**NDSU** **NORTH DAKOTA STATE UNIVERSITY** **Tel.: (701) 231-8443**
**Fax: (701) 231-8474**
**phillip.mcclean@ndsu.nodak.edu**

**Department of Plant Sciences**
**Loftsgard Hall**
**P.O. Box 5051**
**Fargo, ND 58105-5051**

26 November 2007

To: Dr. Ed Kaleikau

From: Dr. Phillip McClean Phil McClean
Re: Letter of Intent: Applied Plant Genomics – Coordinated Agricultural Project

## Project Director

Phillip McClean, North Dakota State University

## Project Members

**Howard Schwartz**, Colorado State University – Extension Coordinator; **James Beaver**, University of Puerto Rico, Mayaguez – Dry Bean Breeding, Education Co-Coordinator; **Juan Osorno**, North Dakota State University – Dry Bean Breeding, Education Co-Coordinator; Agronomic Phenotyping; **Mark Brick**, Colorado State University – Dry Bean Breeding, Education Co-Coordinator, Molecular Breeding; **James Kelly**, Michigan State University – Dry Bean Breeding, Molecular Breeding, Informatics; **Carlos Urrea**, University of Nebraska – Dry Bean Breeding, Agronomic Phenotyping; **Shree Singh**, University of Idaho – Dry Bean Breeding, Agronomic Phenotyping; **Phil Miklas**, USDA/ARS, Prosser, WA – Dry Bean Breeding, Molecular Breeding, Molecular Mapping; **Timothy Porch**, USDA/ARS, Mayaguez, Puerto Rico – Dry Bean Breeding, Association Mapping; **Jim Myers**, Oregon State University – Snap Bean Breeding, Molecular Mapping, Molecular Breeding; **Jim Nienhuis**, University of Wisconsin – Snap Bean Breeding, Molecular Breeding, Agronomic Phenotyping; **Phillip Griffiths**, Cornell University – Snap Bean Breeding, Molecular Breeding; **James Steadman**, University of Nebraska – Disease Phenotyping Coordinator; **Judith Brown**, University of Arizona – Disease Phenotyping; **Rubella Goswani**, North Dakota State University – Disease Phenotyping, Education Program; **Paul Gepts**, University of California – Molecular Marker Development Co-Coordinator; **Greg May**, National Center for Genome Resources – Molecular Marker Development, Informatics; **Scott Jackson**, Purdue University – Molecular Marker Development; **Henry Thompson**, Colorado State University – Cancer Prevention Phenotyping; **Maurice Bennink**, Michigan State University – Cancer Prevention Phenotyping; **Jianming Yu**, Kansas State University – Association Mapping, Statistical Analysis; **Edward Kee**, University of Delaware – Extension and Education Programs; **Samuel Markell,** North Dakota State University – Extension and Education Programs; **Greg Varne**r, U.S. Dry Bean Council – Stakeholders Committee; **Ken Kmiecik**, Seminis Vegetable Seed, Inc. – Stakeholders Committee; **Kirstin Bett**, University of Saskatchewan – Research Advisory Committee; **Fred Bliss**, Seminis Vegetable Seed, Inc. – Executive Committee

## Program Priority

Improvement in U.S. crop and forestry production through the application and translation of knowledge generated via genome-wide discoveries and high-throughput technologies for traditional breeding practice.

## *Bean CAP: Tools for the Future, Knowledge and Training for the Present*

The Bean CAP is an integrated community-wide effort whose primary objectives are: 1) to develop marker-assisted selection tools, a knowledge base encompassing phenotypic and genotypic data for agronomic and nutritional traits, and a MAS implementation strategy that supports the long-term and sustainable improvement of common bean; 2) to disseminate knowledge about genomics, plant breeding, and nutrition to producers and consumers and how the agricultural sciences support the end-user; and 3) to develop plant breeding educational activities that will enhance the recruitment of students into the discipline and offer continuing education in genomic-based breeding for both private and public plant breeders.

**The Organization**: The Bean CAP is a national collaboration involving 27 scientists representing 21 organizations. The collective expertise encompasses a wide-range of scientific disciplines including plant breeding, agronomy, plant pathology, biochemistry and cancer prevention, genetics, genomics, statistics, and informatics. In addition, experts involved in day-to-day bean extension activities, and those developing plant breeding education programs are members of the project team and will lead those aspects of the project. The research component is organized around the national multidisciplinary W1150 project, "Exotic Germplasm Conversion and Breeding Common Bean (*Phaseolus vulgaris* L.) for Resistance to Abiotic and Biotic Stresses and to Enhance Nutritional Value". This project meets annually to review progress and set organizational goals for the following year. As shown on the first page, the project is integrative with all participants involved with multiple aspects of the project.

**Research Program**. Common bean (*Phaseolus vulgaris* L.) is an important agronomic and nutritional crop cultivated as dry edible or edible pod snap beans. The species consists of two gene pools (Mesoamerican and Andean), and within each gene pool multiple ecogeographic races are found. Importantly, the multiple market classes of beans grown in the U.S. are distributed across these races. Each market class reflects consumer preference and is defined by specific seed traits (size, color and pattern), growth habit, and phenology that are difficult to reconstitute from inter-market class crosses. Therefore, any national molecular breeding project must balance the need for both species-wide and market class specific tools. At the same time, many of the agronomically important abiotic and biotic stresses are common to all dry bean and horticultural snap bean market classes. Therefore, generalized discovery of the genetic factors controlling these will be of wide utility.

The primary tool for molecular breeding will be a suite of single nucleotide polymorphism (SNP) markers. The extensive EST collections and the availability of BAC-end sequences will be the initial resource for SNP discovery. Additional SNPs will be defined by high-throughput sequencing of cDNAs using the sequencing-by-synthesis (Solexa) technology. This will focus on defining race and market class specific SNPs. Because breeders make crosses primarily within gene pools, two molecular maps (~1000 SNP each) will be developed based on interracial Mesoamerican x Mesoamerican and Andean x Andean crosses. To further aid breeders, ~300 SNPs will be defined by screening a broad panel of genotypes for each of the following classes of beans: pinto, navy, black, kidney, great northern, and snap. These were chosen because they represent the major bean types grown in the U.S. Each of the eleven U.S. public breeding programs will also provide important historical and modern genotypes used as parents in their programs for SNP genotyping. The recently developed species-wide association mapping population, which represents the full range of diversity in cultivated common bean, will also be SNP genotyped. The association mapping population and the six panels of cultivars from all of the breeding programs will be grown in multiple locations and phenotyped for agronomic and biotic and abiotic stress traits important to the US bean production systems. Additionally, nutrient and seed (for dry beans) and pod (for snap beans) profiles for each of the lines will be developed from field-grown material. The data from all of these analyses will be pooled, and association or QTL mapping procedures will be used to uncover important marker/trait associations that will support future bean improvement efforts. The SNP, mapping, and association data will be incorporated into the Legume Information System. The data will be combined with all of the existing genetic and physical map data that are already available to the community. A user-friendly interface that captures SNP-based haplotypes and provides links to pedigree and performance data will provide support for parental and marker selection.

**Extension Program**. We will build upon two distinctive aspects of common bean to enhance the eXtension Communities of Practice (COP) activity. First, bean breeders have a long history of using marker assisted selection for cultivar development. Based upon this experience, one COP will be entitled "**M**arkers **A**nd **P**lant breeding (**MAP**)". The content will consist of a plant breeding primer, the principles of selection in plant breeding (including genotype x environment interactions), the basics of genetics and linkage, and the use of MAS. Using the important nutritional features of common bean as a starting point, we will also develop another eXtension COP entitled "**NUTR**ition, **A**gronomy, and **GEN**omics (**NUTRAGEN**)". The community content will consist of basic information regarding the field of genomics, $N_2$ fixation and legumes, the screening for genes related to nutrition, and the application of genomics for agronomic and nutritional improvement of plants with an emphasis on legumes. The target audience for these two new COPs will be extension educators, crop producers, and the general public. The COPs will be featured in regional workshops held in conjunction with activities such as Bean Days in North Dakota. Those workshops will also describe specific activities, progress, and successes of the Bean and other CAP projects.

**Education Program**. Currently, many plant breeding positions are going unfilled in the U.S. For example, over 30 positions were open at the 2007 Agronomy Society of America meeting. Additionally, with the advent of genomics-based breeding, the scope of knowledge required of public and private breeders has broadened and additional training is needed.

To help with the shortage of plant breeding graduates, we will develop educational materials at the university freshman level to raise awareness of career opportunities in plant breeding. These will include modules that describe the discipline as one of discovery, innovation, and implementation. The emphasis will be on the science that underlies the important technology implementations. The use of technology as a tool to reduce production costs, enhance yield potential, and improve the nutritional and health properties of bean will also be highlighted. We will collaborate with instructors at the BeanCAP universities, as well as their nearby non-agricultural schools, to incorporate these modules into plant science curriculums. Students will be recruited for summer internships following their sophomore years to work side-by-side in plant breeding programs. Advising sessions will be held that recruit students into graduate plant breeding programs.

The private and public plant breeding industry has a group of personnel with a wide-range of trainings. Some of these companies are small with one or a few breeders that strictly do phenotypic breeding, while others are international in scope with sophisticated breeding programs that tightly integrate the process from the lab to the field. To increase the knowledge base of these plant breeders, the regional workshops (see above) will include training sessions that emphasize applications of genomics-based breeding.