as adjunct graduate faculty at Mississippi State University and Alabama A&M University, respectively. Four Ph.D. students and four M.S. students have successfully completed their degrees under his supervision as a Co-major advisor. He has also supervised several Ph.D. level visiting scientists from Uzbekistan, India and China for six months to one year period in his lab.

He also worked as an agricultural extension worker for eight years with farmers in India before immigrating to the US. His research productivity is well documented in about 130 publications including 77 peer-reviewed journal articles in many prominent journals, one germplasm release notice, a co-edited book, additional multiple papers and abstracts in presentations at conferences.