

From: [Scott Allen Jackson](#)
To: [PAMELA JEAN Brown](#); [Laura D Burris](#)
Subject: Fwd: Application for Assistant Professor in UGA (Position ID: 25598)
Date: Sunday, August 31, 2014 9:12:00 AM
Attachments: [UGA_APPLICATION_KANG_CV.docx](#)
[ATT00001.htm](#)
[UGA_APPLICATION_KANG_LETTER.docx](#)
[ATT00002.htm](#)
[UGA_APPLICATION_KANG_PUBLICATIONS.zip](#)
[ATT00003.htm](#)
[UGA_APPLICATION_KANG_REFERENCES.xlsx](#)
[ATT00004.htm](#)

Another application

Begin forwarded message:

From: 강양제 <kangyangjae@gmail.com>
Subject: Application for Assistant Professor in UGA (Position ID: 25598)
Date: August 31, 2014 at 4:38:31 AM EDT
To: sjackson@uga.edu

Dear Dr. Scott Jackson

I am writing to apply for the assistant professor position of genetics based on high-dimensional data analysis, statistical genomics, genome-wide analysis, gene-environment interactions, and/or epigenetics of crop plants in the Department of Crop & Soil Sciences in University of Georgia posted at Applicant Clearinghouse with Position ID: 25598.

I am a currently senior researcher of Plant Genomics and Breeding Institute (PGBI) at Seoul National University in Korea. As my attached curriculum vitae shows, I have been working to analyze the next generation sequencer-derived data for several genome projects such as mungbean (*Vigna radiata*), adzuki bean (*Vigna angularis*) and Jatropha (*Jatropha curcas*). This includes *de novo* genome and transcriptome assembly, re-sequencing, intensive analyses of genomic variations, high-density genetic map construction with SNPs, gene prediction and annotation, gene expression profiling with RNAseq, transcriptome-based

speciation estimation, and statistics/visualization of genome analysis. Beside of the genome projects, I am preparing manuscript regarding the small scale genome duplication events such as tandem duplication and ectopic duplication. These mode of duplications show fast evolution compared to large scale duplications and I studied the evolution of tandem duplicates in so-far sequenced plant genomes to understand their duplication preference toward stress response genes and putative driving forces including the types of LTR retrotransposons. I believe that my bioinformatics skills and the insights of genomics which has been gained during several genome projects make me a strong candidate for the assistant professor position.

My representative research as a first author is “Genome sequence of mungbean and insights into evolution within *Vigna* species” (under review at Nature Communications). This genome paper is consisted with the several main topics such as genome assembly and gene prediction, genome evolution, speciation and domestication. I covered most of bioinformatics in this project including *de novo* assembly, re-sequencing, gene prediction, SNP/SSR development, genetic map construction using genotype by sequencing (GBS) data, comparative genomics among legumes, and construction of species tree among *Vigna* species based on Bayesian MCMC method. The species tree was constructed from *de novo* assemblies of RNAseq data of 22 *Vigna* species with careful selection of conserved orthologous loci. Additionally, the genome of allopolyploid *Vigna* species (*V. reflexo-pilosa*, $2n=4x=44$) was *de novo* assembled to understand allopolyploidization. I could successfully split the donor genomes within the assembly of *V. reflexo-pilosa* using synteny relationship with *V. radiata*, and placed each genome into the phylogenetic tree of *Vigna* species. This revealed that *V. trinervia* and un-sampled or

extinct *Vigna* species close to *V. angularis* were merged to create the allopolyploid genome.

Even though there have not been the open teaching courses regarding bioinformatics for crop genomics in Seoul National University, I have taught programming language, python, major bioinformatics tools such as BWA, Bowtie, Tophat, ALLPATHS-LG, and etc. and bioinformatics analysis pipelines such as MAKER for gene prediction, GATK for variation calling, and several custom pipelines for genome analyses to organize our bioinformatics team. I have been trying to teach the context of NGS-based genomics to solve confronted questions in plant science and breeding as well as the importance to know and handle the bioinformatics tools.

I attached my curriculum vitae, information of four professional references, and my publications. I can be reached via email address k821209@snu.ac.kr or kangyangjae@gmail.com. I thank you for your consideration and look forward to hearing from you.

Best regards,

Kang, Yang Jae