Project Summary

PROJECT SUMMARY

Instructions:
The summary is limited to 250 words. The names and affiliated organizations of all Project Directors/Principal Investigators (PD/PI) should be listed in additions to the title of the project. The summary should be a self-contained, specific description of the activity to be undertaken and should focus on: overall project goals(s) and supporting objectives; plans to accomplish project goal(s); and relevance of the project to the goals of the program. The importance of a concise, informative Project summary cannot be overemphasized.

Title: Common Bean Coordinated Agricultural Project

PD: McClean, Phillip E.	**Institution**: North Dakota State University
CO-PD: Garden-Robinson, Julie	**Institution**: North Dakota State University
CO-PD: Johnson, Christina	**Institution**: North Dakota State University
CO-PD: Osorno, Juan	**Institution**: North Dakota State University
CO-PD: Slator, Brian	**Institution**: North Dakota State University
CO-PD: Kelly, Jim	**Institution**: Michigan State University
CO-PD: Brick, Mark	**Institution**: Colorado State University
CO-PD: Ryan, Elizabeth	**Institution**: Colorado State University
CO-PD: Thompson, Henry	**Institution**: Colorado State University
CO-PD: Myers, Jim	**Institution**: Oregon State University
CO-PD: Gepts, Paul	**Institution**: University of California, Davis
CO-PD: Urrea, Carlos	**Institution**: University of Nebraska, Lincoln
CO-PD: Grusak, Michael A.	**Institution**: USDA Children’s Nutrition Research Center, Houston, TX
CO-PD: Cregan, Perry	**Institution**: USDA Soybean Genomics and Improvement Lab, Beltsville, MD
CO-PD: Hyten, David	**Institution**: USDA Soybean Genomics and Improvement Lab, Beltsville, MD
CO-PD: Cichy, Karen	**Institution**: USDA Sugarbeet and Bean Research Unit, East Lansing, MI.
CO-PD: Porch, Tim	**Institution**: USDA Tropical Agriculture Research Station, Mayaguez, PR
CO-PD: Miklas, Phillip	**Institution**: USDA Vegetable and Forage Crops Research Lab, Prosser, WA

The Common Bean Coordinated Agricultural Project (BeanCAP) will significantly impact the future direction of research by providing new tools and research directions for this important nutritional and commodity crop. The first market-class-specific markers, whose value will extend well beyond the project duration, will be a major outcome affecting all bean research. When genotypic data, generated by using these markers, is coupled with nutritional profiling data, also generated by the project, species-wide and market-class-specific loci affecting the nutritional traits will be discovered. This will set the stage for significant common bean improvements for years to come. All public US bean breeding programs will also be supported by 1) a genotyping program that will aid the discovery of genetic factors controlling traits of local agronomic importance; and 2) conversion of high throughput markers into low cost makers for day-to-day use in breeding programs. The nutrition, genetic, and genomic scientists will coordinate the development of an eXtension Community of Practice that will utilize high-quality animations and other multimedia to educate the general public and educational communities about the biology of nutrition and how genetics/genomics technology assists with the improvement of nutritional traits. The BeanCAP will also initiate a modern plant breeding training program focusing on early career recruitment and practical breeding/genomics training that illustrates, as an example, how the integration of genomic and phenotypic data can be used to improve nutritional traits in plants. This will provide a stream of students interested in filling the plant breeding human resource pool.

PROJECT NARRATIVE

A. Introduction

The Common Bean Coordinated Agricultural Project (**BeanCAP**) will strengthen the bean research, education, and extension communities by focusing on the genetics and genomics aspects of nutrition in this important food crop.

The **research component** will translate current and newly developed genomic information into the first suite of market-class-specific markers with broad utility to improve ***any trait*** of interest. The markers will be used in the first ever nation-wide project to define loci controlling a large collection of nutritionally important traits at both the species and market-class-specific levels. Each breeding program can then design the best strategy for the nutritional improvement of the market classes they work with. A genotyping service will support all public US breeding programs improving traits of local importance. Low cost markers that leverage the information from the high throughput marker screening will be developed for the long-term improvement of common bean. The marker and phenotypic data generated by this project will be organized along with all available genetic map, marker, and loci data into a database that is fully operable with other legume databases.

The **extension component** will develop a new Community of Practice (COP), "**Nutritional Genetics and Genomics: Healthy Foods from the Field to the Table."** The COP will inform educators and the public about the biology, genetics, and genomics of nutrition. High quality, narrated animations will be the primary learning tool.

The **educational component** will design models for the recruitment of new students into the plant breeding discipline. Participants will be a trained in a program that introduces the basics of plant breeding, genetics, and genomics using nutritional genetics and genomics as the theme. The education and extension participants will collate all education materials developed by other plant genomics CAP projects into a newly designed learning environment that integrates those materials with those developed for this project. The specific project objectives are:

- **Objective 1**: Develop high throughput, market-class-specific markers for the predominant common bean market classes produced in the US, convert those markers into breeder-friendly markers, and genotype breeder-defined populations with these markers.
- **Objective 2**: Discover genetic loci associated with nutritional traits that define "healthy beans" by combining genotype and nutritional profile data of association mapping and bi-parental populations.
- **Objective 3**: Integrate common bean phenotypic, genotypic, and molecular marker data with other emerging legume genomic resources into breeder-friendly bioinformatic tools.
- **Objective 4**: Launch the "**Nutritional Genetics and Genomics: Healthy Foods from the Field to the Table"** eXtension Community of Practice (COP). The COP will utilize high-quality animations and other multimedia to highlight the biology and technology associated with the genomic-based improvement of nutritional traits.
- **Objective 5**. Initiate a modern plant breeding training program that focuses on early career recruitment and provides practical training that illustrates how the integration of genomic and phenotypic data can be used to improve nutritional traits in plants.

Genesis of the Project. The BeanCAP team is drawn from a well-organized community of individuals who exhibit a high degree of coordination and cooperation. Team members interact with local commodity groups and industry to seek input on their research direction. These meeting guide the W1150 experiment station project entitled "Exotic Germplasm Conversion and Breeding Common Bean (*Phaseolus vulgaris* L.) for Resistance to Abiotic and Biotic Stresses and to Enhance Nutritional Value". The project recently received the 2009 Excellence in Multistate Research Award by the Western Association of Agricultural Experiment Station directors. (The Statement of Issues and Justification for this project can be viewed at: http://nimss.umd.edu/homepages/home.cfm?trackID=7076). **That white paper provided the impetus for the project**.

BeanCAP participants coordinate with the private sector and the international research community during the biennial Bean Improvement Cooperative (BIC) meeting. BIC is an international organization that provides a focal point for worldwide interactions and is an important venue for private industry to also provide input into the public research effort. **The feedback that we have received from all of these groups informed our decision to focus on the nutritional status of common bean.**

Large, integrated projects such as the BeanCAP can make significant educational impacts beyond the research component. The general public wants to understand health and nutrition yet they need unbiased, peer-reviewed information that is presented in a manner that facilitates learning. Numerous research reports have demonstrated that animations are a superior learning tool (McClean et al. 2005) especially when integrated with other learning materials. **This research has informed our decision to use animations as the primary learning tool for our nutrition oriented COP.**

Multiple reports have described industry's need for plant breeding training. Yet the number of individuals obtaining degrees in plant breeding has been relatively stagnant in recent years (Guner and Wehner, 2003; Bliss, 2006), and current numbers of plant breeding graduates do not meet the number of open plant breeding positions. **This human resource need is the basis for our decision to focus our education efforts on developing models for filling the plant breeding training pipeline.**

B. Rationale and Significance

A significant aspect of the BeanCAP project is the full integration of the research, extension, and education components around the theme of nutrition, genetics, and genomics. This theme was chosen because common bean is a nutritionally important crop. By mobilizing all three components around a single theme, we will 1) **develop research tools** in order to better understand the genetic and genomic factors that define a nutritional crop; 2) **create effective delivery methods** to disseminate this knowledge in a way that assists the public as they make informed decisions regarding biology and health; and 3) **design and implement a training program** for young plant breeders that emphasizes how a crop can be improved nutritionally by using all of the research tools available.

From a **research perspective**, little is known about the genetic and genomic control of important nutritional traits in common bean or any crop. The modern genetic tools developed here will be most effective when we evaluate the expression of the nutritional traits in experiments that consider the full breadth of genotype (market classes) and environmental (production regions; abiotic stresses) factors important in the US. ***The development of market class specific markers that fully supports all US research programs will be a significant outcome of the BeanCAP****.*

For learners to comprehend nutrition and how genomic tools can effectively improve the nutrition of a plant, they must learn basic cellular, molecular and physiological processes. These three-dimensional processes are best learned by visualizations that contain a motion component that promotes a better understanding of interrelationships that involve space and time. The **extension component** of the project will develop a Community of Practice featuring a suite of high-quality animations of important biological processes that are integrated with other animations that teach the methods of modern crop improvement using nutritional crops as an organizing theme. These animations will also be coupled with other educational media designed to enhance the learning experience.

In the current job market, there is a strong demand for plant breeders, especially in the private sector. Yet the number of individuals obtaining degrees in plant breeding has been relatively stagnant in recent years (Frey, 1996; Guner and Wehner, 2003; Trexler et. al., 2005), and the current number of plant breeding graduates does not meet the number of open plant breeding positions. To address this growing need, the **educational activities** will provide early exposure of high school students to plant breeding as a profession, and recruit young undergraduates into a year-round internship program that involves students in the field and lab components of a plant breeding program. The theme of nutrition, genetics and genomics will be prominent in all high school and undergraduate recruitment and training materials.

C. Approach

1. BeanCAP Research Program: Nutritional Genetics and Genomics of Common Bean

a. Background. Common bean, an important US economic crop. Common bean (*Phaseolus vulgaris* L.; 2n = 2x = 22) is in important economic crop in the US where 1.7 million acres of dry and snap beans were planted in 2008. While production of dry bean is primarily located in North Dakota, Michigan, Nebraska, and Colorado (90% of production), the crop is also grown in 15 other states. US dry bean production is primarily restricted to five market classes - pinto, navy, black, red kidney, and great northern (in descending order of importance) - that account for 81% of the US production. Snap bean are grown for the fresh and processing markets on 300,000 acres, primarily in Oregon, Wisconsin, and New York. **Collectively, the value of common bean production at the farm gate in 2008 was $1.5 billion.** This exceeds the value of all other vegetable legumes combined (chickpea, lentil, pea, and peanut). The 16% increase in common bean value in 2008 was one of the largest increases among major crops.

Common bean genome, genetic organization, and diversity. The common bean genome is moderate in size (450-650 MBp/haploid; Bennett and Leitch. 2005). It appears to be a “true” diploid since nearly all loci are single copy (Vallejos et al. 1992; Freyre et al. 1998; McClean et al. 2002) while, the traditionally large families such as resistance gene analogs (Rivkin et al. 1999) and protein kinases (Vallad et al. 2001) are smaller than most crops.

Two major domestication events appear to have resulted in the Middle American and Andean gene pools (Kaplan and Lynch 1999). These are distinguished by biochemical (Gepts and Bliss

1986; McClean et al. 2004a, b) and morphological (Gepts and Debouck 1991) traits. Following domestication, gene pool divergence lead to the development of several races within each of the two major domesticated gene pools (Singh et al. 1991).

US breeders focus on five dry bean classes (pinto, navy, black, Great Northern, kidney) and snap beans for the fresh and processing markets. Each market class is defined by a specific seed size, color, and pattern, traits controlled by many genes (McClean 2002). Crosses are typically made between genotypes within a market class because it is difficult to recover a market class phenotype from inter-market-class crosses This has lead to limited sequence variability within each market class (McClean et al. 2004, 2007). The variability is lowest with the kidney and Andean-derived snap beans and is greater within the Middle American races Durango and Mesoamerican. By contrast, a large amount of variability is observed between genotypes from the two gene pools. This has been exploited extensively during the development of populations used to map important agronomic traits (Miklas et al. 2006).

Bean breeders: early adopters and innovators of molecular breeding. Marker-assisted selection (MAS) has become an essential tool in public bean breeding to introgress and pyramid resistance genes (Kelly et al. 2003; Miklas et al. 2006). Bean breeders pioneered the discovery and application of markers by using advanced generation segregating lines and cis- and/or trans-markers to effectively integrate desirable traits (reviewed in Kelly et al. 2003). Currently, 41 markers linked to qualitative and quantitative loci important for disease resistance and other production traits (http://www.css.msu.edu/bic/PDF/SCAR%20Markers%202007.pdf) are available. Since 2000, over 90% (17/19) of the disease-resistant germplasm released in the US were developed using molecular markers. Since this germplasm is being broadly used by all public breeding programs, the impact of molecular marker breeding on the bean industry will be long lasting. These tools are critical for private breeding companies, as they too become increasingly active users of these molecular markers. (See industry support letters.)

To repeat this success, bean breeders face a number of challenges to improve important agronomic traits. Because of the narrow genetic basis of beans in the US (McClean et al. 1993; Sonnante et al. 1994), bean breeders increasingly use exotic, unadapted germplasm as a source of useful traits. This raises significant breeding challenges because each market class has strict phenotypic characteristics that must be maintained. Molecular markers are needed not only to introgress gene(s) but also to facilitate the recovery of the adapted (domesticated *P. vulgaris*) genetic background. **Yet market-class specific markers are few in number and are needed to facilitate bean improvement.** Most markers were developed one at a time using the cumbersome process of identifying RAPD markers and converting these to SCAR markers (Kelly et al. 2003). **Therefore, a national effort to develop and apply high-throughput marker technology for bean improvement is necessary.**

Common bean, a major nutritional crop. Plants are a rich source of basic sugars, proteins, and lipids essential for our normal growth and development, and supply vitamins and minerals required for many of the basic cellular processes necessary for life. Recent research has focused on phytochemicals, plant-derived molecules that while not essential for human growth and development, positively affect human health. Legumes are considered to be some of the healthiest foods in our diet. Although some provide the full complement of 15 minerals required for human metabolism (Grusak 2002), levels of the minerals vary among crops within the family. **Among legumes, common bean are consumed by humans more than any other crop.**

Health benefits from eating beans are numerous and include reducing the blood cholesterol and sugar levels which in turn prevents or alleviates certain types of cancer, Type 2 diabetes, and cardiovascular diseases (Andersen et al. 1984; Tietyen-Clark, 1986). Diets rich in zinc and iron, two micronutrients abundant in bean, can delay the onset of AIDS (Savarino et al. 1999; Buys et al 2002), and as such, HIV positive patients are encouraged to include beans in their diets (SADH 2001; Jackson et al. 2007; Malete et al. 2007). Bean seeds also contain a protein that inhibits the HIV-1 reverse transcriptase (Wong et al. 2006). Recent research has shown that beans significantly reduce the onset of breast cancer (Thompson et al. 2009), colon cancer (Hangen and Bennink 2002; Feregrino-Perez et al. 2008), and biomarkers for heart disease risk (Winham et al. 2007).

From a crop improvement perspective, it is important to know the range of the natural variation of any nutritional factor. In common bean, colored beans have greater antioxidant activity than white beans (Madhujith et al. 2005), and that among the colored beans, the antioxidant activity of black beans was higher than for yellow-seeded beans (Rocha-Guzman et al. 2007). These experiments are typical not only for common beans but, all crops in general where only a few genotypes or market classes are profiled during an experiment. **Species-wide variation is simply not assessed.**

Obviously, it is foolish to claim any one plant species is a superfood that contains abundant amounts of all the basic nutrients of life and is a rich source of those health boosting phytochemicals. That is why a balanced diet is necessary. But that fact does not preclude the possibility of improving the health value of a crop plant like common bean by 1) **assessing its natural variation** for food nutrients, 2) **discovering the genetic factors** controlling the amount of the nutrients, and 3) **applying modern plant breeding practices** to increase the amount of these nutrients in the food. These three activities define the BeanCAP research component.

b. BeanCAP Research Products

The following research products will significantly improve common bean for many years into the future:

- A suite of market-class specific SNP markers for whole genome screening
- Breeder friendly CAP markers linked to nutritional traits and all known single gene and known QTL in common bean
- Discovery of species-wide and market class specific loci affecting expression of nutritional traits
- Breeder accessible database of phenotypic and genotypic data

c. Research Activities – Specific Experiments

i. SNP marker development **(Cregan, Hyten)**. A 1536 oligonucleotide pool array (OPA) set (Illumina Golden Gate Assay) is currently available. It was developed from ~7000 SNP discovered using a combination of genome resequencing of a large number of common bean loci utilizing soybean gene-specific primers, 454 sequencing of BAT96, and Solexa sequencing of Jalo EEP558 (Cregan et al. 2009). To uncover the level of diversity among and within the six major common bean market classes (pinto, black, navy, great northern, kidney, and snap), an equal distribution of genotypes from each of the market classes will be surveyed using this OPA.

Many previous studies have shown that while between gene pool sequence diversity is substantial, within gene pool, and more importantly, within market class variability is more limited. Therefore, we anticipate that while the initial screening with the 1536 SNPs will reveal polymorphisms among market classes, it will not meet our goal of developing a large collection of within market class markers.

To discover within market class SNPs, we will use the high-throughput Solexa "Paired-End Module" sequencing protocols to collect ~100 bp of sequence data per fragment. The source DNA will be a reduced-representation library developed by cutting genomic DNA with a group of restriction enzymes. Two diverse modern cultivars (based on the above diversity screening) from the pinto, navy, black, great northern, and kidney market classes will be surveyed. Since the snap bean market class is derived from both Middle American and Andean germplasm, a total of four cultivars, two each from the two gene pools, will be sequenced. The SNP data will then be compared with our reference sequence data to discover market-class-specific SNPs. The reference sequence will be constructed from 454 runs of the Andean landrace Jalo EEP558. The current collection of 454 data for this genotype is small. This project will augment that data set with ~1 million reads of about 400 bp in length.

Based on previous sequencing experiments (McClean et al. 2004a, 2004b, 2007), much of the market class diversity is also captured with the Durango (pinto and great northern market classes), Mesoamerican (navy and black market classes), and Nueva Granda (kidney and most snap market classes) races. If also observe stratified diversity based on race, then we will design a 768 OPA set for each race. Alternatively, if SNPs are confined to market class, then 384 OPA sets specific to each market class will be designed. We should mention that the larger OPA is preferred because we will be able to collect a greater number of data points for a smaller cost.

***ii. Discretionary SNP screening; a service for ALL public US bean breeding programs* (Cregan, Hyten, Gepts)**. The project will offer a **genotype screening service**. SNP genotypes will be collected for 8256 individual DNA samples in years 2-4. In general, two types of materials will be screened. First, all members of the association mapping populations used to discover genetic loci associated with nutritional traits will be screened. In addition, individual members of all bi-parental populations developed to confirm nutritional loci within the various market classes will also be genotyped. (Details of the experiments that will use these populations are described below.) Genotypes submitted by interested common bean breeder or geneticists will also be screened. The follow are examples of materials to be screened.

1. All members of the **common bean core collection** housed at the Pullman, WA site of the National Plant Germplasm System (NPGS). This will support future research by providing a genotypic basis for any phenotyping efforts that use the core collection to discover new useful traits of agronomic importance.
2. The **association mapping populations**, consisting of 400 dry bean and 200 snap bean lines, respectively, that will be used for the nutritional genomics experiments. All of these lines will be genotyped, and that data will be used for the statistical analysis to discover loci associated with the nutritional traits under study.
3. All **members of bi-parental populations** used by multiple geneticists to discover disease resistance loci (Miklas and Singh 2007). This will include any internationally developed population that has important utility to the US common bean breeding. This

effort, when coupled with phenotypic data, will enable the discovery of markers more tightly linked to major disease resistance loci.

4. **Breeder contributed genetic materials**. Plant breeders are either evaluating parents for hybrid breeding or screening populations for loci linked or associated with agronomic traits of interest. The genotyping of these populations will greatly increase the efficiency of the efforts to discover important traits. To participate in the program, breeders will agree to collect phenotypic data using local funds and to submit that phenotypic data to the bioinformatics group for inclusion into the program database.

The final decision regarding genotyping will be made by breeders that are members of the Steering Committee (**Kelly, Miklas, Myers, Osorno**). To ensure Golden Gate assays quality control, the **Gepts Lab** (UC, Davis) will isolate DNA from seed provided by breeders or geneticists. That DNA will then be sent to USDA/Beltsville where the Cregan lab will perform the SNP genotyping. The OPA set that will be used for genotyping will depend upon the market class or race of the materials that will be screened.

iii. Conversion of SNP loci into breeder-friendly CAP markers linked to all known agronomic genes in common bean **(McClean)**. Although the SNP technology provides a highly-efficient method of performing whole genome scans for important marker trait associations, it is cost prohibitive to use this technology to screen only a single or a few markers of interest within a breeding program. For that purpose, we will develop cleaved amplified polymorphic (CAP) markers for important regions and traits of interest. To effectively link the SNP discover and the down-stream breeder screening, we will, whenever possible, select SNPs for the OPA set that are part of an inexpensive restriction enzyme site (e.g. *Hin*dIII, *Eco*RI). Given the large number of SNPs that will be generated by the Solexa sequencing effort, we do not foresee any difficult with this type of SNP selection process.

We will first define the location of all known single genes and QTL associated with important agronomic traits using the database tools described below. SNPs that colocalize with these loci will be converted into CAP markers. The first year of the project will focus on disease resistance loci. As nutritional trait loci are discovered, the emphasis will switch to those loci. By the end of the project, our goal is to define at least 15 CAP loci for each common bean chromosome in a race (Durango, Mesoamerican, Nueva Granda) specific manner. This will enable breeders to select the best CAP marker for their particular application based on genetic location and genotyping cost. The **McClean Lab** (NDSU) will develop the CAP markers

iv. Nutritional genetics and genomics.

Year 1: Nutritional profiling the common bean germplasm. In year 1, the project will develop nutritional profiles of 600 genotypes representing all of the major market classes of common bean grown in the US. Because this same collection will also be grown under field conditions at multiple US locations in year 2, only genotypes adapted to US production conditions (maturity, photoperiod) will be considered. To study the maximum potential for each of the traits under consideration, plants will first be grown under controlled greenhouse conditions (Waters and Grusak 2008) at NDSU. Seed (for dry bean) and pods (for snap beans) will then be sent to the testing locations for nutritional profiling. The following set of nutritional traits will be evaluated by the investigators noted in parentheses. (**Note:** Because of cost, some traits will only be evaluated with the greenhouse materials, whereas other nutritional traits will be profiled with cultivars used in all experiments. That information is listed for each trait.)

1. **Minerals** (Grusak; all experiments). Common bean is a rich source of minerals (Wang et al. 2003; Grusak 2002), and therefore it is important to measure the full range of variation. Samples will be delivered to **USDA Children's Nutrition Research Center** in Houston where data for 16 minerals (P, Ca, K, Mg, Cu, Fe, Zn, Mn, Co, Ni, B, Se, Mo, Na, As, and Cd) will be collected using ICP-MS (inductive coupling plasma mass spectrometry) technology.
2. **Nutritional availability and CaCo-2 cell tests** (Grusak; greenhouse experiment only). Although content of a specific mineral may be high, it is necessary to determine the nutritional availability of that mineral. CaCo-2 cells cultures are typically used for these analyses as a substitute for the much more expensive rat or human studies. These analyses correlate well with whole animal experiments (Fairweather-Tait et al. 2005) and have already been applied for studies in common bean (Hu et al. 2006; Laparra et al. 2008). The analyses will be performed at the **USDA Children's Nutrition Research Center** in Houston.
3. **Antioxidants, phenolics, and anthocyanins** (Brick/Thompson/Ryan; all experiments). The colored components of the various common bean market classes are products of various steps along the anthocyanin biosynthetic pathway and are extracted as phenolics. The molecules themselves have beneficial antioxidant activity (Madhujith et al. 2005; Rocha-Guzman et al. 2007), but variation both within and among various market classes is unknown. The **Cancer Prevention Laboratory at Colorado State University** will perform these analyses.
4. **Soluble/insoluble carbohydrates** (Brick/Thompson/Ryan; greenhouse experiment only). As beans pass through the gut, some carbohydrates are broken down and absorbed, while others are insoluble and pass into the colon. In the colon, they may be broken down into various short-chain fatty acids that decrease the onset of colon cancer (Hangen and Bennik 2002; Feregrino-Perez et al. 2008). Therefore, a crop wide survey at The **Cancer Prevention Laboratory at Colorado State University** will be performed.
5. **Protein, oil, fiber** (Tulmek ; all experiments). Protein, oil and fiber are three basic components that determine a crop's nutritional value. In particular, common bean is recognized as a major protein source, especially in developing countries. The **North Crop Institute at NDSU,** with a long history of seed diagnostics, will evaluate these traits.
6. **Phytate** (Cichy; all experiments). Phytate has been implicated as both a nutritional (Zhou and Erdman 1995; Thompson and Zhang 1991) and anti-nutritional (Oatway et al. 2001) molecule. This important trait will be analyzed by Karen Cichy, a new researcher at the **USDA Sugarbeet and Bean Research Unit** in East Lansing, MI.
7. **Carotenoid, vitamin C, fiber** (Myers). Snap beans have different nutritional features than dry bean. For this crop, the pod rather than the dry seed is the organ of importance. Carotenoid and vitamin C provide antioxidant protection, while fiber reduces risks of cancer, heart disease, diabetes, and obesity. The nutritional traits will be analyzed in common bean pods at **Oregon State University**. The fiber test is different than that performed at NDSU (see above).

Year 2: Association mapping experiments. Association mapping (AM), an alternative to linkage analysis, uses the natural sequence diversity within a species to define the various loci controlling a complex trait (Jorde 2000; Mackay 2001; Nordborg and Tavaré 2002). As an example, the McClean lab used this approach to discover loci associated with iron deficiency chlorosis in soybean (Wang et al. 2008). Other recent examples of association mapping in plants include fiber quality (Abdurakhmonov et al. 2008), plant height (Brown et al. 2008), and flowering time (Ducrocq et al. 2008; Stracke et al. 2009). Association mapping has also been used to discover genes associated with nutritional traits such as vitamin A content (Harjes et al. 2008), starch content and composition (Wilson et al. 2004), and carotenoid content (Palaisa et al. 2003).

An AM experiment consisting of the 400 dry bean genotypes described will be performed in replicated trials under normal production conditions in **North Dakota** (Osorno), **Michigan** (Kelly), **Nebraska** (Urrea), and **Colorado** (Brick). These sites were chosen because 90% of the US dry bean production comes from these states. For this experiment, standard production trait data (**days to flowering, days to maturity, plant height, lodging, growth habit, 100 seed weight, and yield**) will be collected to determine if any trait is correlated with any nutritional trait. A snap bean AM population, consisting of 200 lines, will be grown in **Oregon** (Myers), a primary snap bean production state in the US. Standard production data (**yield, pod shape, pod color, days to harvest, concentration of set, lodging, and architecture**) will be collected, and correlations with nutritional traits will be calculated. AM statistical analyses will also be performed to discover those loci associated with each nutritional trait. (See details below.)

Year 2: Effects on abiotic stress effects on nutritional traits. Some genetic loci exert their effect regardless of the environmental conditions; whereas others affect the trait only under a specific condition. From a genetic perspective, these can be considered **constitutive QTL** and **adaptive QTL** (Collins et al. 2008), respectively. Distinguishing between these two types of loci is important as plant breeders decide what loci to follow in a marker-assisted breeding program. We are sensitive to the fact that breeding for optimum performance under abiotic stress conditions is now an important consideration of all bean breeding programs. Therefore, it is important that nutritional traits also be compared under drought and normal conditions. Therefore, an AM field trail will be conducted with 100 lines that compares performance under drought and normal conditions. (This number was chosen because it is not practical to perform experiments of this nature with more gentotypes.) Drought will be simulated in **North Dakota** (Osorno), **Michigan** (Kelly), **Nebraska** (Urrea), **Washington** (Miklas), and **Puerto Rico** (Porch) by applying irrigation water at 50 to 70% of normal application for optimum yield. Non-stress trials will be planted at all three locations. The same dry bean agronmic trait data will be collected as described above. Correlations between the agronomic and nutritional trait data will be determined. Statistical analyses will be performed to distinguish between constitutive and adaptive loci.

Years 2-4: Within market-class nutritional trait QTL. While AM mapping is a powerful tool, it is necessary to confirm the loci using a different genetic base such as a bi-parental population. Following the nutrient profiling in the first year, parents will be selected from all market classes that vary for many of the nutritional traits. These parents will be crossed, and F5 recombinant inbred populations will be developed and evaluated in the field. In addition, a full nutrient profile will be conducted. QTL analysis will be performed to confirm those loci important for different nutrients. The following market classes (with geneticisits in parentheses) will be evaluated: pinto (**Osorno**); navy (**Kelly**); black (**Kelly**); great northern (**Urrea**); kidney (**Osorno**); and snap (**Myers**).

v. Statistical analysis. As described above, AM has become an accepted genetic analysis approach. Coupled with that has been the development of user-friendly software for the analysis of AM experiments, including STRUCTURE (Falush et al 2003; Pritchard et al 2000) and TASSEL (Bradbury et al 2007). **McClean** (NDSU) is fully adept at using the software (Wang et al. 2008) and will provide guidance to the breeder group (**Brick, Kelly, Miklas, Osorno, Porch, Urrea)** that will perform the analysis. The **AM statistical analysis** will include 1) genotypic data analysis; 2) phenotypic data analysis; and 3) association analysis of genotypic and phenotypic data. The SNP data from the AM population will analyzed for subpopulation structure (Q) using STRUCTURE software. The final population subgroups will be determined based on Wilcoxson test (Wang et al. 2008) and breeders' knowledge about these germplasm (Camus-Kulandaivelu et al 2007; Flint-Garcia et al 2005). Because of the importance of relative kinship in controlling for false positives in association analysis (Weber et al 2008; Yu et al 2005), a pair-wise kinship relationship matrix using SPAGeDi (Hardy and Vekemans 2002; Yu et al 2005) will be developed. . The relative kinship information will be fitted as a random term to control polygenic effects in the mixed model analysis. Next, a combined analysis of phenotypic data from the multiple-year multi-location nursery trials will provide critical information on the precision of the field experiment and generate the mean performance for each line. A mixed model framework will be used to evaluate each trait of each line (Bernardo 2002). Data inspection with descriptive statistics as well as residual analysis will be conducted for quality control. The final step involves association analysis of genotypic and phenotypic data. First, model fitting will be conducted to determine the influence of population structure and relative kinship on different traits (Yu et al 2005). Individual SNPs will be tested with the selected model (Yu et al 2005) using the TASSEL software. Given the number of SNPs we will evaluate, our association analysis represents a first genome-wide scan that is critical for future experiments designed to discover causative SNPs.

The **bi-parental statistical analysis** will use composite interval mapping approaches. We will use Q-Gene (Johanes and Nelson 2008), a statistical package specifically designed for such analyses. Permutation tests (Churchill and Doerge 1994) will be performed to determine experiment-wise error rates.

vi. The BeanCAP portal and storage of research data. The BIC WWW site (hosted at Michigan State; http://www.css.msu.edu/bic/) is the primary on-line resource for bean research information. **Kelly**, the current BIC site curator, will continue to provide leadership for this site. For example, this site provides all of the accepted disease screening procedures at http://www.css.msu.edu/bic/ResearchTechniques.cfm. Therefore, it is logical to utilize the BeanCAP portal as the project server (http://www.css.msu.edu/bic/BeanCAP.cfm). The portal will advertise BeanCAP activities and provide a schedule of all of the project activities.

From a research perspective, it is our experience that less-experienced database users prefer pre-designed tables to those generated by the user. As examples, the BeanCAP portal will provide:

- research experimental design and data collection methods
- complete pedigree data for all historical varieties and advanced lines

- passport and performance data for the NPGS common bean core collection
- complete passport, genotypic, and phenotypic data for members of the association mapping population (provided by UC Davis database personnel)
- a continuously updated master table containing complete marker/trait association information including linkage distance, allele effect, and PCR detection conditions (provided by UC Davis database personnel)

The Phaseolus Genes database (http://phaseolusgenes.bioinformatics.ucdavis.edu/search/), housed at UC Davis, will be developed as the long term site curating common bean genetic and genomic research data. All of the historical mapping and QTL data generated by the bean research community prior to this project, and all BeanCAP generated phenotypic and marker information, will be incorporated into the database. The database will also include the soybean genome sequence and synteny references between common bean and soybean. This will allow us to anchor a given common bean genetic location to additional electronically mapped common bean loci. For example, all QTL and AM loci will be located on a cMap linkage group that is linked by sequence to additional common bean loci through a GBrowse soybean intermediate. Data mining queries will allow the user to discover additional markers that might be more tightly linked to a trait of interest. The McClean lab has recently demonstrated the value of leveraging the soybean genome by converting a common bacterial blight QTL, that spanned an entire linkage group (Nodari et al. 1993), into one that spans only 5 cM (Jackson et al. 2009). During the analysis and visualization step, users can freely move around GBrowse, CMap and marker database to discover related genome sequences, genetic marker details, and locus annotations. Custom hyperlinks will be provided to facilitate browsing among different types of information. The analysis and visualization module will lead tonew marker discovery by interacting with various custom tracks of sequence information generated by bioinformatics tools and algorithms that implement the necessary steps for marker discovery. These tracks will be based on BLAST of Phaseolus sequences against soybean sequences and primer development for PCR amplification of candidate markers. Throughout the establishment of this tool, we will remain in touch with the National Center for Genomic Research (Santa Fe, NM) to assure close links with the Legume Information System.

To ensure applied utility, Executive Committee plant breeders (**Brick, Kelly, Osorno, Myers**) will also work with a UC Davis staff to exploit the coming interoperability of cMAP and gBrowse. The immediate goal is to design approaches that allow breeders to select markers for incorporation into their projects. This tool will significantly impact breeding by enabling breeders to discover previously unrealized parental combinations that are genetically diverse at regions of the genome highly associated with important agronomic traits. To ensure a more basic utility, Executive Committee molecular geneticists (**Gepts, Grusak, McClean, Myers**) will provide guidance regarding the development of linkages to candidate genes. The linkages will be based on the annotation of the common bean sequences and their soybean orthologs and the physical location of the gene models relative to known genetic loci. This linkage will provide users a more knowledge-rich information basis from which to choose new useful markers. Myers and McClean (unpublished) have shown this functionality by identifying a putative gene for the “stay-green” phenotype in common bean based on the location of an annotated gene model in soybean that genetically cosegregated with the soybean “stay-green” trait.

2. BeanCAP Extension Program: A Nutrition and Health Community of Practice

a. Background. Visualization and learning. Life science courses now emphasize that cellular life is maintained by molecular and cellular processes. The use of **visualization** is a compelling approach that assists biology educators to teach these molecular and cellular processes. From an educational perspective, visualizations greatly aid student understanding of complex processes because they assist in the conversion of an abstract concept into a concrete visual object that can be mentally manipulated (Sekular and Blake 1985). With well-designed visual tools, students can digest large amounts of information in a relatively short time and construct their own personal vision of a process (Kraidy 2002). Graphical visualizations augment textual information (Mayer 1989) and are most effective when they support content for which the learner has had little or no knowledge (Mayer and Gallini 1990).

Computer **animations** foster long-term learning by calling attention to objects during the early steps of instruction. They are effective for learning processes that change over time by reducing the abstractions associated with the temporal transitions of the process (Gagné 1985; Rieber 1994). The benefit of animations is only realized if it is incorporated into a lesson plan that includes lecture and other learning inputs (Rieber 1990). The dual-coding theory (Paivio 1979, 1991) suggests long term memory requires both verbal and visual cues. As such, when animations are combined with narration, dual-coding learning is shown to be supported (Mayer and Moreno 2002). The most effective visualizations reveal the complexity of the objects involved in the process, illustrate how and where the objects interact, provide a spatial representation of the molecules during the process, and smoothly represent the transitional states the objects undergo during the length of the process. High quality, three-dimensional animations have all of these attributes.

The Virtual Cell development team. The NDSU Virtual Cell research and development team has developed a suite of >16 high quality animations depicting basic molecular and cellular processes (http://vcell.ndsu.edu/animations). **The motivation for these animations is to assist novice and advanced students to learn general principles of molecular and cellular biology.** These animations were featured prominently in the Netwatch section of Science Magazine (December 2, 2005; http://www.sciencemag.org/cgi/reprint/310/5753/1401a.pdf), as well as the NSF Discoveries WWW site (http://www.nsf.gov/discoveries/disc_summ.jsp?cntn_id=106839). Over 1,200 users have registered, and more than 300 instructors have created accounts so they can download the animations for local usage in their teaching materials. All of the animations were deposited on YouTube in the past year. The YouTube Virtual Cell Channel (http://www.youtube.com/user/ndsuvirtualcell?ob=1) has >1,600 subscribers, and since uploading, the animations have been viewed more than 600,000 times. At times, the Photosynthesis animation was the third (now fifth) most watched video among the featured Education videos on YouTube. The animations are also widely disseminated at the TeacherTube (http://www.teachertube.com/) and Multimedia Educational Resource for Learning and Online Teaching (MERLOT: http://www.merlot.org/) sites.

In addition to animation development, the project team also researches how animations affect the learning of science. A recent publication from our research group clearly demonstrated that animations improve learning (McClean et al. 2005). Those results are supported by other educational researchers in fields such as cell biology (Stith 2004) and biochemistry (Schonborn and Andernson 2006) and for topics such as cholesterol uptake and apoptosis (O’Day 2008). This research has informed our choice of animations as the learning media for the new COP.

b. The Nutritional Genetics and Genomics Community of Practice: Healthy Foods from the Field to the Table

i. The BeanCAP COP – General Concept. The BeanCAP will launch the "**Nutritional Genetics and Genomics: Healthy Foods from the Field to the Table"** eXtension Community of Practice. The **Community of Interest** consists of two **target audiences**: 1) the **general public** seeking knowledge regarding nutrition, health, genetics, and genomics; and 2) the **educational community** looking for education resources that teach students modern components of biology in a manner that links science to the day-to-day health concerns. We will coordinate closely with the plant breeding component of the BeanCAP project to provide materials that are relevant to their educational efforts.

ii. COP Leaders. The first set of COP leaders will be drawn from the BeanCAP project itself. The leaders are: **NDSU**: McClean (Genetics/Genomics), Garden-Robinson (Nutrition/Health), Osorno (Breeding/Genetics), Johnson (Animation Development); **Colorado State University**: Brick (Breeding/Genetics), Thompson (Health and Disease); **USDA/Children's Nutrition Research Center**: Grusak (Genetics/Nutrition/Physiology); **University of California, Davis**: Gepts (Genetics/Genomics). As other individuals become interested in the material, we will look to adding other leaders.

iii. Development of the COP: Animations, Multimedia Materials, Site Management, Design, and Review.

General design approach. The purpose of the COP is **to provide modern, multimedia resources that educate the public regarding the role that plant genetics and genomics play in improving the nutritional status of plants**. Clearly, the materials must be interdisciplinary and integrate a wide range of topics including plant and human physiology, nutritional aspects of health, molecular and cellular biology of metabolism, and genetics and genomics of plant improvement. These materials must be designed in a manner that provides immediate answers to questions, but are also be part of a learning path that integrates the multiple disciplines.

To ensure consistency, we will adopt the VCell development model and build two interrelated modules simultaneously. The **first pair of modules** will focus on 1) root biology and the role soil chemistry plays on nutrient uptake; and 2) the flow of soil minerals from the root to various parts of plants. The purpose of these modules is to explain a) that important food minerals come from the soil, b) that soil chemistry (e.g. low or high pH) dictates what minerals are taken up, and c) how minerals move through the plant and eventually end up in the edible part of the plant. The **second pair of modules** will focus on a few minerals and show how they move from our digestion system to the various organs in our body, and what health problems arise from mineral deficiencies in our diet. The **third pair of modules** will be a basic lesson in genetics that emphasizes the fact that many genes are involved in the uptake and distribution of the minerals throughout the plant, and that the genome of the plant is required to produce all of the proteins necessary for functional uptake and distribution of minerals throughout the plant. And the **fourth pair of modules**, will focus on how plant breeding utilizes the genetic information for trait (mineral uptake) improvement, and the role of genomics in developing the tools that assist the breeder in trait selection.

This development plan is intended to illustrate a continuum that demonstrates 1) how plant metabolism dictates the nutritional status of a crop; 2) how the plant nutritional status affects human nutrition and directs our choice of foods; and 3) how knowledge of the genes controlling plant nutritional status can be improved using genetics and genomics approaches. It is our initial intention to follow this model, but if inherent education flaws arise, it will be modified.

Animation development cycle. Each module will consist of a narrated animation and supporting multimedia WWW pages. Animation development begins with the development of a storyboard and narrative by project scientists. The artists then use ***Autodesk Maya***, a powerful software environment that supports all aspects of modern animation. For example, it has been used for such recent motion pictures as *Spiderman*, *Ice Age*, and *The Lord of the Rings* trilogy. (The Academy of Motion Pictures Arts and Sciences recently awarded Autodesk an Oscar for scientific and technical achievement for its development of Maya.) **Our project has a working relation with Autodesk, and they provide ten Maya Complete (full commercial version) licenses at no charge.**

To expedite the development process and promote visual consistency, we will reuse, whenever possible, the VCell library that currently contains over 250 molecular and cellular objects. In addition to speeding up the development process, reusing objects provides the students with a degree of familiarity and consistency that aids student learning and provides a visual understanding that all processes are part of a continuum of interrelated steps.

Once the animations are complete, they will be rendered at the NDSU Center for High Performance Computing (CHPC; http://www.ndsu.edu/chpc/) Bewoulf cluster that consists of 64 dual-processor computers. Computation time is balanced based on user needs, and our animations are typically rendered in 18-36 hours. Following rendering, lead in stills and voiceover narrations are added to the animations. Currently, it takes an artist about six to eight weeks to develop a completed animation, and an additional one week to implement the WWW pages used to deliver the learning module. Given that our budget provides for one full-time and one half-time artist, we safely estimate that we will be able to produce **4-6 animations** and their associated WWW pages **per year**. We thus anticipate that we will develop **between 16 and 24 modules during the BeanCAP project**.

Alternative animation formats. All animations are rendered at a high quality 640x480 resolution and saved in the .wmv file format because it is the easiest format for embedding the animations in a WWW page. The internet connection of some instructors is too slow to download these large size files. Some instructors wish to embed the animations in their learning modules, such as MS PowerPoint presentations. To meet these needs, all animations will be offered in alternate formats (.avi, .mov, and .mpeg4) rom the VCell server at http://vcell.ndsu.nodak.edu/animations/downloads. The user will register so we can keep track of usage. All stills and narrations will be available from the same download site.

Supporting multimedia materials. We will adopt the VCell model of offering still images of the animation as supporting materials. A selection of images that focus the learner on important learning points will be extracted from the rendered animation, and information bubbles that feature the key knowledge points of the animation will be added. One set will be developed for the general public at the ninth grade level. A second (and more comprehensive) set will be developed for the college freshman to junior level.

COP site activities. During the first 12 months, we will develop an extensive list of **Frequently Asked Questions (FAQ)**. These will be drawn from our knowledge of the field, questions found in textbooks, and those we receive in the classroom or from our colleagues in other fields. As the COP goes public, we will begin to collate questions and expand the FAQ as appropriate. The leaders will share the FAQ and their answers among themselves to ensure accuracy.

Prior to the launch date, the content portion of the Wiki site will be created. A chart will be created that will suggest possible learning paths. The content will be organized around the animations. Users will select a topic, link to a page where they will have the choice of either directly reviewing 1) the animation; 2) stills; 3) the animation narrative; or 4) learning objectives. All of these topics will be interlinked to allow the user multiple learning paths.

Given the time consuming nature of animation development, the **peer review** process will be **ongoing**. Reviews will be provided initially at the time the storyboard and narration are drafted. This is a critical point because it will dictate the visual nature of the animation objects as well as the interactions and timing of interactions among objects. The National Standards for Science Learning for grades 9-12 (http://www.nap.edu/openbook.php?record_id=4962&page=106) that relate to “The cell”, “matter, energy, and organization in living systems”, and “interdependence of organisms” will be considered during development. That will be important as we offer these learning modules to the grade 9-12 audience. The next review will consider the visual nature of the objects to ensure their appearance is appropriate for the target audience. When an animation is completed, it will be reviewed to ensure the interactions are smooth and not confusing. Finally, the lead-in materials added in post-production will be reviewed to ensure they are engaging and spur the interest of the learner. All of the **reviews** will be performed **by project leaders**.

iv. Launching and Marketing the COP. Because of their extensive experience with animation development and dissemination, the NDSU members of the COP will serve as the marketing team. The obvious first venue is educators. The large database of VCell Animation users and those registered with the YouTube channel will be contacted within six months of the start of the project. The announcement will describe the nature of the site, the resources available, and the utility of the site as an educational venue. In the second year of the project, we will make a presentation at the Plant and Animal Genome Conference. The goal will be expose educators to the value of the materials that we are developing. Similar presentations will be made by leaders who attend other meetings, for example, the Crop Science Society of America.

v. Managing the COP. Project leaders will provide overall governance of the COP. **McClean and Garden-Robinsion** will take the initial responsibility for direct leadership at the onset and will be assisted by other leaders. **Deb Pankow** (NDSU), the past chair of the Financial Security for All COP, will act as our COP mentor. (See attached commitment letter.) A monthly organizational meeting will be held either via conference call or video conference. Progress in all aspects of the COP will be reviewed and specific assignments will be made to leadership. Christina Johnson will be the direct contact person with the eXtension organization. She handles all animation design, still development, and interactions with youtube.com and teachertube.com for the VCell Animation project. She will be directly responsible for uploading all project information and ensuring it meets eXtension organizational and formatting requirements. She will also work directly with eXtension to ensure the COP site design complies with eXtension guidelines.

III. BeanCAP Education Program: Engaging Students to Broaden the Human Resource Base for the Plant Breeding Industry

Although there is a **strong demand** for plant breeders, especially in the private sector, the **applicant pool** has **decreased** in recent years (Frey, 1996; Guner and Wehner, 2003; Trexler et. al., 2005). Importantly, the current numbers of plant breeding graduates do not meet the number of open plant breeding positions. The gap between demand and supply of plant breeders has been caused by several factors including decreased funding, increased retirements of experienced breeders, and lack of interest from students. Another factor is the emphasis made at universities towards training in molecular biology and other new technologies rather than conventional plant breeding. Yet, plant breeding remains a vibrant, multi-disciplinary science characterized by its ability to reinvent itself by absorbing and using novel scientific findings and approaches such as those offered by the science of genomics (Gepts and Hancock, 2006). Therefore, as the training arm of the plant breeding, universities need to engage students earlier and expose them to the breadth of activities in which a plant breeder is engaged.

From an industry perspective, new hires lack the ability to walk the field and observe important phenotypic differences, and to conduct field experiments with the optimum management practices and statistical design to distinguish genotypic differences (Bliss, 2006; Fehr, 2007). These are essential skills for an individual to be a successful plant breeder. Simultaneously, the breeder should be able to sit with the molecular geneticist and discuss the integration of classical and molecular genetics in a manner that more efficiently reduces the time to new cultivar releases. Therefore, the key to being a successful plant breeder today resides in the ability to integrate both the field breeding techniques and the molecular tools. In addition, the plant breeder needs excellent communication and teamwork skills because plant breeding is a team-oriented effort involving professionals from different disciplines and locations (Baenzinger, 2006). We believe exposing students to all of these aspects of plant breeding will provide them with the necessary information to make an informed career decision.

The BeanCAP will organize three activities in order to assure a flow in the human resource pool for plant breeding. These activities will target students from different education levels ranging from high school students to undergraduate, and graduate students in some instances. We believe that early exposure of high school and undergraduate students to plant breeding is the best way to generate interest in pursuing a career in this area of agriculture. Undergraduate students often only learn about plant breeding in their junior and/or senior year. By this time, most of them have already chosen another career. **Therefore, direct high school and undergraduate experiential learning activities and recruitment are our main activities of the BeanCAP education component.** Other CAP projects have focused on training graduate students whom are already involved and/or pursuing careers in plant breeding. Therefore, **our plan is to show the opportunities that plant breeding offer by bringing exposing new students to the discipline**.

***i. Objectives and Activities*:** The BeanCAP education program has two main objectives:

1. Early exposure of high school students to encourage them to pursue of careers in plant breeding.
2. Hands-on training of undergraduate students at the interface of plant breeding, genetics, and genomics.

Presentations, field/greenhouse trips, and hands-on training will expose students to the general functions of plant breeding. This includes the science of plant breeding (what a plant breeder does), Mendelian genetics, breeding for nutritional traits, qualitative vs. quantitative trait breeding, and marker-assisted selection. Potential students will be invited to participate in summer and year-round internships that demonstrate the applied and basic activities involved in a breeding program. These activities will directly expose many high school students to the day-to-day activities of plant breeding and genetics across the four years of the project. The collaborators of these education activities are: **Brick** (CSU), **Kelly** (MSU), **Osorno** (NDSU), and **Urrea** (UNL). **Drs. Osorno and Urrea will lead this aspect of the project**.

ii. Early Exposure High School Activities. Early exposure activities will target high school students. Participants from each university will visit on an annual basis at least three local and regional high schools to discuss the science of plant breeding. Secondly, follow-up visits by these high school students will be arranged. Our **goal** is to reach at least **1,200 high school** students (75 students per year per location) over the 4 years of the project. Additionally, one interested and motivated high school student will be recruited annually into the breeding program to serve an apprenticeship.

Individual high schools will be contacted and interested science teachers will be identified that are willing to host a class visit. Given the connection that rural students have with agriculture, rural schools will be one of the target clientele. The visit by the breeder will be general in nature and focus on genetics as a science and plant breeding as an applied genetics career. These will be generally, 30-45 minutes in length.

Following the in-class presentation, visits by high school classes to a breeding program will be arranged. These visits will emphasize key concepts of plant breeding such as genetic variability and the importance of selection. The need for crops with better nutritional quality will be a featured example. Classroom materials will be developed for school teachers to take back to the school where they can demonstrate important concepts such as the importance of water and light for plant development. This activity would help teachers have more general discussions of water, agriculture and society.

At all schools, one motivated and interested student will be brought into the program. Where possible, students will enroll in a program to receive college credit for their internship. For example, Huskers Horizons is a program offered through the College of Agricultural Sciences and Natural Resources at UNL that offers high school seniors college credit for activities like those we are planning. High school students from a Scottsbluff area high school working with Dr. Urrea will take part in this program. We will look for similar opportunities at the other locations.

Promotional materials such as brochures, flyers, and posters describing plant breeding will be developed for the high school audience (**Osorno and Urrea leads**). A brochure describing the science of plant breeding will be prepared for distribution during high school visits and campus activities. The brochure will be question oriented and answer questions such as: 1) What does a plant breeder do on a daily basis? 2) What is the role of in plant breeding? 3) How are genetic concepts applied to solving several production problems? 4) What roles have famous plant breeders and geneticists played in solving society problems? The main goal is to show students the career possibilities and excite them about a career in plant breeding. All materials generated will be publicly available in a website of general access so they can be used in recruiting activities and workshops made by other groups and institutions in the future.

iii. Early Undergraduate Activities. Summer and year-round internships will be offered by all participant universities each year. A total of eight students per year (two per campus), will have an 11 week summer internship opportunity to gain hands-on experience in a US dry bean breeding program. These will come for the local universities. In the case of UNL, students attending Scottsbluff Community College will be recruited.

The **summer program** will be announced during the fall and spring semesters. In some cases, students in the program may register for a 1-3 intern credits. **This experience will focus on field** (whole plant phenotyping, field operations, production and agronomy, experimental design, disease evaluation), **and lab** (nutrition profiling, DNA isolation, molecular marker screening and detection, analysis of marker data) **aspects of plant breeding**. Students will also visit other breeding programs. For example, NDSU has 13 breeding programs that the students can learn from. These activities will be designed to be informative to the undergraduate students and are not intended to duplicate the graduate training offered by the other CAP projects. At the same time, though, we will leverage the more advanced materials developed by the other CAP projects by collating all of the learning materials and hosting them on the BeanCAP WWW site. This will not only serve our students, but provide additional coordination for all CAP educational activities.

Students will be admitted into this program based on their potential to be recruited for M.S. or Ph.D. programs at one of the participating institutions. All the applicants should have at least a 2.8 GPA. An informational seminar about research opportunities in this program will be offered each fall semester. Candidates will apply in fall semester and are interviewed early in the spring of each year. Students will be required to report on their experiences in a departmental seminar or other appropriate forum. The goal is to motivate these students to pursue a graduate degree in plant breeding.

Undergraduate students (sophomore or early juniors) that express an interest in plant breeding will be recruited into **school year internships** at each university. They will work part-time during the fall and spring semesters (10 hours per week). **These students will participate in a student-centered research project that couples breeding activities such as selection, field and greenhouse trials, nutritional screening with molecular marker, and genomics-assisted breeding techniques.** This will give them an exposure to all aspects of a breeding program. At each campus, a ½ time Ph.D. student (**on non-BeanCAP funds**) will supervise the interns' activities and act as mentors. Faculty will participate actively and interact with the interns on a regular basis through group meetings and mentoring sessions.

iv. Assessment and Tracking Participant Accomplishments. The success of the educational component of the project will be measured based on both quantitative and qualitative evidence. A data base of all student participants will be maintained and contact information will be periodically updated. Exit interviews will be conducted at the conclusion of each project activity. Tracking of participants will continue throughout the project as well as after the termination of the project. The database will be used as a way to periodically contact ex-participants and document what impact participation in the project has had on recruitment and education of plant breeders.

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Key Personnel

(a) Key Personnel

The following table describes the roles of the PD, the Co-PDs, and other service providers. The table is organized around the major activities of the BeanCAP Project. These are also noted in the Project Narrative.

Participant (Location)	**Role and responsibility**
Phillip McClean (NDSU)	Project administrator CAP marker development
Perry Cregan and David Hyten (USDA/Beltsville)	Solexa sequencing within market classes 454 sequencing of Jalo EEP558 SNP marker development Illumina Golden Gate Assays
Mike Grusak (USDA/Houston)	Mineral analysis CaCo-2 cell tests
Mark Brick (CSU) Elizabeth Ryan (CSU) Henry Thompson (CSU)	Antioxidant tests Phenolics tests Anthocyanins test Soluble/insoluble fiber determination
Mehmet Tulbek (NDSU)*	Protein analysis Fiber analysis Oil analysis
Jim Kelly (MSU) Karen Cichy (USDA/East Lansing)**	Phytate test
Jim Myers (OSU)	Carotenoid test (snaps only) Vitamin C test (snaps only) Fiber (snaps only; different than CSU test)
Mark Brick (CSU)[1,5] Jim Kelly (MSU)[1,2,4,5] Phil Miklas (USDA/Prosser)[2,5] Jim Myers (OSU)[3,4,5] Juan Osorno (NDSU)[1,2,4,5] Tim Porch (USDA/Mayaguez)[2,5] Carlos Urrea (UNL)[1,2,4,5]	[1] Dry bean association mapping field test [2] Dry bean abiotic stress field test [3] Snap bean association mapping test [4] Bi-parental population field test [5] Statistical analysis
Paul Gepts (UC, Davis)	DNA analysis cMAP implementation gBrowse implementation Electronic marker selection

Key Personnel

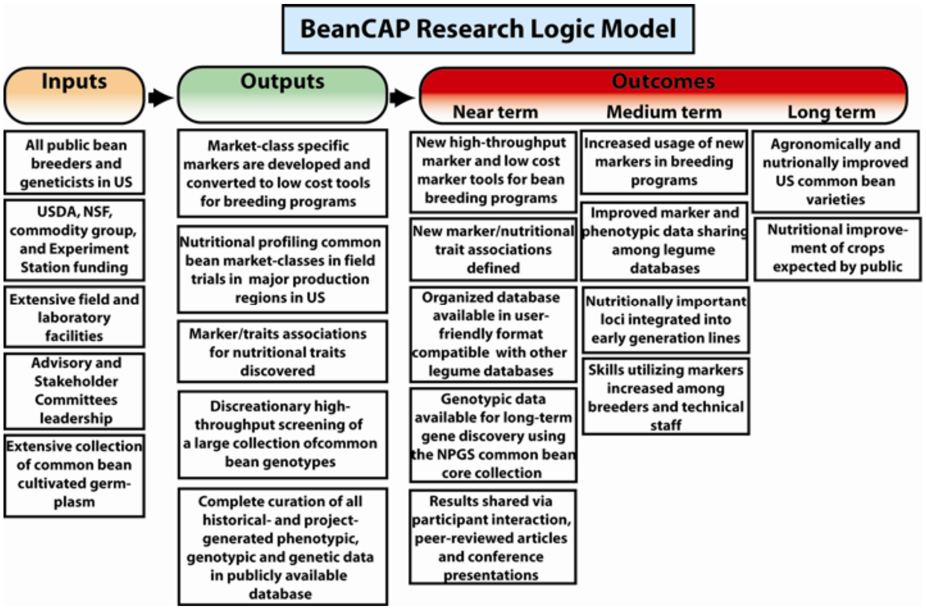
Mark Brick (CSU)[1,2,3] Julie Garden-Robinson (NDSU)[1,2,3,4] Paul Gepts (UC, Davis)[1,2,3] Mike Grusak (USDA/Houston)[1,2,3] Christina Johnson (NDSU)[1,2,3,4] Phil McClean (NDSU)[1,2,3,4] Juan Osorno (NDSU)[1,2,3] Deb Pankow (NDSU)[5] Henry Thompson (CSU)[1,2,3]	[1]COP leaders [2]COP FAQ development [3]COP experts [4]COP launch [5]COP mentor
Christina Johnson (NDSU) Phil McClean (NDSU) Brian Slator (NDSU)	Animation development
Mark Brick (CSU) Jim Kelly (MSU) Juan Osorno (NDSU) Carlos Urrea (UNL)	High school visits Undergraduate recruitment and training Plant breeding education materials Plant breeding recruitment materials

*Not listed as Co-PD. See letter of cooperation in “Documentation of Collaboration.”
**Dr. Karen Cichy will begin at the USDA/Sugarbeet and Bean Research Unit, East Lansing, MI in the summer of 2009.

(b) Logic Model

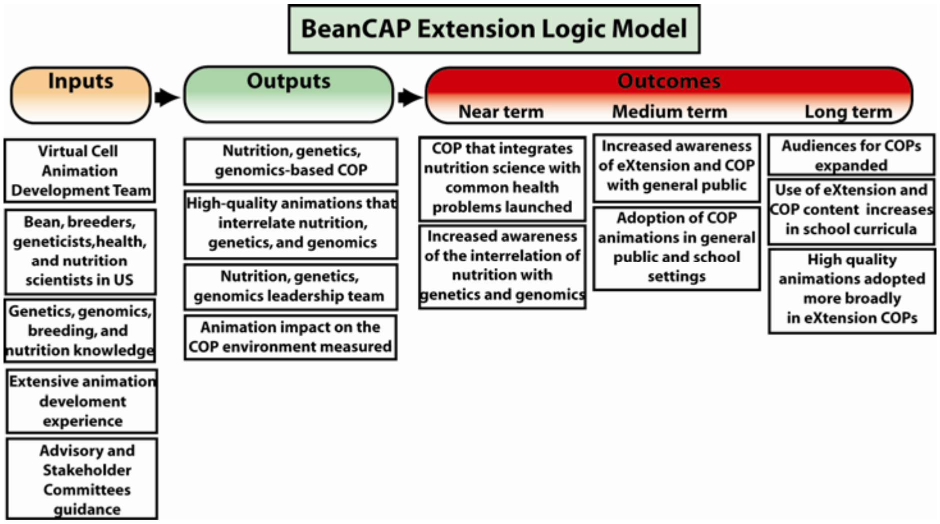
Research Logic Model

The current situation is that common bean is considered a major nutritional crop. **Improvement of nutritional traits is limited** by the fact that loci controlling a large collection of nutritional traits have not been discovered in a systematic species-wide or market-class-specific manner. Also, large scale, species-wide nutritional profiling is lacking, and the tools for genome-wide screening for important nutritional loci are not available. To systematically change the nutritional status of common bean, discovering the specific nutritional trait/loci associations is a **priority**. Genome-wide tools that have utility for all, not just nutritional traits, should be developed and converted into low cost breeder markers to support this priority. This data must be shared for national and global improvement. To accomplish this, **we assume that** 1) within market-class (or race) variation is sufficient to discover within market class loci that can improve all (or at least most) market classes; 2) species-wide profiling will uncover new loci with major impact on nutritional trait expression; and 3) addressing such a broad suite of nutritional traits is best approached using community-wide human and technical resources.



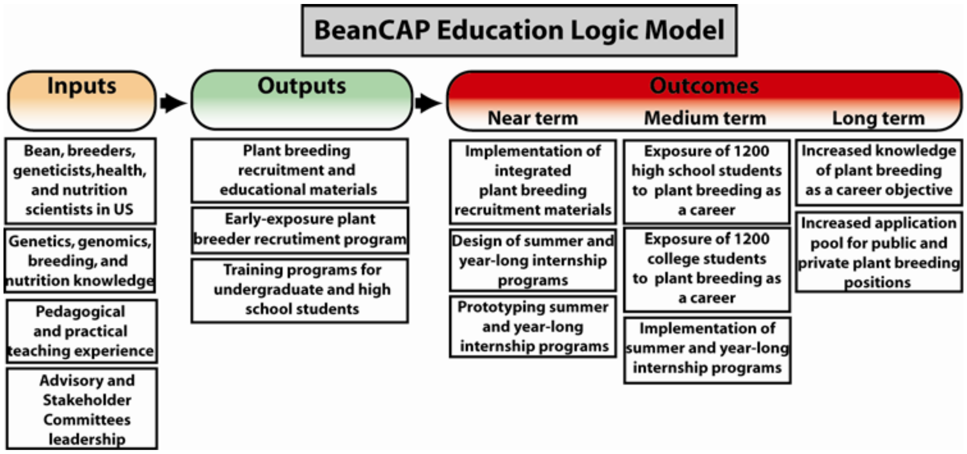
Extension Logic Model

The current situation is that the relationships between nutrition, genetics, and genomics are not understood by the general public. **Changing this knowledge gap is limited** by the fact that effective learning tools that capture the dynamic nature of the interactions and cover the multiple biological aspects of nutrition are not available. To remedy this situation, the development of learning modules that capture the interrelationships are a **priority**. Animations that capture the dynamic nature of nutrition should be developed and coupled with a broad-reaching learning environment such as an eXtension Community of Practice. To ensure the public's awareness of the interrelationship increases, the COP learning modules must be shared both nationally and globally. To accomplish this, **we assume that** 1) the public is interested in this topic; and 2) animations are the most appropriate learning media.



Education Logic Model

The current situation is that human resource pool for plant breeding falls far short of meeting the needs of the profession. **Increasing the pool is limited** by the fact that fewer and fewer students are knowledgeable about the profession and hands-on early experiences are not widely available. Developing early exposure programs are a **priority** to address the shortfall. Face-to-face interactions and breeder-guided training that focus on a single improvement goal, such as nutritional status, would support this priority. These programs must be shared to have a national or global impact. To accomplish this, **we assume that** 1) face-to-face interactions that focus on the daily aspects of a profession is an effective initial recruitment approach; and 2) extensive hands-on training is an effective tool that transitions interest into commitment.



(c) Management Plan

1. Administrative Groups. The direction of the BeanCAP project will be guided by four committees. The **Advisory Committee** will provide all guidance to the project. The **Executive Committee** will provide operational leadership of the project. The **Industry Stakeholders Committee** will provide guidance from an industry perspective. The **International Stakeholders Committee** will provide a mechanism to introduce BeanCAP outputs throughout the world, while ensuring duplication is minimized and avenues of cooperation remain strong. Committee members and their expertise follow.

Advisory Committee members are: **Fred Bliss**, long time bean geneticists and former head of plant improvement at Seminis, Inc.; **Charlie Brummer**, forgage molecular geneticist, University of Georgia; **Chuck Hibberd**, director, Purdue Extension Service; and **David Sleper**, plant breeder and author of "Breeding Field Crops", University of Missouri.

Executive Committee members are: **Paul Gepts**, molecular geneticist, UC, Davis; **Julie Garden-Robinson**, human food and nutrition extension specialist, North Dakota State University; **Mike Grusak**, human nutrition and plant physiologist, USDA, Houston; **Jim Kelly**, dry bean breeder, Michigan State University; **Phil Miklas**, bean molecular geneticist, USDA/Prossser, WA; **Jim Myers**, snap bean breeder, Oregon State University; and **Juan Osorno**, genetics and breeder educator, and dry bean breeder, North Dakota State University.

Industry Stakeholders Committee members are**: Tom Grebb**, Central Bean owner, and member of US Dry Bean Council, Qunicy, WA; **Ken Kmecik,** snap bean breeder for Seminis, Inc.; and **John Ryapati**, dry bean breeder, Archer Daniels Midland.

International Stakeholders Committee members are: **Kirsten Bett**, bean breeder/geneticist, Univ. of Saskatchewan; **Horacio Guzman**, bean nutrition expert, INIFAP, Mexico; **Susan Nchimbi Msolla**, bean breeder, Tanzania; **Federico Sanchez**, bean molecular genetics, UNAM, Mexico; **oe Tohme**, bean biotechnology lead, CIAT, Colombia; and **Rajeev Varshney**, legume genomics, ICRISAT, India..

2. Management Roles and Responsibilities. The BeanCAP reporting lines are graphically presented in Fig. 1. **Co-PDs** will provide one-page quarterly reports to program leads highlighting progress and problems. **Program leads** will review the reports to ensure that the Co-PDs activities are being achieved according to the project timeline. During monthly conference calls with the Executive Committee, the **Project Director** (McClean) will summarizes the reports and discuss other project issues with an emphasize on project activities that are working in an integrative manner and how further integration can be enhanced in the future. The Executive Committee provides direction to the Project Director who in turn provides guidance to the program leads. The **Advisory Committee** reviews all reports and provides guidance to the Executive Committee in the form of semi-annual reports. The **Stakeholder Committees** inform the Executive Committee and the Advisory Committee on issues relating to the outputs of the three programs.

The program **Evaluator** (to be hired upon funding) will prepare an annual report for the Advisory and Executive committee based on the BeanCAP Formative Evaluation Plan (Appendix Table 1). To assess progress and impact of the project, four major questions, each with multiple sub-questions, were developed. These questions focus on the research, extension, and education components of the project, as well as the integration of the components. Data will be collected from a combination on questionnaires and interviews. Interviewees will include appropriate project personnel, Stakeholder and Advisory Committees, plant breeding education interns, and on-line users of the newly developed Community of Practice.

Management Plan

The Advisory Committee will meet with the Program Director and Executive Committee at the annual Plant and Animal Genome Conference to receive additional detailed input. The Advisory Committee will summarize overall progress based on project timeline (**Table 2**) and suggest improvements in an annual report that will be delivered to the Executive Committee and the USDA/Plant Genome, Genetics, and Breeding program officer. The Advisory Committee will ensure that the project is integrative by highlighting points of contact and information exchange between the three programs in the annual report.

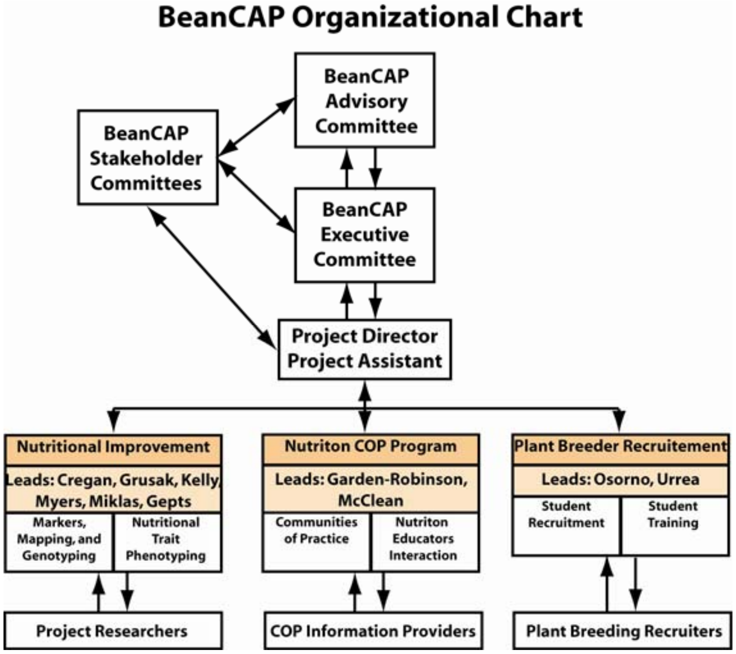


Figure 1. The BeanCAP Organizational Chart that depicts the reporting lines among the various participants and administrative groups.

Table 2. BeanCAP Project Timetable

	Date							
Program/Activity	**9/09**	**3/10**	**9/10**	**3/11**	**9/11**	**3/ 12**	**9/12**	**3/13**
Research Program								
SNP development	X	X						
Genotyping		X	X	X	X	X	X	X
Nutritional phenotyping	X	X	X	X	X			X
Marker associations/QTL discovery		X	X	X	X	X	X	X
Drought and heat stress study	X	X	X	X	X	X	X	X
Database development	X							
Database delivery		X	X	X	X	X	X	X
Extension Program								
COP development	X	X	X	X	X	X	X	X
Stakeholders communication	X	X	X	X	X	X	X	X
Education Program								
Year-round research internships	X	X	X	X	X	X	X	X
High school recruitment	X	X	X	X	X	X	X	X
Plant breeding literature development	X	X						
Hands-on program development	X	X	X	X				

3. Discretionary genotyping funding. Intrinsic to this project is a large scale, high-throughput genotyping service. The service will provide the full common bean improvement community (project as well as non-project PD/Co-PDs) an opportunity to collect data that would be of value to full research community. The materials to be screened will be determined annually, and those materials determined to be of broad utility for common bean improvement will be chosen. All individuals requesting the service must agree to submit the genotypic, and all associated phenotypic data, into the project database within six months of the service.

4. Modifying the Project. Reviews by the Executive Committee and the Advisory Committee and Evaluator reports will be used to evaluate progress of each Co-PD. That person's activities will be modified if it is determined by Executive Committee that the initial plan for that activity was overly aggressive. The Executive Committee reserves the right to halt a Co-PDs activities for neglect of responsibility. Those funds would be redirected to another Co-PD or another individual will be recruited to assume that project role.

It is understood by the BeanCAP management team that science and technology progresses often in unforeseen directions. If the Executive Committee and Advisory Committee determine that a new technology or scientific design would improve the efficiency of the project or significantly increase the value of the outputs, the project will be modified by reassigning Co-PD activities or redirecting funds to another Co-PD.

5. Managing Intellectual Property (IP). IP issues will be resolved among those researchers involved in the discovery using the IP policies in place at the appropriate universities.

6. Publications and Data Release. All Publications will be written in a timely manner and appear in established peer-reviewed journals. Authorship will be properly ascribed to individuals associated with a specific BeanCAP research activity at time of publication. The BeanCAP project supports the concept of open access to all research results. We will share our research results and education and extension materials in a timely manner to all stakeholders by placing them in public databases with direct access via the BeanCAP portal (http://www.css.msu.edu/bic/BeanCAP.cfm). The raw results will be incorporated into a database hosted at University of California, Davis. The mapping data will be displayed using cMAP, while sequence related data will be presented using gBrowse. The legume research database organizers have agreed upon these two applications for continuity between species data. Continuity will enable future data integration that will significantly leverage all data.

7. Sustainability. The BeanCAP will be sustained as the genetics and genomics tools are adopted by the bean research and extension community and stakeholders throughout the United States. That will result in continued long-term support from our federal, regional, local, commodity groups, and private funding sources. Related efforts such as those of the W 1150 regional research and extension committee will incorporate BeanCAP advances into its ongoing efforts and future strategic plans to genetically improve beans, and use the BeanCAP successes and wealth of information to interest and recruit highly promising students into our genetic improvement programs. The BIC will continue to provide the infrastructure as a portal for the BeanCAP outputs. The extensive data will continue to be maintained by the UC, Davis database. The National Plant Germplasm System will continue to function as depository for unique genotypes and/or germplasm identified by the program.