PROJECT NUMBER: W-150

GENETIC IMPROVEMENT OF BEANS (*PHASEOLUS VULGARIS* L.) FOR YIELD, PEST RESISTANCE AND FOOD VALUE

DURATION: October 1, 2000 to September 30, 2005

"For millennia humans have recognized the curative power of plants. The use of plants to reduce the discomfort from and/or prevent ills from toothache to gout has been preserved in the lore of countless tribes of people inhabiting the earth". G.L. Hosfield, 1999.

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I. STATEMENT OF THE PROBLEM:

More efficient procedures are needed to transfer desirable traits to avoid unwanted phenotypic alterations often associated with conventional breeding strategies in plants. Although backcrossing is often used to transfer a single gene (or a few genes), breeders frequently cannot completely recover the phenotypic expression of the recurrent parent. Molecular biology techniques provide a tool to manipulate individual DNA sequences.

Relative to cereal grains, beans have low yields and suffer from several limitations. While the world average yield is 600 kg/ha, yields in the U.S. range from 100 kg/ha in the Upper Midwest to 2200 kg/ha in the Pacific Northwest. Problems affecting beans include susceptibility to many diseases, reduced productivity due to environmental stresses, reduced digestibility from antinutritional factors, and poor utilization of seed proteins. These problems are amenable to genetic solutions; however, it often is difficult to identify and incorporate appropriate traits. On a global scale, genetic diversity does not seem to be lacking, but the germplasm base in the U. S. is narrow (McClean, et al., 1993) with restricted exchange between temperate and tropical germplasm pools. In addition, some useful traits are available only by utilizing related species, such as *P. ciccineus* and *P. acutifolius*, or through genetic engineering technology.

Economic productivity can be increased by selecting genotypes with superior morphological characteristics. For example, yields can be improved if plants direct more photosynthate into seeds, due to either increased light penetration in the canopy, higher net CO_2 fixation, or improved remobilization of stored carbon during periods of stress. This requires identification of genes controlling photosynthate partitioning and yield stability. Cultivars also must be disease-resistant, wholesome, with desirable culinary and nutritional qualities. Changes in nutritional guidelines and culinary habits portend a promise to increase domestic bean consumption.

II. JUSTIFICATION:

Extent of Problem

Some of the major factors affecting bean yield are: daylength, temperature, moisture, partitioning and remobilization of photosynthates, disease and insect pests, mineral deficiencies and toxicity and air pollutants. Although daylength and temperature strongly control maturation, the physiological basis underlying these mechanisms is not yet fully understood. More needs to be

learned about the genetic processes that regulate adaptation, and about the genetic control of days to flowering and partitioning. Plant diseases can markedly decrease yield and can affect seed appearance and characteristics associated with quality. Consumers reject blemished and discolored pods and beans. Low yields often mean growers of beans are at a competitive disadvantage with growers of cereals and other foods. Moreover, there are additional losses if beans are unacceptable for purchase and consumption. The increased awareness of the nutritional value of beans in the diet should increase consumer demand.

Gastrointestinal discomfort, including flatulence and diarrhea, is the single most important factor that limits the consumption of dry beans in the diets of American consumers. The intestinal discomfort associated with eating beans is caused by microbial fermentation of particular compounds in the seed that pass into the lower gastrointestinal tract undigested. Factors that may limit digestibility and reduce the nutritional quality of food legumes include complexing of protein with natural polymers such as heat stable trypsin inhibitors, phytates, soluble dietary fiber and flavonoid compounds. Such reactants limit the bioavailability of nutrients and, thus, limit the nutritional potential derived from eating dry beans. It is not clear how flavonoids, fiber, and other complex carbohydrates interact in the bean seed to limit digestibility; however, there is good evidence suggesting that macromolecules form complexes in the seed. These complexes are genotype, post harvest age and storage environment dependent and are resistant to break down by digestive enzymes and/or inhibit the digestive enzyme themselves. Before digestibility can be improved through genetic intervention or food processing technology, a knowledge base needs to be established concerning the genetic and internal controls that restrict break down of bean seed reserve proteins and carbohydrates and render these important bionutrients unavailable in human diets. Studies of interactions between proteins, fiber and other carbohydrates, and flavonoids will provide the means to improve the digestibility of beans through genetic intervention and food processing technology.

Conventional breeding techniques and selection have been used to improve bean varieties. However, gene transfer promises to be the best method to improve disease, insect, and herbicide resistance; improve nutritional composition of bean; improve ease of cooking; and reduce flatulence. Additional research is warranted to identify the appropriate molecular genetic and biotechnological techniques that are required.

Need and Advantages of a Cooperative Approach

Since its initial approval in 1977, W-150 has established a rich history of procedures that are vital to a successful collaborative plant improvement project. The development and composition of the current revision was accomplished by the formation of three committees comprised of participants in the project. Each committee was composed of scientists with an expertise and interest in each of the three stated objectives. Each objective and subsequent supporting procedure was agreed upon by the membership of the regional committee. The planning was accomplished by joint input and consensus with collaboration as the vehicle by which the objectives were to be achieved.

No single research program or agency can conduct all the research necessary to improve beans as a food source. For example, the Agricultural Research Service of the USDA allocates 4.5 scientific years (SY) to in house research on beans under the aegis of National Programs 301,

302, 303, 306, and 107. Additional resources are required to solve the production, disease, and food-quality problems that currently limit the consumption of beans in human diets.

These resources can be provided by a comprehensive approach involving regional collaboration to maintain germplasm and pathogen strains, exchange samples of seeds, pathogens and insects, pool information and equipment, and exchange research data. A coordinated effort will make the most efficient use of genetic resources and avoid duplication of research efforts.

III. RELATED CURRENT AND PREVIOUS WORK:

A CRIS survey conducted by USDA-CSREES, Washington, D.C., identified 416 projects in the U.S. directed toward *P. vulgaris*. Among these, 216 projects concerning dry beans (code 1211) and 155 projects concerning green/wax beans (code 1212) were identified. These projects address breeding and genetics problems, germplasm screening and enhancement, development and use of molecular markers, and use of recombinant DNA techniques. The projects address several problem areas, e.g., heat and drought stress, nitrogen fixation, pest resistance or protein digestibility, and high and stable yield through interspecific hybrids that should contribute to the overall improvement of *P. vulgaris*.

Bean research on a national and international basis is also conducted through a Bean/Cowpea Collaborative Research Support Program (B/C CRSP), a research and training partnership involving U.S. land grant universities, agricultural institutions in Africa and Latin America, and the U.S. Agency for International Development (USAID). As of December 1999, eight of the twelve B/C CRSP projects involved bean research. The focus of this research was on insects, diseases, plant responses, physical environment, production, consumption and economics, food quality, nutrition and health, and research education and training capabilities. These projects concern developing superior disease-resistant, drought-tolerant, high-yielding cultivars; using molecular techniques to characterize the viruses that cause bean golden mosaic virus; developing insect pathogens as pest management tools on small farms; characterizing rust and other fungal and bacterial pathogens; improvement in bean productivity by altering daylength and temperature sensitivities; improving the food value of beans; investigating genetic diversity among landraces; studying the coadaptation of pathogens and the host cultivar; and ascertaining the socio-economic impact of growing disease, insect and stress resistant bean cultivars on smallholder farm families.

Collaboration among members of the B/C CRSP and the W-150 is close, with many members participating in both groups. This close working arrangement has allowed for a liberal flow of germplasm between B/C CRSP participants and members of the regional project, resulting in broadening the genetic base of bean cultivars worldwide. Because of the international scope of the B/C CRSP, there is in the W-150 a renewed awareness of the pathogenic variability present worldwide and the ability to be proactive in the U.S. to breed for resistance to potential new races/strains of common pathogens. Also, this close arrangement with the B/C CRSP allows W-150 participants to utilize beneficial material identified by the B/C CRSP participants for improved biotic and abiotic resistance, yield, and culinary quality. For example, research conducted by the B/C CRSP has provided U.S. snap bean breeders with sources of resistance and molecular markers to breed for resistance to Bean Golden Mosaic Virus in snap bean production region in South Florida. Also, B/C CRSP breeding programs in Central America have extensively

utilized multiple disease resistance germplasm with pyramided rust resistance genes, which were developed through research efforts by W-150 participants.

Attaining these research objectives should lead to techniques or germplasm suited for local conditions. Most of the constraints listed in the B/C CRSP projects are important to specific countries, although some concern affect all locations where beans are grown and utilized. Duplication of research efforts will be avoided through the participation of the various investigators in W-150.

IV. OBJECTIVES

1. **Maximize Productivity and Global Competitiveness.**
2. **Improve Abiotic and Biotic Stress Management Strategies through a Combination of Classical and Biotechnological Approaches.**
3. **Elucidate Genetic Controls for Food Quality and Value Added Components.**

OBJECTIVE 1: MAXIMIZE PRODUCTIVITY AND GLOBAL COMPETITIVENESS.

SUBOBJECTIVE 1A. Broaden the genetic base of common bean through: (a) use of wild bean populations; (b) increase cross-pollination; (c) use and conversion of promising tropical and sub-tropical germplasm; and (d) intra-racial and inter-racial gene pool hybridizations.

SUBOBJECTIVE 1B. Investigate the physiology and genetics of yield potential and its stability (gene interaction) through the Cooperative Dry Bean Nursery, the Midwest Regional Performance Nursery, and other nurseries.

SUBOBJECTIVE 1C. Maximize yield potential of common bean cultivars of major market classes using elite x elite hybridizations among selected high yielding parents of diverse origin.

To maintain competitiveness in national and world markets, bean yields must be increased. Recent shifts in bean production regions within North America underscore the lack of competitiveness with other crops in those states where land prices are higher (Kelly et al., 1999a). Approaches to improve bean yields can be multifaceted, including selection for resistance to biotic and abiotic stresses, introgression of wild germplasm, or the integration of molecular technologies to improve efficiency or incorporate novel genes; in all cases these efforts need to be better integrated. The premise that the germplasm of contemporary bean cultivars is narrow suggests that an integrated approach to improving yield while maintaining or increasing genetic diversity needs to be developed. Breeding for high yield in beans must be conducted within the major constraints of growth habit, maturity, local adaptation, specific disease resistance factors, seed size, and quality preferences. Selecting for yield outside these major potential to improve yield, while not being limited by major agronomic and quality constraints.

In order to emphasize yield breeding in beans, given the production and quality constraints, Kelly et al. (1998) proposed a structured program based on a three-tiered breeding pyramid

shown in Figure 1. The approach to yield breeding is different at each level of the breeding pyramid, and is designed to utilize the maximum variability within available dry bean germplasm. Genetic diversity and development time would be greatest at the lowest level. Improved materials developed at the lower level of the pyramid would be moved sequentially to higher levels for additional improvement. Exploiting and maintaining diversity would be optimized at the lower level of the breeding pyramid, while the focus at the apex of the pyramid would be directed toward yield performance and uniformity. Breeding approaches will differ at each level, while a strong continuity among all three levels is essential. Different breeding procedures are needed to combine and exploit the genetic differences in beans and the breeding pyramid allows for a structured and integrated approach to meet that approach. The approach has been adopted by the bean breeding program at the International Center, CIAT, and a more detailed description of the yield breeding pyramid is discussed elsewhere (Kelly et al., 1998,1999a).

The base of the breeding pyramid represents a foundation of diversity upon which the intermediate and, eventually, elite populations will utilize for future progress. The failure to dramatically increase yield in beans can be attributed to a lack of desirable alleles in the base population, low heritability of yield-related traits, high genotype by environment (G x E) interaction among these traits, yield component compensation, low or negative combining ability within and between gene pools, and dependence on visual selection for yield in early generation. Improvement in any one of these areas should reflect higher yield potential in beans. An analysis of individual elements suggests that all the elements are interdependent, so any change in one component will affect the others. The lack of desirable alleles for yield in the base population is a fundamental limitation, as is the ability to effectively identify sources of useful variability for complex traits. Once desirable alleles are identified, they can easily be transferred into new germplasm. Factors such as dwarf lethal genes, negative combining ability and yield component compensation, however, can limit the exploitation of inter-gene pool variability in cultivated beans. Increasing diversity, through programs that involve germplasm conversion, use of the wild species, intraspecific and interspecific hybridization, would be exploited at the base level. The value of the base population is dependent on its utilization in the higher levels of the breeding pyramid. In order to achieve this, long-term selection and hybridization programs, combined with the advance of progeny from these wide crosses, needs to be rigidly structured.

When crosses are made between lines that are highly diverse, the progeny generally lack a trait vital for the economic production of the crop. Thus the intermediate level of the breeding pyramid is structured to introgress greater levels of diversity into breeding materials, and to identify top performing intermediate lines for crossing with elite breeding material. Crosses in this level would be restricted within gene pools but be freely made among races and market classes differing in seed size. There also would be flexibility to cross between growth habits among different architectural types and between adapted material differing in maturity from different countries. A larger number of crosses would be made since no prior prediction of combining ability is known among diverse germplasm. Use of three-way crosses, pedigree, modified inbred-backcross, and limited cyclic selection procedure, ideotype breeding and physiological genetic approaches should all be considered as breeding methods in the intermediate level. A major focus at the intermediate level is to utilize diverse germplasm to improve tolerance to abiotic stresses that indirectly contributes to improved yield.

Typically, newly released cultivars represent the highest available yield potential at the time

of release (Kelly et al., 1999b). A review of the pedigree information of contemporary bean cultivars illustrates that they are the result of elite x elite crosses (McClean et al., 1993). The need to focus on elite by elite crosses in beans within the apex of the breeding pyramid will ensure the short term improvement of yield in the different commercial classes, provided adequate levels of new and novel variability is being introduced into these elite materials. Every attempt should be made to cross parents with maximum diversity but within the limits of the market class. High levels of disease resistance can be maintained as elite lines represent the best sources of pyramided disease resistance genes. Crosses would be restricted to within gene pools, within races, and among bean market classes of similar seed size to ensure economic potential of the progeny.

The W-150, through recognized collaborative programs with different research s, affords the ideal vehicle, modeled on the yield pyramid, to effectively integrate activities directed toward the common goal of improving yield in beans. Breeders recognize the level of the breeding pyramid at which they expend the most effort with the realization that they are not achieving their desired Realistically, most breeders cannot effectively function at three levels of the pyramid. Our challenge in the W-150 is to integrate, through collaboration, coordinated activities at all levels of the pyramid, since individual breeding programs may be restricted to one level. Collaboration and germplasm exchange, fostered by W-150, between breeding programs worldwide will continue to be the most effective strategy to maximize the diversity entering breeding programs and allow for future improvements in yield. Strong public breeding programs with liberal germplasm exchange policies and effective collaborative nurseries for testing new germplasm need to be maintained to ensure that these objectives can be met. The W-150 offers such a model.

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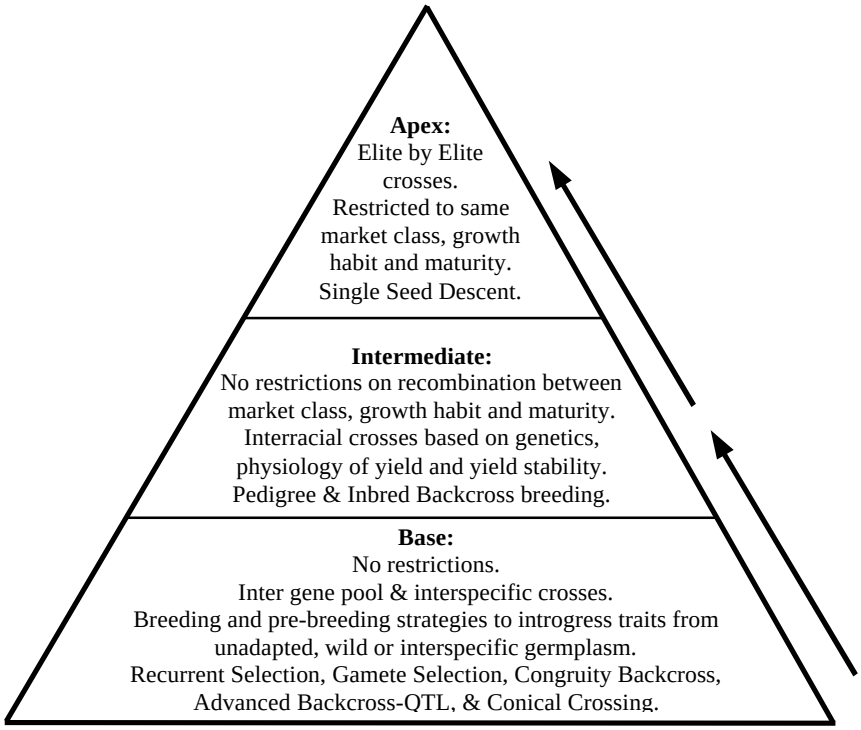

FIGURE 1. Breeding pyramid. A three-tiered approach to maximize productivity and global competitiveness (Based on breeding for yield in common bean, Kelly et al., 1998)

SUBOBJECTIVE 1A. BROADEN THE GENETIC BASE OF COMMON BEAN THROUGH:
PROCEDURES:
(A) Use of wild bean populations;
(B) Increase cross-pollination;
(C) Use and conversion of promising tropical and subtropical germplasm; and
(D) Intra-racial and inter-racial gene pool hybridizations.

Use of wild beans as a source of useful genes for yield potential

1) Map domestication syndrome and yield potential genes, 2) compare the inbred backcross and congruity backcross methods for introgression of yield potential from wild beans to cultivated beans, and 3) determine role of the parental combination in recovering high-yielding progenies.

Increase cross-pollination in common bean

Nienhuis and Singh (1986) observed average heterotic effects of 30% above the best parent, with the best crosses yielding up to 100% above the best parent. The single most important problem from an economic standpoint is the production of hybrid seeds. These have to be produced both abundantly and reliably. Difficulties in achieving this objective should not be underestimated, as common bean is a predominantly self-pollinated species. In most

environments, levels of outcrossing are very low (well below 5%) (Brunner and Beaver, 1989; Park et al., 1996; Ibarra-Pérez et al., 1997). Higher levels of outcrossing have been noted, however, by Wells et al. (1988) and Ibarra-Pérez et al. (1997).

Development of high yielding dry bean cultivars and germplasm lines

Increased yield potential is a major goal of bean breeding programs. In addition, more upright plant type, greater levels of tolerance to biotic and abiotic stresses, and better canning and cooking qualities will be sought.

Genetics, Germplasm Conversion, and Genetic Diversity

The maintenance of genetic diversity in a breeding program can contribute to realized gain from selection for quantitative traits like yield and reducing genetic vulnerability to changes in biotic and abiotic stress conditions. Recent reports about genetic resources used in common bean cultivar development (Silbernagel and Hannan, 1992; McClean et al., 1993) indicate a relatively narrow germplasm base existed in many breeding programs in the past, and may be partly responsible for the relatively slow increase in bean yields when compared to the yield increase for other crops like corn, wheat, and soybean (Silbernagel and Hannan, 1992), Today, our better understanding of the geographic origin and genetic isolation of common bean races and gene pools (Gepts, 1998) has directed research and breeding activities toward wide intra- and interracial gene pool crosses to generate genetic diversity (Kornegay et al., 1992; Singh et al., 1992; Kelly and Adams, 1987; Beaver and Kelly, 1994). Generally wide crosses involving tropical germplasm have not been exploited in the development of US germplasm because of complications arising from photoperiod sensitivity.

A population of recombinant inbred lines will be developed from the cross ICA Pijao x Montcalm. This population will be evaluated in field trials to estimate genetic correlations among traits associated with bean yield. The information from the field trials will be used to generate genetic coefficients in the bean yield model**.** Research is also being conducted to establish the level of unadapted germplasm that can be used in crosses with adapted material to obtain useful commercial pinto and black lines. Numerous advanced breeding lines with commercially acceptable grain types are in final stages of evaluation and confirmation for yield and disease resistance, and will be released as germplasm sources and/or commercial cultivars in the near future.

A recombinant inbred (RI) population has been developed in the cross ICA-Pijao x G12864 (a wild *P. vulgaris* accession). This is the parental combination that gave the highest yield in early generation tests (Singh et al. 1995). Phenotypic evaluations of the domestication syndrome as well as yield of individual RI lines will be carried out in replicated field trials. Concurrently, a molecular linkage map based primarily on AFLP and ISSR markers will be developed, with addition of some RFLP or STS markers to provide correlations with existing bean linkage map (Freyre et al., 1998). A QTL analysis will then be conducted for the traits concerned. Of particular importance will be the linkage relationships between genes for yield potential and domestication syndrome as well as the magnitude of individual yield potential genes.

Two different introgression methods will be tested – inbred backcross and congruity

backcross - by developing the corresponding populations in the cross ICA-Pijao x G12864 (this is the same cross as for the recombinant inbred populations in 1). Low-density maps will be established in these two populations with AFLP and ISSR markers, as well as with a framework of previously mapped RFLP and STS markers. The yield performance and phenology of the progeny lines of the two populations will be evaluated in multi-location and multi-year field experiments. The combination of field data and mapping results will lead to a QTL analysis of yield and phenology (Johnson and Gepts, 1999). Concurrently, an analysis will be conducted on domestication syndrome traits to identify lines most closely resembling the cultivated bean phenotype. Stability of yield and yield-related traits over environments will be analyzed with various parameters. The relative merits of the two introgression methods will be evaluated according to the average length of the introgressed segment. Because break-up of undesirable linkages is of prime importance in this type of mating, we suggest that the mating system that leads to the smallest average introgressed segment is the most desirable. We expect this mating system to be the congruity backcross.

Crosses will be made between selected U.S. cultivars from different commercial classes and wild beans from the same corresponding gene pool. Crosses will be advanced according to the congruity backcross method. Progenies will be evaluated as described above. It is anticipated that this may not be fully accomplished by the end of the 5-year project period.

The objective of the cross-pollination study is to obtain a better understanding of the factors influencing levels of outcrossing in common bean. The following specific s will be pursued:

1) Inheritance of contrasting outcrossing levels within *P. vulgaris.* The inheritance of these differences will be investigated in the cross FM53 (high outcrossing) x Sal (low outcrossing). A recombinant inbred population will be established. Outcrossing in this population will then be evaluated in the field as described by Wells (1988). Concurrently, a molecular linkage map will be established in this population and the outcrossing levels will be subjected to a QTL analysis.

2) Inheritance of outcrossing traits from *P. coccineus,* a cross-pollinated species related to *P. vulgaris.* A recombinant inbred population between a *P. vulgaris* and a *P. coccineus* genotype will be established. Segregation of specific traits mentioned above will be evaluated and correlated with levels of outcrossing measured in the field.

3) Compare reproductive fitness (seed yield) of common beans in self pollinated and mixed mating populations where insect visits to bean flowers are encouraged by proximity to bee hives. Experiments that place honeybee hives in bean fields will determine the yield advantage of bee tripping over several seasons and locations.

4) Compare pollination biology of common and lima bean flowers. Lima bean is 60 to 80% outcrossed at Riverside and up to 100% in some southeastern States (Waines and Barnhart, 1997). We will determine the characteristics of Lima flowers that promote cross pollination relative to common bean flowers. Concurrent tests of the effects of bee visits to common and Lima flowers will be conducted in field and glasshouse conditions. It may be beneficial to compare

pollination biology in common, Lima and scarlet runner bean as way to improve seed yield in beans.

A diverse group of parental germplasm from U.S. and international programs, especially CIAT, will be used to broaden genetic base of cultivars and maximize selection gains. The value of broad based germplasm lines and cultivars of different market classes developed by private and public institutions will be assessed through yield evaluation in the CDBN, MRPN, and other regional and state nurseries. Also, genotype x environment analyses will be performed on the CDBN and other data to determine stability of new cultivars and physiological genetic changes realized**.**

SUBOBJECTIVE1B. INVESTIGATE THE PHYSIOLOGY AND GENETICS OF YIELD POTENTIAL AND ITS STABILITY (GENE INTERACTION) THROUGH THE COOPERATIVE DRY BEAN NURSERY, THE MIDWEST REGIONAL PERFORMANCE NURSERY, AND OTHER NURSERIES.

PROCEDURES:

National Cooperative Dry Bean Nursery

The NCDBN will compare approximately 30 cultivars in 20 locations in the U.S. and Canada on an annual basis. A major component of this nursery is to identify the highest yielding and best cultivars for a particular region. The nursery is open to both public and private breeders. Breeders are encouraged to place a line in the nursery for three years. Seed provided to the nursery must be western grown to ensure freedom from bacterial and fungal seedborne diseases. Trials are replicated with at least three reps, and cooperators are encouraged to record the following data: days to flower, days to maturity, seed weight, yield, and biomass. Cooperators may also take data on plant architecture or biotic and abiotic stresses that occur in the nursery at their location. As part of yield system analysis, four additional yield components are calculated. These are Yield per day, Yield per day of seed fill, Biomass accumulation per day, and Harvest Index. The data are displayed visually in graphs which allow patterns in "yield strategies" to be observed. These data and mutivariate techniques will be used to dissect the genotype x environment interaction. Yield system analysis compares rates and duration of vegetative and reproductive growth over environments. Analysis of GxE interaction will use AMMI analysis to partition the GxE into one or more principal component axes, which will be correlated to environmental factors that appear to exert a strong influence on the GxE interaction.

Midwest Regional Nursery

Locations for this nursery are Ft. Collins, CO; Scottsbluff, NE; Saginaw, MI; and Fargo, ND. Entries are composed of advanced pinto and great northern bean breeding lines, with commercial cultivars as checks. Collaborators have the flexibility to manage this nursery as their other yield tests, but RCBD's or lattices are recommended, with a minimum of three replicates. Each collaborator may enter up to five advanced lines for testing, with the understanding that these entries should be maintained for at least two years. North Dakota State University acts as the coordinator of this nursery and is responsible for receiving and distributing entries and preparing a summary of data collected. Data on flowering, maturity, architecture, yield, and seed weight are recorded. A summary of these data is provided to participants and the technical committee of the

W-150 regional project for further dissemination of trial results. Seed requirements of the MRPN are minimal. This is sufficient for each collaborator to plant a three replicate test using one-row plots. If additional seed is available, the entries may be tested in local disease evaluation nurseries. Entries should have minimal seedborne disease problems, although, since all collaborators are breeding in areas where some seedborne diseases exist, the requirements for this nursery are less stringent than those required by other regional or national trials.

Winter Nursery

Winter nurseries will be conducted in Puerto Rico to accelerate development of breeding lines and conversion of tropical bean germplasm. Cooperators who participate in the harvest of the winter nursery will also have the opportunity to evaluate tropically adapted bean germplasm in Bean/Cowpea CRSP, PROFRIJOL and CIAT nurseries planted in Puerto Rico. During the proposed extension period bean germplasm will be screened in Puerto Rico for resistance to common bacterial blight, bean rust and leafhoppers. Germplasm with useful levels of resistance will be included in the conversion program.

Modeling of Bean Growth, Development, and Yield as a Function of Environmental Conditions

The previous W-150 project has shown that models can be used to analyze the potential impact of various weather conditions on crop growth and yield. As the current project has a stronger integrative approach, a crop modeling and systems analysis approach can be used to integrate the research outcomes of various individual projects. This will result in a more realistic simulation that can be used to help explain some of the GxE interaction. The existing crop simulation CROPGRO-Dry Bean will be enhanced and additional processes will be added. Simulation studies will be conducted to help understand the GxE interaction for various locations. Optimum management strategies for farmers and crop consultants will be determined. The latter will provide alternate management options that allow farmers to cope with the variability of weather conditions and could lead to yield improvement and a reduction in use of natural resources. The final outcome should lead to an improvement of both the economic as well as the environmental sustainability of farmers in rural areas.

SUBOBJECTIVE 1C. MAXIMIZE YIELD POTENTIAL OF COMMON BEAN CULTIVARS OF MAJOR MARKET CLASSES USING ELITE X ELITE HYBRIDIZATIONS AMONG SELECTED HIGH YIELDING PARENTS OF DIVERSE ORIGIN.

PROCEDURES:

At the apex level of the breeding pyramid, one primary objective is to develop cultivars that maximize productivity, reduce production costs, and improve seed and culinary quality. This is achieved by hybridizing high yielding cultivars and elite lines of similar market classes. Development of superior cultivars for (a) small, (b) medium, and (c) large seeded market classes require different breeding and selection strategies.

(a) Small seeded genotypes - Market classes of small seeded beans represent a high level of yield potential, adaptation, and stability. Cultivar development and selection efforts on yield potential will remain for these important classes. Improvements in early maturity, plant

growth habit, and improved harvest index can be made, since cultivars with high biomass and seed yield exist, but these genotypes are generally late maturing.

(b) High yielding, medium seed-size genotypes - Market classes in this category exhibit strong GxE interaction effects for yield, adaptation, maturity, and architecture. Efforts will be focused on exploiting GxE responses to develop broadly adapted, high yielding cultivars with stable growth habit for U.S. production regions.

(c) Large seeded genotypes – Market classes of this category have historically exhibited the lowest levels of biomass and seed yield, and have strong GxE interactions. Breeding efforts to improve biomass, maturity, and harvest index while maintaining excellent seed and culinary quality will be enhanced.

OBJECTIVE 2: **TO IMPROVE ABIOTIC AND BIOTIC STRESS MANAGEMENT STRATEGIES THROUGH A COMBINATION OF CLASSICAL AND BIOTECHNOLOGICAL APPROACHES.**

SUBOBJECTIVE 2A. Identify new and novel sources of resistance, develop insight into the molecular basis of host-pathogen interaction, and develop a bean transformation system.

SUBOBJECTIVE 2B. Investigation of pathogen variability, development of efficient pathogen detection and disease screening techniques and characterize genetic resistance.

SUBOBJECTIVE 2C. Develop multiple disease resistance germplasm and complement resistance with disease management strategies.

Improving abiotic and biotic stress management in beans will be approached on an integrated three-tiered pyramid, similar to the concept being utilized for the goal of maximizing productivity and global competitiveness. Given the wide diversity among the pathogens and abiotic stresses, the approach will be structured to focus on basic issues common to the range of constraints. Issues common to the basic level will involve developing efficient transformation systems, cloning resistance genes, identifying and utilizing interspecific crosses to utilize resistance sources in secondary gene pool. Materials and technologies developed at the basic level would be utilized at the intermediate level, where research would focus on characterizing pathogenic variability, race identification, genetic inheritance studies in the host, and developing linked molecular markers. The genetic and pathogenic information generated at the intermediate level would be the basis of activities at the apex of the pyramid. Strategies would focus on pyramiding resistance genes for diverse pathogens, multiple disease resistant germplasm released to breeders, disease management strategies including cultural and chemical control methods would be developed to protect both resistance and contemporary cultivars in the immediate short term (Figure 2).

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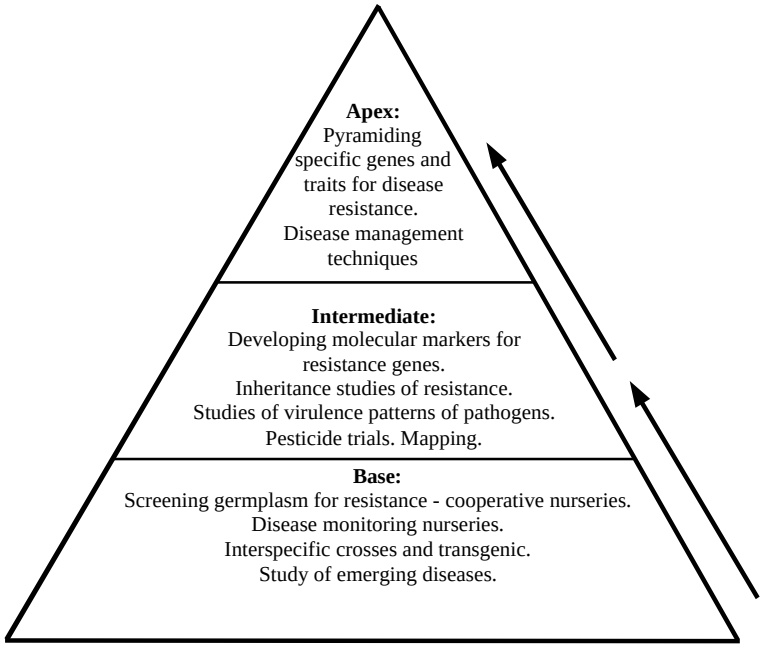

Figure 2. A three-tiered approach to improve abiotic and biotic stress management through a combination of classical and biotechnological approaches.

SUBOBJECTIVE 2A. Identify new and novel sources of resistance, develop insight into the molecular basis of host-pathogen interaction, and develop a bean transformation system.

PROCEDURES:

Identify new and unique sources of resistance to broaden and strengthen resistance to diseases caused by fungi (e.g., anthracnose, rust, root rots, and white mold), bacteria (e.g., common blight bacteria), viruses (bean common mosaic, bean golden mosaic and other bean-infecting geminiviruses) and abiotic stresses (e.g., heat stress). Approaches will include the use of core collections including wild and cultivated species for direct and indirect screening. Use would be made of gene conversion programs to identify and test for new sources of resistance in adapted genetic backgrounds. The USDA Plant Introduction collection currently includes more than 11,000 accessions, which makes screening this collection a difficult task. The development of

core collections has permitted the identification of disease resistance in a more limited, but representative, group of accessions without significant loss of diversity. The inability to test unadapted materials in the field necessitates the development of laboratory and greenhouse screening methods. Methods such as the straw test, detached leaf, oxalate test screening for white mold resistance and agroinoculation for bean golden mosaic virus have been developed. These methods need to be standardized to correlate better with field nurseries. These methods have the potential to facilitate identification of resistance in unadapted accessions from the plant introduction core collections. Upon identification of resistance genes, related germplasm from similar geographic regions will be tested for presence of the resistance.

Insight into the molecular basis of the host-pathogen interaction can provide new strategies for developing disease resistant plants. For the geminiviruses, one such strategy has been targeting the viral replication-associated protein. A novel approach to do this is to use combinatorial chemistry techniques to develop RNA and protein ligands that will interfere with the rep protein or the viral origin of replication. Another potential approach involves the characterization of the resistance of Mesoamerican beans to bean dwarf mosaic geminivirus. Identification of the gene(s) involved will involve identification of the viral avirulence determinant and using this factor to 'fish out' proteins encoded by resistance genes and/or use of degenerate primers to amplify resistance gene-like sequences and use these as molecular markers.

Research on plant transformation systems would be continued to develop techniques to introduce novel genes where resistance is lacking in current germplasm. For example, use of the oxalate oxidase gene to control *Sclerotinia sclerotiorum* as oxalic acid is the major determinant for pathogenicity of this fungus. For bean golden mosaic virus, strategies using antisense genes and trans-dominant lethal rep protein mutants will be explored. At least two methods of transformation will be investigated (i) DNA electroporation in which DNA is introduced into the cells of the meristem via an electric current and (ii) inocluation of sliced explants with *Agrobacterium tumefaciens*.

SUBOBJECTIVE 2B. Investigation of pathogen variability, development of efficient pathogen detection and disease screening techniques and characterize genetic resistance

PROCEDURES:

Characterization of pathogenic variability within the fungal pathogens such as those that cause rust, white mold, and root rots (particularly *Fusarium* spp.), bacterial pathogens such as common blight bacteria, and viral pathogens such as geminiviruses and potyviruses will continue to be done using traditional as well as molecular techniques. Standard inoculations of differential lines/cultivars will be used to identify race, strain and/or pathotype variability. Molecular techniques such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPDs), repetitive sequence PCR (repPCR), amplified fragment length polymorphism (AFLPs) and others will be used to identify variability, and the significance of this variability in terms of the biology of the pathogen will be determined for a number of these pathogens. Relevant strains/pathotypes will be identified for use in resistance screening. Efforts

will continue to develop improved methods for detecting bean-infecting geminiviruses through the development of virus-specific primers and nested PCR, and non-radioactive DNA probes. Bean-infecting potyviruses will continue to be detected using standard approaches such as enzyme linked immunosorbent assay (ELISA), although efforts will continue to develop nucleic acid-based detection methods.

Improved screening techniques will be developed to better identify genes conditioning resistance. Screening for white mold has been complicated by environmental factors and plant morphological traits. This has necessitated that lab and greenhouse tests be used to corroborate results from field nurseries. Collaborative field nurseries, planted at multiple sites are an integral part of the regional project and will be continued. To screen for heat and drought tolerance, specific sites have been developed in PR, ID, CO, and CA to facilitate selection for higher levels of stress tolerance. White mold nurseries are very important and regional nurseries will be conducted in NE, ND, OR, CO, MN and MI. The regional common blight nurseries will be coordinated in NE. Root rot nurseries will be developed in WA, CO, MI, MN, ND, and PR. Rust nurseries will also be continued in CO, MD, MI, NE, and ND.

Resistance genes will need to be characterized and identified using various methods, such as using molecular markers (e.g., chromosome walking) and/or degenerate primers designed for highly conserved motifs present in resistance-like genes. These approaches will have to be integrated with inheritance studies and development of genetic populations for mapping and linkage studies in order to utilize these genes in the development of multiple disease resistant germplasm. Recombinant inbred populations have been developed for numerous resistance sources for different pathogens and these will be field tested across bean production areas of the U.S. Use of the integrated bean linkage map to identify markers linked to resistance genes will be critical for marker assisted selection, to facilitate combining epistatic genes and to eliminate the traditional variability associated with field screening at different locations.

Marker-assisted selection in combination with traditional breeding (resistance gene recombination) will be used to pyramid resistance genes. This may be aimed at a single pathogen and/or as an approach to develop multiple disease resistance germplasm for a wide array of pathogens. In some cases, such as those involving a highly variable pathogen such as that causing rust or a highly pathogenic agent such as BGMV, specific resistance genes need to be pyramided to stabilize resistance across bean producing regions of the US, or in Florida/PR in the case of BGMV. Efforts, involving some or all of these approaches, will be focused on common bacterial blight, rust, white mold, anthracnose, root rots, bean golden mosaic, and heat tolerance. For example, introgression of root rot resistance from Mesoamerican black beans into highly susceptible Andean red kidney beans is a priority. Another priority is the pyramiding of common blight resistance genes; there are now a number of sources of resistance and robust markers are available or are being developed for QTLs associated with these resistances. Another important example is BGMV resistance. Markers linked to genes conferring BGMV resistance have been developed and this will facilitate introgression of this resistance into a number of classes, including snap beans. When transgenes are identified and cloned, they will be inserted into the bean genome via plant transformation, into elite multiple resistance germplasm.

SUBOBJECTIVE 2C: Develop multiple disease resistance germplasm and complement resistance with disease management strategies.

PROCEDURES:

Disease resistance will not remain durable unless integrated resistance management strategies that would include clean seed programs, crop rotation, irrigation management, and judicial use of appropriate chemical control. Such approaches would involve low toxicity, low volume pesticide applications combined with forecast systems that would minimize chemical use and environmental side effects. For example, many current bean cultivars are susceptible to local rust races; thus, judicious use of chemicals will be needed to reduce growers losses under disease pressure. Cultural practices are of limited value in reducing major disease epidemics. Ultimately, disease resistance will be expected to replace use of chemicals, but cultural practice management will be needed to extend the longevity of resistant varieties in the U.S.

The VegNet Technology program will be continued with support from Colorado State University and clientele in the Inter-Mountain region. Plans include the testing of a disease forecast model that is based upon pathogen biology, cropping systems, and environmental conditions that contribute to overwintering and infection of volunteer and new crop beans. Additional research will be conducted on evaluation of new fungicide chemistry, especially products that pose less risk to the environment and humans.

OBJECTIVE 3: Elucidate Genetic Controls for Food Quality and Value Added Components.

SUBOBJECTIVE 3A. Identify cell structural and chemical factors causing (a) bean seed indigestibility, suboptimum nutrient bioavailability, and flatulence; (b) elucidate through genetic engineering, the role of the raffinose-family oligosaccharides (RFO) as components of flatulence-causing factors; (c) alleviate the hard-to-cook and hard seed phenomena that occurs in dry bean during storage and; (d) develop preventative measures to reduce the incidence of hard-to-cook beans.

SUBOBJECTIVE 3B. Screen germplasm to (a) improve dry bean digestibility and release new and valuable germplasm with favorable consumer acceptance and; (b) determine the inheritance of traits influencing food quality.

SUBOBJECTIVE 3C. Develop value added bean products/compounds.

Increased antioxidant potential of bean flavonoids and constraints to bioavailability of nutrients and consumer acceptance of dry bean are amenable to genetic and technological solutions. The use of processing technology will be helpful in the short term; however, long term and permanent correction of defects limiting nutrient bioavailability and quality constraints in bean will be best accomplished through genetic change within the crop. The challenges to be confronted in improving dry bean as a food source during the next five years are illustrated in

Figure 3.

COOPERATORS: B. DE LUMEN (UC-B, **CA**), M. BRICK, H. SCHWARTZ (CSU, **CO**), C. VALLEJOS, R. MCMILLAN (UF, **FL**), J. KELLY, M. UEBERSAX (MSU, **MI**), P. GRIFFITHS (CU, **NY**), K. GRAFTON (NDSU, **ND**), D. MOK, J. MYERS (OSU, **OR**), B. SWANSON (WSU, **WA**)

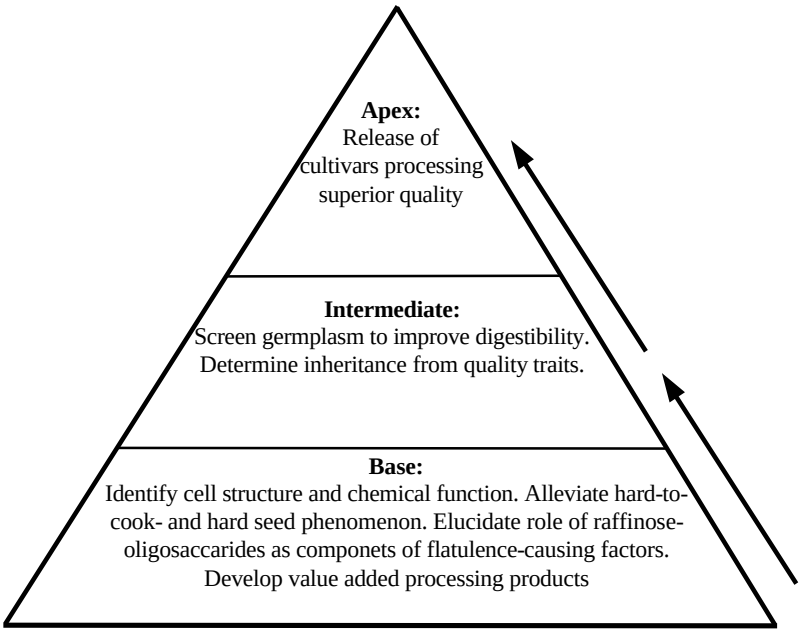

Figure 3. A three-tiered approach to elucidate genetic controls for food quality and value added components through a combination of classical and biotechnological approaches.

SUBJECTIVE 3A: Identify cell structural and chemical factors (a) causing bean seed indigestibility, suboptimum nutrient bioavailability, and flatulence; (b) elucidate through genetic engineering, the role of the raffinose-family oligosaccharides (RFO) as components of flatulence-causing factors; (c) alleviate the hard-to-cook and hard seed phenomena that occurs in dry bean during storage and; (d) develop preventative measures to reduce the incidence of hard-to-cook beans.

PROCEDURES:

Any material that is not digested and absorbed in the small intestine of humans is available for microbial digestion in the colon. Large quantities of undigested food can cause cramps, diarrhea, and flatulence. Undigested starch may be one of the contributors to gastrointestinal discomfort from eating cooked dry beans. Cooking of beans induces cell wall crystallization and decreases starch bioavailability. An enzymatic procedure using β-amylase and pullulanase will be used to selectively digest gelatinized starch to estimate starch bioavailability of different bean

lines.

Variability exists between bean genotypes in the amount and percent of indigestible starch (PTIS) and indigestible protein seems to affect the amount of total dietary fiber. Higher IS, PTIS, and IP values correspond to higher TDF values. The variability among bean genotypes for total dietary fiber, indigestible starch, and indigestible protein should be of interest to breeders. Further research is necessary to ascertain whether the genotypes used in our experiment are representative of their respective market classes. Thermal processing in tin cans provides the best consistency between samples, the lowest TDF, IS, and PTIS values, and the best reflection of how beans are processed in industry.

Elucidate, through genetic engineering, the role of the raffinose-family oligosaccharides (RFO) as components of flatulence-causing factors

The ultimate objective of this project is to reduce flatulence in beans by inhibiting the biosynthesis of flatulence-causing raffinose family oligosaccharides (RFO) in kidney bean seed. The strategy consists of blocking the expression of the gene encoding galactinol synthase (GS), the key enzyme in RFO biosynthesis. To reduce the level of RFO in the seed without adversely affecting seed viability, the biological role of RFO in plants needs to be understood. Galactinol synthase (GS) catalyzes the first committed step in RFO biosynthesis and is a major metabolic control point to manipulate in planta the levels of RFO in the seed and other tissues. Our basic strategy is to make gene constructs (sense and antisense) that would drive cotyledon-specific, and constitutive overexpression and repression of the GS gene in kidney bean and in tobacco. The cotyledon-specific expression experiments in kidney bean are designed to test the hypothesis that RFO play the crucial role of osmoprotectant in the axis to provide desiccation tolerance while serving the less crucial role of reserve carbohydrates in the cotyledon and could be replaced by sucrose and other carbohydrates. The constitutive expression experiments in the whole tobacco plant are designed to test the second hypothesis that RFO protect against cold and salinity.

The full GS cDNA from an *Arabidopsis* silique library has been obtained. The GS cDNA will be driven by the 5'untranslated region of the genomic clone for a developmentally regulated, cotyledon specific cDNA (Gm2S-1) we isolated in our lab. The 35S promoter will be used to drive the constitutive expression of *Arabidopsis* GS cDNA in tobacco. The s are to (1) Test whether the full *Arabidopsis* cDNA codes for a functional GS by expression in bacteria, (2) Make 35S:GS cDNA constructs for constitutive expression in tobacco. Test transgenic plants for chill and salt tolerance, (3) Isolate the genomic clone for Gm2S-1 and obtain its 5'untranslated region, (4) Make Gm2S-1:GSc DNA constructs for cotyledon-specific expression and transform into kidney bean. (This will be done in collaboration with people working on bean transformation). Test transgenic seeds for gene expression levels and viability.

Alleviate the hard-to-cook and develop preventative measures for the hard seed phenomena that occurs in dry bean during storage

Black Turtle Soup (BTS) beans stored for two years under ambient conditions (AC) of

23-25°C and 30-50% relative humidity demonstrated a significant increase in cooking time, solids loss, electrolytes leached, percentage of hardshell, and fat acidity value (FAV) compared to BTS beans stored under refrigerated hypobaric conditions (RHC) of 4.5°C, 50-60% relative humidity and atmospheric pressure of 125 mm Hg. Scanning electron microscopy demonstrated only internal structural characteristic differences between beans stored under AC and RHC, while cotyledon cells of BTS beans stored under RHC exhibited many large intercellular spaces characteristic of freshly harvested beans. The effect of high hydrostatic pressure (HHP) on water imbibition , cooking times, in vitro protein digestibility, texture, and microstructure of black beans increased the rate of water imbibition of untreated black beans by 50%, and increased in vitro protein digestibility. The study will be repeated with different bean genotypes to help alleviate the hard to cook phenomenon.

SUBOBJECTIVE 3B. Screen germplasm to (a) improve dry bean digestibility and release new and valuable germplasm with favorable consumer acceptance and; (b) determine the inheritance of traits influencing food quality.

PROCEDURES:

A genetic stock nursery for food quality research has been in existence for 20 years. The lines represent an extensive collection of diverse genotypes of the Middle American gene pool. The genetic stocks are adapted in both tropical and North temperate environments. Over the years, data have been accumulated on 25 of the 42 genotypes that make up the nursery. The nursery is useful to establish the range of variability for particular food quality traits and provide plant breeders and other researchers with information on screening methods and appropriate germplasm to improve particular traits through genetic intervention. The distribution of seed from the genetic stock nursery to project collaborators ensures that all investigators use the same genetic materials from the same production systems in their research. This procedure aids laboratory-to-laboratory concordance of research results. A determination of indigestible starch showed that cell walls of beans crystallize when bean seeds are cooked, preventing enzyme digestion of starch. All new high yielding, disease-resistant genotypes will be processed to ensure that they are acceptable by the processing industry and presumably by consumers.

Determine the inheritance of traits influencing food quality

Knowledge of the relative proportion of additive and nonadditive genetic variances for complex quality traits in a population forms a basis for studying trait inheritance and can be used as tool in plant breeding. Heritability estimates for three quality traits including visual appeal, texture, and washed drained mass will be determined. Appearance and degree of splitting of each sample and the check varieties will be scored subjectively on a 1-7 scale to represent the minimum and maximum acceptability levels of the traits, respectively. DNA bulks will be used for bulked segregant analysis in order to screen for molecular markers associated with QTLs controlling canning quality. Markers aligned in the integrated linkage map of beans will be given priority to find marker-QTL associations. Marker assisted selection will be for the improvement of quality associated traits in beans.

Reduction of bean cooking time may save considerable energy. Use of fast cooking bean cultivars with fuel efficient cooking methods is a good strategy to reduce energy consumption and conserve valuable natural resources when cooking. Large differences in the ability of bean plants to accumulate elements in the seed, including zinc, phosphorus, iron, and calcium. Segregating populations derived from crosses between low and high nutrient accumulators are being grown to elucidate the genetic control of nutrient accumulation. Other studies are planned to identify the relationship between elemental concentration and levels of phytate, zinc, and folate in the seed. Molecular markers will be sought that are associated with the seed nutrient accumulation trait.

SUBOBJECTIVE 3C. Develop value added bean products/compounds.

PROCEDURES:

Value added processing

A broad spectrum of value-added processing strategies have been undertaken to provide enhanced marketing opportunities for dry edible beans. These techniques have been directed to whole bean and fractionated ingredients suitable for nutritious and convenience based foods. Extraction and fractionation of dry beans resulted in specialty ingredient of improved nutritive value. Ultra filtration technology has been applied to milled protein concentrates suitable for aseptically processed beverages. High Temperature Start Time processing procedures suitable for whole beans has been applied to accelerate the hydration and tissue softening of diverse classes of dry beans. Process procedures have enabled rapid cooking of beans that are subsequently frozen as a food service recipe ingredient. These processes enable a fully cooked bean product similar in quality to canned beans in a pre-cooked frozen format.

The composition of drum-dried bean meals varied with hot water and enzymatic pretreatments (Occena et al., 1996). Bean meals obtained using drum-drying technology are acceptable as food ingredients that may be used directly (weaning food for infants in developing countries) as a component of formulated foods (cookies, spaghetti, etc.). Legume residues can be recommended as a food ingredient if supplemented with wheat flour. Further, studies are needed to demonstrate the potential for producing rapidly hydrated pre-cooked beans. These produces possessed highly palatable beans suitable for ingredients and food formulation in value-added products. Beans were described as being of "canned bean consistency without canning". Additional time and temperature studies are needed to demonstrate potential for process control optimization variation to yield beans of defined quality specification. These examples of value added processing improve market potential for beans grown in multiple regions within the scope of the project.

Develop near-white seeded snap beans for processing with low levels of flavonol glycosides

Nearly all snap beans in commercial production in the U.S. are white seeded. White seed, is conditioned by the recessive "ground gene," p. Varieties with the recessive p, "ground gene," are required by processors because these beans produce a clear product not contaminated by water-soluble pigments. However, white seeded beans are more susceptible to imbibitional and stand loss during germination and emergence. The development of near-white beans could possibly mitigate the emergence problems, while allowing for the production of a product that is acceptable to the processor. Green bean isolines in a 91G background will be quantified for flavonol glycosides (tannins, anthocyanins, lignin). The genotype for 91G is pVCDJ. Three

isolines are being developed: p^{gri}VCDJ, Pvc^{u}DJ, and PVcDj. These combinations of genes give low levels of pigment production. The isolines and 91G will be compared in the field for emergence and for canning quality. Data from these tests will be compared to flavonol-glucoside profiles.

High value phytochemicals derived from dry bean provide specialty market chemicals

Bean seed coats contain chemicals called flavonoids, which have antioxidant potential, and these may be useful in preventing some types of cancer in humans. Five genotypes of dry bean corresponding to "white," "yellow," "brown," "red," and "black" seeded market classes were previously examined for antioxidant potential. All of the methanolic extracts from the "white," "brown," and "black" seeded genotypes had very good antioxidant activity in the liposome assay. Knowledge of the type of flavonoid compounds present in beans is essential to providing consumers with information on possible health benefits that can be derived from including beans regularly in the diet. Work will be conducted to determine the antioxidant levels of different commercial bean types differing in seed coat color. The data from this research should provide plant breeders with a genetic basis on which to enhance the antioxidant activity of beans and, at the same time, improve digestibility through plant breeding.

V. INTERDEPENDENCY:

The W-150 regional project combines research activities, directed toward bean improvement, of state scientists in 15 cooperating states and USDA-ARS scientists at five locations. The project offers a framework for the genetic improvement of beans through basis research on the evaluation of wild germplasm and the optimization of its use through research on pollination mechanisms, conversion and testing programs, located in temperate and tropical locations. This basic science component is integrated through four adaptation nurseries that are the backbone of the W-150 project. The National Cooperative Dry Bean Nursery has eight collaborating states and four states collaborate in the Midwest Regional Performance Nursery. The functional structure of the regional project is that unadapted wild materials enter at the base of the pyramid (Figure 1) and are converted to germplasm for evaluation in temperate zones in the intermediate level followed by widespread regional testing of elite lines, conducted at the apex of the pyramid. Given the strong G x E interaction for yield and adaptation, the collaboration within the W-150 provides the necessary structure to determine these critical interactions and identify elite germplasm for release. The interdependence between the 12 states and five USDA- ARS programs is essential to the success of the improvement efforts in beans as each scientist brings different local expertise to the overall effort.

Under Objective 2, where the focus is on biotic and abiotic stresses, the integration between state programs is critical as unique and variable pathogens and stresses that affect bean production, occur in different regions of the U.S. Due to contrasting disease problems, and pathogenic variability present in different regions of the country, work on resistance must be integrated as the research can only be effectively conducted at specific locations. The W-150 project affords the opportunity to test for broad based resistance and stability across environments to a wide range of virulent races of specific pathogens affecting bean production. In contrast to the research on yield-based traits in dry edible seed types, diseases attack both the green bean pod

types and the dry edible beans. Work on resistance breeding is vital to both market types and is quite complementary. The development of rust resistance is the best example of collaborative research over a number of states where breeders work with different combinations of rust races in different market types each with its own unique local adaptation. Pyramiding resistance genes through the use of molecular markers linked to new and unique resistance sources requires integrated regional testing to determine its effectiveness. The interdependency afforded by the W-150 project provides the mechanism for such testing. A similar structure for the integration of basis and applied research is proposed and encouraged between programs, as efforts toward plant transformation are underway and, if successful, the protocol can be integrated into a number of different programs interested in developing novel disease resistance.

The quality aspects proposed under objective 3 are vital to the overall bean improvement effort as changes in agronomic traits need to be integrated with corresponding positive changes in quality. Quality and value added traits are a critical component of a food product such as beans where both pods and seeds are consumed directly. Through the W-150, there is an integrated team effort to ensure that research is conducted on these vital quality traits across a number of states where the expertise and interest resides. Characteristics such as indigestibility and flatulence reduce the value of beans as a food, and through the W-150 project these characteristics are being addressed as a national need in bean improvement. The health value of beans, whether available in seed or pods traits, likewise, gets national attention through the W-150. Research findings can be incorporated directly into many state improvement programs as a result of the interdependency outlined in the W-150 project.

VI. EXPECTED OUTCOMES:

OBJECTIVE 1: Maximize Productivity and Global Competitiveness.

Development of an efficient germplasm conversion program in *Phaseolus* to exploit the unique variability present in the cultivated tropical germplasm and related wild species.

Potential to increase cross pollination as the first step in the development of hybrid beans.

The four nurseries, National Cooperative, Midwest Performance, Modeling and Winter Nurseries form the basis for the strong collaborative effort within the W-150. These nurseries will continue to contribute valuable information and germplasm vital to the future improvement of beans in the U.S.

OBJECTIVE 2: Improve Abiotic and Biotic Stress Management Strategies through a Combination of Classical and Biotechnological Approaches.

Identify wild gerrnplasm with increased levels of resistance to white mold, common blight, Fusarium root rot, and bean golden mosaic virus.

Develop further insight into the pathogen and host genes involved in the host pathogen interaction as an aid to improving levels of disease resistance.

Improved technologies for the efficient transformation of beans.

Understanding the variation in the pathogens such as rust, white mold, Fusarium root rot, common blight, bean golden mosaic, and bean common mosaic virus.

Identify resistant germplasm and genes for fungal and bacterial resistance effective at multiple sites in bean production areas of the U.S.

Have available for public use, additional molecular markers linked to major resistance genes and QTLs controlling abiotic and biotic stresses in common bean.

Release of multiple disease resistant germplasm and/or cultivars in a range of commercial classes adapted to major bean production areas in the U.S. Disease management strategies to stabilize resistance longevity will accompany these releases.

OBJECTIVE 3. Elucidate Genetic Controls for Food Quality and Value Added Components

New and more cost effective methodologies including the use of DNA markers will be employed for screening bean germplasm for improved quality.

Bean germplasm with improved digestibility and concomitant nutritional benefits will be identified.

Other quality characteristics, that influence cookability and ease of preparation, will be combined with the traditional seed characters preferred by consumers. The improved germplasm will be released for use by SAES and federal breeding programs in the U.S.

Alternate processing procedures that are energy-efficient, environmentally sound and convenient to use, will be developed to promote new bean-based products.

VII. ORGANIZATION:

Present officers of the W-150 Regional Project are:
Chair, Kenneth F. Grafton, North Dakota State University, Fargo, ND
Vice-Chair, Robert Gilbertson, University of California, Davis, CA
Secretary, Rusty Smith, USDA-ARS, Tropical Agriculture Research Service, Mayaguez, PR

Members of the Technical Committee are designated by the directors of the various participating states and agencies. The project is considered a Western Regional Research Project, but has always had substantial participation by states in other regions of the U.S. and from abroad.

The Technical Committee officers are a Chairperson, Vice-Chairperson, and Secretary. Unless he/she declines to serve, the Vice-Chairperson will succeed the Chairperson. The Secretary is elected annually and the previous Secretary will succeed the Vice-Chairperson, unless he/she declines to serve. An election will be held if any officer declines to serve in his/her office. The officers will be elected from the officially designated representatives. The Administrative Advisor will be selected by the Western Association of Agricultural Experiment Station Directors. The Administrative Advisor will serve without a vote.

The Technical Committee will meet annually, unless otherwise planned, at a place and on a date designated by a majority vote of the committee. Minutes will be recorded and an annual progress report will be prepared by the Technical Committee and submitted through proper channels.

VIII. SIGNATURES:

PROJECT NUMBER: W-150

TITLE: GENETIC IMPROVEMENT OF BEANS (*PHASEOLUS VULGARIS* L.) FOR YIELD, PEST RESISTANCE, AND FOOD VALUE

	8-15-00
ADMINISTRATIVE ADVISOR	DATE
	8-15-00
CHAIR, REGIONAL ASSOCIATION OF DIRECTORS	DATE
	9-18-00
ADMINISTRATOR, COOPERATIVE STATE RESEARCH, EDUCATION AND EXTENSION SERVICE	DATE

Appendix:

Plant Variety Protection - PVP certificates issued.

9300261, Aztec pinto bean	2/28/97
9300258, Alpine great northern bean	5/30/97
9300262, Chinook light red kidney bean	8/29/97
9500062, Isles dark red kidney bean	12/31/97
9500064, Raven, black bean	2/27/98
9500063, Huron navy bean	9/30/99
9600288, Newport navy bean	7/13/99

REGIONAL PROJECT: W-150: GENETIC IMPROVEMENT OF BEANS (*PHASEOLUS VULGARIS* L.) FOR YIELD, PEST RESISTANCE, AND FOOD VALUE

REFERENCES – OBJECTIVE 1 (1995-2000) :

OBJECTIVE 1. Improve the efficiency of breeding through elucidation of biological and environmental controls regulating yield potential and adaptation, enhancement of breeding methodologies (including genome mapping and gene database development), and improved use of germplasm diversity.

Anonymous. 1998a. USDA Agricultural Statistics. Washington, D.C.

Anonymous. 1998b. USDA-ARS Nutrient Data Laboratory. http://www.nal.usda.gov/fnic/foodcomp/

Beaver, J.S., and J.D. Kelly. 1994. Comparison of selection methods for dry bean populations derived from crosses between gene pools. Crop Sci. 34:34-37.

Brunner, B.R., and J.S. Beaver. 1989. Estimation of out crossing of the common bean in Puerto Rico. HortScience 24:669-671.

Gepts, P., 1998. Origin and evolution of common bean: past events and recent trends. HortScience 33: 1124-1130.

Johnson, W., and P. Gepts, 1999. Segregation for performance in recombinant inbred populations resulting from inter-gene pool crosses of common bean (*Phaseolus vulgaris* L). Euphytica 106.

Ibarra-Perez, F.J., N.C. Ellstrand, and J.G. Waines. 1996. Multiple paternity in common bean (*Phaseolus vulgaris* L., Fabaceae). Amer J. Botany 83:749-758.

Ibarra-Perez, F.J., B. Ehdaie, and J.G. Waines. 1997. Estimation of outcrossing rate in common bean. Crop Sci. 37:60-65.

Kelly, J.D., and M.W. Adams. 1987. Phenotypic recurrent selection in ideotype breeding of pinto beans. Euphytica 36:69-90.

Kelly J.D., J. M. Kolkman, and K. Schneider. 1998. Breeding for yield in dry bean (*Phaseolus vulgaris* L.). Euphytica 102:343-356.

Kelly, J.D., K.A. Schneider, and J.M. Kolkman. 1999. Breeding to improve yield. In: Developments in Plant Breeding Vol. 7. p.185-222. *In* ed. S.P. Singh. Common bean improvement in the Twenty-First Century. Kluwer Acad. Pub. Dordrecht, The Netherlands.

Koinange, E.M.K., S.P. Singh, and P.Gepts.1996. Genetic control of domestication syndrome in common bean. Crop Sci. 36:1037-1045.

Kornegay, J., J.W. White, and O Ortiz de la Cruz. 1992.Growth habit and gene pool effects on inheritance of yield in common bean. Euphytica 62: 171-180.

Maynard, D.N. and G.J. Hochmuth. 1997. Knott's handbook for vegetable growers. John Wiley & Sons, Inc. New York, NY USA.

McClean, P.E., J.R. Myers, and J.J Hammond JJ. 1993. Coefficient of parentage and cluster analysis of North American dry bean cultivars. Crop Sci. 33:190-197.

Myers, J.R. 1992. Values and use of the National Dry Bean Nurseries. Ann. Rep. Bean Imp. Coop. 35:1-2.

Myers, J.R., and J.R. Baggett. 1999. Improvement of snap bean. Pages 289-329. In: Singh, S.P. (Editor), Common Bean Improvement in the Twenty-First Century. Kluwer, Dordrecht, Netherlands.

Nienhuis, J., and S.P. Singh. 1986. Combining ability analyses and relationships among yield, yield components, and architectural traits in dry bean. Crop Sci. 26:21-27.

Park, S.J., T.E. Michaels, J.R. Myers, D.W.A. Hunt, and K. Stewart-Williams. 1996. Outcrossing rates of common beans grown in Ontario and Idaho. Annu. Rept. Bean Improv. Coop. 39:90-91.

Pereira, P.A.A., J.E. de Souza Carneiro, H. Torres da Silva, M.J. Del Peloso, and P. Gepts, 1996. Introgressão de genes de feijões silvestres em feijão cultivado. In Anais V Reunião Nacional de Pesquisa de Feijão, 14-18 outubro de 1996, Goiânia, GO. EMBRAPA-CNPAF, Goiânia, GO, Brazil, pp 393-396.

Silbernagel, M.J., and R.M. Hannan. 1992. Use of plant introductions to develop U.S. bean cultivars. *In* Use of plant introductions in cultivar development, Part 2, CSSA Special Publication no. 20, Madison, WI.

Singh, S.P., C.A. Urrea, A. Molina, and J.A. Gutierrez. 1992. Performance of small-seeded common bean from the second selection cycle and multiple-cross intra- and interracial populations. Can. J. Plant Sci. 72:735-741.

Singh, S.P., A. Molina, and P. Gepts, 1995. Potential of wild common bean for seed yield improvement of cultivars in the tropics. Can. J. Plant Sci. 75: 807-813.

Sonnante, G., T. Stockton, R.O.Nodari, V.L. Becerra Velasquez, and P. Gepts. 1994. Evolution of genetic diversity during the domestication of common bean (*Phaseolus vulgaris* L.). Theor. Appl. Genet. 89:629-635.

Stewart-Williams K, J.R. Myers, and D. Wallace. 1993. 43rd Annual Report of the Cooperative Dry Bean Nurseries, (1992) IAES Misc. Series No. 162. 18pp.

Waines, J.G., and D.R. Barnhart, 1997. Outcrossing rates and multiple paternity of common and lima beans. Annu. Rept. Bean Improv. Coop. 40:44-45.

Wells, W.C., W.H. Isom, and J.G. Waines. 1988. Outcrossing rates of six common bean lines. Crop Sci. 28:177-178.

Zobel, R. W., M. J. Wright and H. Gauch. 1988. Statistical Analysis of a Yield Trial. Agron. J. 80:388-393.

REFERENCES – OBJECTIVE 2 (1995-2000):

OBJECTIVE 2. Identification of mechanisms of host-pathogen interactions leading to efficient, environmentally-safe, and economical disease control methods.

Brick, M. A., Wood, D. R., Schwartz, H. F., Pearson, C. H., Ogg, J. B., Ballarin, M., and Shanahan, J. F. 1995. Registration of 'Arapaho' pinto bean. Crop Science 35:1511-1512.

Coyne, D. P., D. S. Nuland, D. T. Lindgren and J. R. Steadman. 1994. 'Chase' Pinto dry bean. HortScience 29:44-45.

Deshpande, R.Y., K.G. Hubbard, D.P. Coyne, J.R. Steadman, and A.M. Parkhurst. 1995. Estimating leaf wetness in dry bean canopies as a prerequisite to evaluating white mold disease. Agron. J. 87: 613-619.

Fisher, A. G., Brick, M. A., Wood, D. R., Stack, M., Schwartz, H. F., Ogg, J. B., Pearson, C. D., Shanahan, J. F., and Ballarin, M. 1995. Registration of 'Fisher' pinto bean. Crop Science 35:1511.

Freyre, R., Skroch, P.W., Geffroy, V., Adam-Blonden, A.F., Shirmohamadali, A., Johnson, W.C., Llaca, V., Nodari, R.O., Pereira, P.A., Tsai, S.-M., Tohme, J., Dron, M., Nienhuis, J., Vallejos, C.E. and Gepts, P. 1998. Towards an integrated linkage map of common bean. 4. Development of a core linkage map and alignment of RFLP maps. Theor. Appl. Genet. 97:847-856.

Grafton, K. F., J. R. Venette and K. C. Chang. 1997a Registration of 'Hatton' pinto bean. Crop Sci. 37:288.

Grafton, K. F., J. R. Venette and K. C. Chang. 1997b. Registration of 'Maverick' pinto bean. Crop Sci. 37:1672.

Grafton, K. R., J. R. Venette and K. C. Chang. 1999. Registration of 'Frontier' pinto bean. Crop Sci. 39: 876-877.

Johnson, E., P.N. Miklas, J.R. Stavely and J.C. Martinez-Cruzado. 1995. Coupling- and repulsion-phase RAPDs for marker-assisted selection of PI 181996 rust resistance in common bean. Theor. Appl. Genet. 90:659-664.

Jung, G., P. W. Skroch, D. P. Coyne, J. Nienhuis, E. Arnaud-Santana, H. M. Ariyarathne, S. M. Kaeppler, and M. J. Bassett. 1997. Molecular marker-based genetic analysis of Tepary bean-derived common bacterial blight resistance in different developmental stages of common bean. J. Amer.Soc.Hort.Sci. 122:329-337.

Kelly, J.D., G.L. Hosfield, G.V. Varner, M.A. Uebersax, and J. Taylor. 1998a. Registration of 'Mackinac' navy bean. Crop Sci. 38:280.

Kelly, J.D., G.L. Hosfield, G.V. Varner, M.A. Uebersax, R.A. Long, and J. Taylor. 1998b. Registration of 'Red Hawk' dark red kidney bean. Crop Sci. 38:280-281.

Miklas, P.N., L. Afanador, and J. D. Kelly 1996. Recombination-facilitated RAPD marker-assisted selection for disease resistance in common bean. Crop Sci.36:86-90.

Steadman, J.R., H.F. Schwartz, E.D. Kerr, A.K. Vidaver and D.P. Coyne. 1996. Common bacterial blight and other bacterial diseases of bean on the central high plains of the USA. Proc. First International Workshop on Common Bacterial Blight of Bean. Univ. Puerto Rico, Feb. 19-21, 1996. PROFRIJOL Doc. 96/2. pp.163-168.

Singh, Shree P. and Carlos G. Munoz. 1999. Resistance to common bacterial blight among Phaseolus species and common bean improvement. Crop Sci. 39:80-89.

Wang, H. L., Sudarshana, M. R., Gilbertson, R. L., and Lucas, W. J. 1999. Analysis of cell-to-cell and long -distance movement of a bean dwarf mosaic geminivirus-green fluorescent protein reporter in host and non-host species: Identification of sites of resistance. Molecular Plant Microbe Interactions 12:345-355.

REFERENCES – OBJECTIVE 3 (1995-2000):

OBJECTIVE 3: Elucidate genetic controls for food quality and value added components.

Berrios, J de-J. 1999. Storage of black beans (*Phaseolus vulgaris* L.), Composition, structure, and bromelain hydroysis of globulin G1. Ph.D. Dissertation, WSU, 123p.

Bolles, A.D. 1997. Ultrafiltration processing of dry bean (*Phaseolus vulgaris* L.) protein fractions formulated into a beverage suitable for small children. Ph.D. Dissertation. Michigan State University, East Lansing, MI.

Chung, Y.S. 1996. Changes in Cell Wall Structure and Starch Digestibility During Cooking of Dry Bean (*Phaseolus vulgaris* L.) Ph.D. Dissertation, Department of Food Science and Human Nutrition, Michigan State University.

Chung, Y.S., Uebersax, M.A., Bennink, M.R. and Hosfield, G.L. 1997. Abstracts, 1997 Meeting of the Institute of Food Technologists, Abstr. #13A-19, 1997.

de Lumen, B.O. 1996. Future developments in improvement: Molecular approaches to improving the nutritional and functional properties of oilseeds, grains and legumes, In Food and Feed from Legumes and Oilseeds. Eds. Nwakolo E., and Smartt J. Chapman and Hall, New York, NY.

de Lumen, B.O. and Uchimiya, F. 1997. Molecular strategies to enhance the nutritional quality of legume protein: An update. AgBiotech News and Information 9:353N-358N.

de Lumen, B.O., Krenz, D.C and Revilleza. M.J. 1997. Molecular strategies to improve the protein quality of legumes. Food Tech. 51:67-70.

de Lumen, B.O., Liu, J.J., Galvez, A.F. and Krenz, D. 1998. Galactinol synthase (GS): Increased enzyme activity and levels of mRNA due to cold and desiccation. Plant Science 134:11-20.

de Lumen, B.O., Galvez, A.F., Revilleza, M.J. and Krenz, D.C. 1999. Molecular strategies to improve the nutritional quality of legume proteins. In Chemicals via Higher Plant Bioengineering. Shahidi, F., Kolodziejczyk, P., Whitaker, J,. Lopez Munguia A., and Fuller G. (Editors). American Chemical Society. 5th Chemical Congress of North America. Cancun, Mexico, pp 117-126.

Elia, F.M. and Hosfield, G.L. 1996. Inheritance of cooking time, water absorption, protein, and tannin content in dry beans and their expected gain from selection. Annu. Rept. Bean Improv. Coop. 39:266-267.

Elia, F.M., Hosfield, G.L., Kelly, J.D. and Uebersax, M.A. 1997. Genetic analysis and interrelationships between traits for cooking time, water absorption, protein, and tannin content of Andean dry beans. J. Amer. Soc. Hort. Sci. 122:512-518.

Engleright, R.M., Bennink, M.R. and Hosfield, G.L. 1999. Determination of total dietary fiber and indigestible protein in dry bean (*Phaseolus vulgaris* L.). Annu. Rep. Bean Improv. Coop. 42:123-124.

Freyre, R., Skroch, P.W., Geffroy, V., Adam-Blonden, A.F., Shirmohamadali, A., Johnson, W.C., Llaca, V., Nodari, R.O., Pereira, P.A., Tsai, S.-M., Tohme, J., Dron, M., Nienhuis, J., Vallejos, C.E. and Gepts, P. 1998. Towards an integrated linkage map of common bean. 4. Development of a core linkage map and alignment of RFLP maps. Theor. Appl. Genet. 97:847-856.

Hertog, M.G.L., Feskens, E.J. M, Hollman, P.C.H., Katan, M.B., Kromhout, D. 1993. Dietary antioxidant flavonoids and risk of coronary heart disease: a Zutphen Elderly Study. Lancet 342:10007-10011.

Hosfield, G.L., Bennink, M.R., Beninger, C.W., Engleright, R.M. and Ospina, M.T. 1998. Variability for starch digestibility in dry bean (*Phaseolus vulgaris* L.). HortScience 33(3):471.

Jackson, J.C. 1999. Compositional, Functional, and Nutritional Characterization of Ultrafiltration Processed Cowpea (*Vigna unquiculata*) and Navy Bean (*Phaseolus vulgaris*) Protein Fractions. Ph.D. Dissertation. Michigan State University, East Lansing, MI.

Kelly, J.D., Hosfield, G.L., Varner, G.V., Uebersax, M.A., Taylor, J. 1999a. Registration of 'Chinook 2000' Light Red Kidney Bean. Crop Sci. 39:293.

Kelly, J.D., Hosfield, G.L., Varner, G.V., Uebersax, M.A., Taylor, J. 1999b. Registration of 'Kodiak' Pinto Bean. Crop Sci. 39: 292-293.

Kelly, J.D., Hosfield, G.L., Varner, G.V., Uebersax, M.A., Taylor, J. 1999c. Registration of 'Matterhorn' Great Northern Bean. Crop Sci. 39:589-590.

Kelly, J.D., Hosfield, G.L., Varner, G.V., Uebersax, M.A., Taylor, J. 1999d. Registration of 'Beluga' Alubia Bean. Crop Sci. 39: 294.

Lee, S.C, Prosky, L. and DeVries, J.W. 1992. Determination of Total, Soluble, and Insoluble Dietary Fiber in Foods-Enzymatic-Gravimetric Method, MES-TRIS Buffer: Collaborative Study. Journal of AOAC International 75 (No.3):395-416.

Liu, J,.J, Odegard, W. and de Lumen, B.O. 1995. Galactinol synthase from kidney bean and zucchini leaf: Purification and N-terminal sequences. Plant Physiol. 109:505-511.

Moraghan, J.T. and Grafton, K.F. 1997. Accumulation of calcium in bean cultivars differing in seed size. J. Sci. Food Agric. 74:251-256.

Moraghan, J.T. and Grafton, K.F. 1999. Seed zinc concentration and the zinc-efficiency trait in navy bean. Soil Sci. Soc. Amer. J. 63:918-922.

Occena, L.G., Uebersax, M.A. and Hosfield, G.L. 1996. Steam and hot water extractive pretreatments of whole beans (*Phaseolus vulgaris* L.) drum-dried meals. Mich. Dry Bean Dig. 20:9-13.

Ospina, M.T., Hosfield, G.L. and Bennink, M.R. 1997. Indigestible starch in a select sample of navy beans. Annu. Rep. Bean Improv. Coop. 40:19-20.

Ospina, M.T., Hosfield, G.L. and Bennink, M.R. 1998. Methodology to determine indigestible starch in dry bean (Phaseolus vulgaris L.). Annu. Rep. Bean Improv. Coop. 41:86-87.

Posa, M.C., Hosfield, G.L., Kelly, J.D. and Grafton, K.F. 1999. Variability for processing quality traits in two recombinant inbred populations of kidney bean. HortScience 34(3):447.

Sangronis, E., Ibarz, A., Swanson, B.G. and Barbosa-Canovas, G.V. 1998. Cooking time and water absorption of black beans treated with high pressure. Abstract 20A-25, Institute of Food Technologists, Atlanta, GA.

Sangronis, E. 1999. High hydrostatic pressure treatment of black beans (Phaseolus vulgaris L.), Ph.D. Dissertation, Washington State University, p.132.

Sangronis, E., Barbosa-Canovas, G.V. and Swanson, B.G. 1999. Microstructure of black bean protein bodies treated with high hydrostatic pressure. Abstract 22D-61, Institute of Food Technologists, Chicago, IL.

Shellie-Dessert, K.C. and F.A. Bliss, 1991. Genetic improvement of food quality factors. p. 649-677. *In* van Schoonhoven, A. and O. Voysest (eds.), Common Beans: Research for Crop Improvement. CAB, Wallingford, UK and CIAT, Cali, Colombia.

Shellie-Dessert, K.C. and Hosfield, G.L. 1990. Implications of genetic variability for dry bean cooking time and novel cooking methods for fuelwood conservation in Rwanda. Ecol. Food Nutr. 24:195-211.

Shellie, K.C. and Hosfield, G.L. 1991. Genotype x environmental effects on food quality of common bean: resource-efficient testing procedures. J. Amer. Soc. Hort. Sci. 116:732-736.

Walters, K.J., Hosfield, G.L., Kelly, J.D. and Uebersax, M.A. 1995. Genetics of canning quality in navy beans. Mich. Dry Bean Dig. 19:8-9.

Walters, K.J., Hosfield, G.L., Uebersax, M.A. and Kelly, J.D. 1997. Navy bean canning quality: correlations, heritability estimates, and randomly amplifield polymorphic DNA markers associated with component traits. J. Amer. Soc. Hort. Sci. 122:338-343.

IX. ATTACHMENTS

A. PROJECT LEADERS

B.

W-150, GENETIC IMPROVEMENT OF BEANS (*PHASEOLUS VULGARIS* L.) FOR YIELD, PEST RESISTANCE AND FOOD VALUE

LOCATION	PRINCIPAL OR CO-INVESTIGATORS	COOPERATORS	AREA OF SPECIALIZATION
California, Berkeley	de Lumen, B.		biochemistry
California, Davis	Gepts, P.		geneticist
	Gilbertson, R.		plant pathology
California, Riverside	Waines, J.		genetics
Colorado	Brick, M.		breeding
	Schwartz, H.		pathology
Florida	Vallejos, C.		molecular genetics
	McMillan, R.		pathology
Georgia	Hoogenboom, G.		Agrometeorology
Idaho	Singh, S.		plant breeding
Michigan	Kelly, J.D.		plant breeding
	Uebersax, M.A.		food technology
Nebraska	Coyne, D.P.		plant breeding
	Steadman, J.		plant pathology
New York	Griffiths, P.		plant breeding
	Halseth, D.E.		plant pathology
	Wallace, D.H.		plant breeding, genetics
North Dakota	Grafton, K.		plant breeding
	McClean, P.		biotechnology
Oregon	Mok, D.		genetics
	Myers, J.		plant breeding, genetics
Puerto Rico	Beaver, J.		plant breeding
	Zapata, M.		plant pathology
	Echavez-Badel, R.		phytopathology
Washington	Swanson, B.		food quality
Wisconsin	Maxwell, D.		molecular virology
LOCATION	**PRINCIPAL OR CO-INVESTIGATORS**	**COOPERATORS**	**AREA OF SPECIALIZATION**
B. **USDA**			
ARS-East Lansing, MI	Hosfield, G.		plant genetics, nutrition
ARS - Prosser, WA	Miklas, P.		plant breeding, genetics
ARS- Mayaguez, PR	Smith, J.		germplasm conversion
ARS-Pullman, WA	Welsh, M.		germplasm

B. RESOURCE PAGE

PARTICIPANT	OBJECTIVES			RESOURCES				
	1	2	3	SY	%Research	%Extension	%Teaching	PY	TY
California SAES									
Berkley									
De Lumen, B.			X	0.15	100%			0.20	0.20
Davis									
Gepts, P.	X			0.10	100%			0.60	
Gilbertson, R.		X		1.00	80%	20%			
Riverside									
Waines, J.	X			0.10	100%			0.10	0.10
Colorado SAES									
Brick, M.	X	X	X	0.20	60%	10%	30%	0.15	0.15
Schwartz, H.	X	X	X	0.20	50%	50%			
Florida SAES									
Vallejos, C.	X	X	X	1.00	90%	10%		1.00	1.00
McMillan, R.	X	X	X	1.00	30%	10%	10%		
Georgia SAES									
Hoogenboom, G.	X			0.10	75%	15%	10%	0.10	0.10
Idaho SAES									
Singh, S.	X	X		0.15	100%			0.15	0.15
Michigan SAES									
Kelly, J.	X	X	X	0.10	75%	00%	25%		
Uebersax, M.			X	0.25	80%	20%	00%	0.50	0.00
Nebraska SAES									
Coyne, D.	X	X		0.20	100%				0.10
Steadman, J.		X		0.20	100%				0.20

B. RESOURCE PAGE

PARTICIPANT	OBJECTIVES			RESOURCES				
	1	2	3	SY			PY	TY
				%Research	%Extension	$Teaching		
New York SAES								
Griffiths, P.	X	X	X	100%	0.10		0.25	
Halseth, D.	X			3%	0.03			
Wallace, D.	X			100%	0.15			
North Dakota SAES								
Grafton, K.	X	X	X	95%	0.15	5%		0.15
McClean, P.		X		100%	0.05			
Oregon SAES								
Mok, D.		X	X	100%	0.05			
Myers, J.		X	X	100%	0.10			0.10
Puerto Rico								
Beaver, J.	X	X		100%	0.25			
Zapata, M.	X	X		100%	0.20			
Echavez-Badel, R.	X	X		100%	0.20			
Washington SAES								
Swanson, B.			X	50%	0.10	25%		
Wisconsin SAES								
Maxwell, D.		X		100%	0.25		0.50	
USDA								
Hosfield, G.L. (MI)	X	X		100%	0.10			
Miklas, P. (WA)	X	X		100%	0.30			
Smith, J.R. (PR)	X	X		100%	0.10			
Welsh, M. (WA)	X			100%	0.50			0.50