



# Dry pea production and breeding – A mini-review

Kevin McPhee

USDA-ARS and Washington State University, P.O. Box 646434, Pullman, WA 99164-6434, USA.

email: kmcphoe@mail.wsu.edu

Received 11 September 2002, accepted 4 January 2003.

## Abstract

Dry pea (*Pisum sativum* L.) was domesticated over 9000 years ago and has been produced in association with cereals since that time. Its seed is highly nutritious and approximately half the world production is fed to livestock while the remaining portion is used for human food, primarily in developing countries. Pea is a cool-season legume crop produced in cool temperate climates worldwide for its highly nutritious seed and many rotational benefits in cereal grain production. Major production constraints for pea include crop pests and adverse environmental conditions such as frost, drought and excessive heat. Viral and fungal pathogens economically impact seed production and quality; however, resistance to several of these pathogens is available and has been incorporated into many adapted cultivars. Genetic improvement of pea began with domestication and has been aided more recently by decades of research beginning with Gregor Mendel's initial discovery of inheritance. Since that time a myriad of geneticists have discovered novel traits and created detailed genetic maps of the *Pisum* genome. Population improvement has been achieved through introduction of novel traits from wild germplasm and landraces as well as pyramiding multiple positive alleles in adapted genetic backgrounds. Marker assisted selection is possible in pea due to the development of detailed genetic maps and DNA markers, however the expense and inconvenience associated with using a number of different protocols which were used to identify the markers has limited their application. Efficient gene transfer through gene technology provides breeding programs an additional tool to overcome deficiencies in genetic variation within *Pisum* germplasm. Nutritional and agronomic benefits of dry pea ensure its inclusion in production systems worldwide while the application of modern DNA technology and gene technology promises to overcome many current production constraints.

**Key words:** *Pisum sativum*, plant breeding, genetics, production, disease, quality.

## Introduction

Pea (*Pisum sativum* L.) is a cool season annual crop produced worldwide for human consumption and animal feed. It originated in the Near East and Mediterranean regions and has been grown since early Neolithic times<sup>1,2</sup>. Evidence from carbonized remains indicates that pea has been cultivated with cereal crops such as wheat and barley since domestication. Limited historical evidence makes it difficult to determine the exact location of domestication; however, soon after domestication pea and other legumes spread to other parts of the world with the movement and activities of man<sup>3</sup>. The genus *Pisum* is a member of the family *Papilionaceae* tribe *Viciae* and is composed of two species, *P. sativum* L. and *P. fulvum* Sibth. and Sm. After a significant amount of study and discussion *Pisum sativum* has been further divided to include several subspecies, *P.s. ssp. sativum*, *P.s. ssp. elatius*, *P.s. ssp. humile*, *P.s. ssp. arvense* and *P.s. ssp. hortense*. The literature indicates that *ssp. elatius* and *ssp. humile* are the progenitors of pea *P.s. ssp. sativum*.<sup>1</sup> *P.s. ssp. arvense*, includes the field pea and the 'Austrian' winter pea, both possessing colored flowers and variously pigmented seeds. The most widely produced pea in the world is the yellow cotyledon dry edible pea, although the green cotyledon dry pea is quite popular in some regions. Green dry peas are typically split and used almost exclusively for human consumption while yellow peas are primary used as a supplement in animal rations. A portion of yellow peas are used for human food, but due to limited reporting from many developing countries it is difficult to estimate an exact quantity. The Austrian winter type pea with colored flowers and pigmented seed is another form of dry pea which when harvested at maturity is commonly used as an

ingredient in bird feed. Due to its excessive biomass production, the Austrian winter pea is commonly used as a green manure crop to improve soil tilth and fertility. A rather minor dry pea type produced for the snack industry in the Orient is the marrowfat pea. It is also harvested dry and is characterized by extremely large and irregularly shaped seed with a dimpled surface. Quality standards in pea vary depending on end use. Human consumption markets require superior physical appearance and nutritional quality is considered generally acceptable while feed markets for livestock focus on compositional quality. The nutritional value of dry pea seed is similar to other grain legumes and contains 18-30% protein, 35-50% starch and 4-7% fiber. Pea protein is deficient in sulfur-containing amino acids, but contains relatively high levels of lysine making it a good dietary complement to cereals. Anti-nutritional factors, although present in pea, are relatively minor and do not adversely affect crop use. The nutritional value and agronomic benefits of pea have contributed to its sustained production and use in cropping systems worldwide.

## Production

Grain legumes including pea, lentil and chickpea are frequently produced in rotation with cereal grains. They break cereal disease cycles, allow grassy weed control through herbicide application and improve soil tilth and fertility. The pea crop enhances soil fertility by forming a symbiotic relationship with the soil bacterium, *Rhizobium leguminosarum*, which has the capability of fixing atmospheric nitrogen into plant-available forms and reduces the need to apply synthetic nitrogen fertilizer. Dry pea ranks second behind dry bean among grain legumes for worldwide production and ranks fourth in harvested area (Table 1). Dry pea is produced in more than 87 countries

worldwide with approximately one-half the world's production occurring in Canada, France, China and the Russian Federation (Table 2). Other leading producers include India, Ukraine, Germany, Australia, United Kingdom and the United States. Production in Canada has increased more than 500 percent during the last decade making them the leading producer and exporter of dry pea<sup>4</sup>. The rapid increase in production is due the rotational advantages of pea and availability of cultivars adapted to the dry land conditions of the northern Great Plains.

Dry pea is most suited to cool environments with evenly distributed precipitation and well-drained soils. Optimum temperatures during the growing season range from 13-18°C; however, many environments where pea is produced experience temperatures between 25 and 30°C without serious yield loss<sup>5</sup>. Young pea seedlings can tolerate short periods of relatively cold temperatures (- 6°C) with little or no frost damage and the pea plant is most sensitive to temperature during bloom<sup>6</sup>. Optimum temperatures are near 20°C while excessively high temperatures (>28°C) result in poor pod set due to flower and seed abortion. Uniform distribution of precipitation during the growing season is important for optimum seed production. Precipitation events during and soon after bloom increase pod set and subsequent seed yield by lowering temperatures and providing additional moisture. Dry pea production occurs predominantly under dryland conditions in environments that are characteristically Mediterranean (ex. US Pacific Northwest) or Continental (ex. northern Great Plains of the US and Canada). Production in Mediterranean environments relies on soil moisture reserves accrued during the winter months with infrequent precipitation during the growing season, while the Continental environments receive the bulk of precipitation during a relatively short summer period coinciding with the growing season. The pea plant is botanically indeterminate and will continue to grow provided sufficient moisture is available. Frequent rains during the latter portion of the growing cycle characteristic of Continental climates may result in continued growth and the presence of immature seed on upper nodes while mature seed on lower nodes could be harvested. Unless crop growth is terminated by herbicide application or swathing, lower pods may shatter causing seed loss and the immature seed on upper nodes may stain the mature seed and cause spoilage during storage. Terminal drought in the Mediterranean environments reduces the risk of contamination with immature seed, but subjects the mature seed to high temperatures and intense sunlight which may cause the seed to bleach, especially if light rains or heavy dews occur. Modern cultivars have been selected for a more determinate and upright growth habit to improve uniformity of maturity and ease of harvest.

Dry pea is typically sown in the spring; however, certain field pea (*P.s. ssp. arvense*) cultivars have been selected for fall sowing and can tolerate harsh winter conditions. The fall-sown field pea establishes in the fall forming a rosette, enters a dormant state and resumes growth in the spring. The most commonly grown winter pea is the Austrian winter type. It has colored flowers and mottled seed coats which give it a bitter flavor making it undesirable for human consumption. Breeding efforts in the US have begun to transfer winter hardiness from the Austrian type to clear-seeded dry pea types. Clear-seeded winter peas are expected to increase seed production up to 50 percent while providing a viable rotation crop for expanding direct seed production systems. Capability to plant the pea

crop in the fall will allow more efficient distribution of field work, reduce soil compaction and avoid difficulties with establishing the pea crop in cold, wet soils typical of spring.

Pea production is constrained by biotic and abiotic stresses. The biotic constraints include several plant pathogens that cause disease on pea. These pathogens include foliar and soil-borne fungi, viruses and bacteria (Table 3). The most devastating pathogens are soil-borne fungi including *Aphanomyces euteiches* (the causal agent of common root rot), *Fusarium solani* (the causal agent of Fusarium root rot), *Pythium* and *Rhizoctonia* spp. (the causal agents of seedling damping off) and *Fusarium oxysporum*, races 1, 2, 5 and 6 (the causal agent of Fusarium wilt). Resistance to each race of *Fusarium oxysporum* is controlled by a single dominant gene and has been incorporated into many recently developed varieties. Complete resistance to the other soil-borne pathogens, *F. solani*, *A. euteiches*, *Pythium* ssp. and *Rhizoctonia* ssp., has not been reported in pea germplasm; however, partial resistance to *F. solani* and *A. euteiches* has been incorporated into improved germplasm and made widely available. The reader is referred to Muehlbauer<sup>7</sup> where a summary of available germplasm lines with tolerance to these two pathogens is presented. Foliar pathogens are also potentially devastating to pea production. Powdery mildew caused by *Erysiphe pisi* can be of epidemic proportion in the drier production regions of the US and Canadian prairies. In addition to reduced crop yield and quality, spore production from powdery mildew can be harmful to human health and significant spore buildups can be a fire hazard for combines during harvest. Resistance to powdery mildew is conferred by a single recessive gene (*er-1*) and has been incorporated into many recently released cultivars. Downy mildew caused by *Peronospora viciae* is important in cool wet environments characteristic of western Washington state and Europe. Resistance has been reported in pea and has been successfully incorporated in many of the cultivars developed in the areas where downy mildew is prevalent.

Disease caused by viral pathogens is transmitted by aphids under field conditions and can sometimes be epidemic. Control of aphid populations with insecticides can minimize the spread of virus particles in many production regions. Pea seed-borne mosaic virus (PSbMV) has the potential to significantly reduce pea production; however, genetic resistance and crop monitoring has minimized the incidence of this disease. Currently, pea enation mosaic virus (PEMV) is the most devastating viral disease in the US. Resistance to PEMV is conferred by a single dominant gene (*En*) and has been incorporated into recently released varieties<sup>8,9</sup>. Symptoms of this virus include stunted growth and possibly plant death, vein clearing or "windowing" on the leaves and stipules, distorted pod development, and reduced seed size<sup>10</sup>. Other virus diseases present in the US include pea streak virus (PSV), bean (pea) leaf roll virus (BLRV) and red clover vein mosaic virus (RCVMV). Additional virus diseases worldwide include bean yellow mosaic virus, faba bean necrotic yellows virus and pea early browning virus. Insect pests such as the pea leaf weevil (*Sitona lineatus* L.) and seed weevil (*Bruchus pisorum*) have the potential to devastate the pea crop and, in the case of the seed weevil, reduce seed quality to unacceptable levels. Resistance to the seed weevil has not been reported in cultivated pea (*Pisum sativum*); however, moderate levels of resistance have been reported in *P. fulvum* germplasm<sup>11</sup>. To date, this resistance has not been successfully transferred to cultivated

varieties of *Pisum sativum*. Resistance to *S. lineatus* is limited at best and shows very poor narrow sense heritability (-2.6%)<sup>12</sup>. Nouri-Ghanbaliani<sup>12</sup> determined that selection for increased resistance among the winter hardy populations they generated would not be successful.

### Genetics

Genetic inheritance in pea has been well defined by numerous geneticists and breeders since the first studies conducted by Gregor Mendel in the mid nineteenth century<sup>13</sup>. This detailed understanding has allowed plant breeders to make significant improvement in crop productivity and quality. Mendel chose pea as the subject of his inquiry because of its self-pollinated habit and easily distinguished phenotypic characters. These same attributes in addition to ease of cultivation and broad range of morphological variation have caused pea to remain the subject of many modern genetic studies. *Pisum* germplasm contains a rich collection of genetic variation suited to commercial applications as well as traits well suited for academic inquiry. Genetic study in the late nineteenth and early twentieth centuries focused on simply inherited morphological traits and disease resistance. The advent of modern DNA technology (markers) and biotechnological approaches (genetic transformation) has extended genetic study to more detailed studies of the *Pisum* genome including physiological traits and metabolic pathways. Crop productivity has benefited from numerous simply inherited morphological traits. Many early cultivars had a conventional plant type with long vines (>100 cm), large stipules and one to three pairs of leaflets per petiole. The conventional plant type is prone to lodge under modest seed loads reducing harvest ease, seed quality and yield due to disease infestation. A collapsed canopy maintains high humidity conditions conducive to pathogen growth and disease development. Discovery of the *afila* gene (*af*) which causes leaflets to be converted into tendrils combined with the dwarf plant type (*le*) has resulted in an upright growth habit that resists lodging<sup>14</sup>. Intertwining of tendrils between neighboring plants allows mutual support resulting in the canopy remaining upright through harvest. Modern cultivars have exploited the tendrilled, semi-dwarf plant type to improve harvesting ease and reduce foliar disease which improves overall productivity and seed quality. Genetic mapping in pea has made use of several simply inherited traits such as alternate leaf and pod morphologies and stem, leaf, flower and pod pigmentation. They serve as useful genetic markers to verify hybridization in the  $F_1$  and allow molecular markers to be anchored to specific linkage groups. Isozymes or alternative forms of a single enzyme are also inherited as single genes and serve as molecular markers in linkage analyses.

Quantitative inheritance is defined as the polygenic control of trait expression and typically shows continuous variation. Improvement of quantitative traits is usually time consuming requiring several cycles of hybridization and selection to pyramid multiple positive alleles in a single desirable genetic background. Environmental influence and epistatic interaction among genes reduce heritability making trait improvement difficult. Important quantitatively inherited traits in pea include seed yield and quality, winter hardiness and tolerance to the fungal pathogens, *Aphanomyces euteiches*, *Mycosphaerella pinodes* and *Fusarium solani* f.sp. *pisi*. Population improvement for these traits has included repeated cycles of hybridization and selection. Low heritability and year to year

environmental variation hinders genetic advancement. Seed yield in pea is highly dependent on environment and is particularly responsive to the amount and distribution of precipitation received during the growing season<sup>15,16</sup>. Additionally, pathogen populations and environmental conditions complicate field evaluation of tolerance to fungal pathogens of pea. Therefore, improved methods to predict genetic gain and evaluate quantitative traits without the environmental influence are needed. Genome mapping has allowed development of DNA markers linked to quantitative trait loci (QTL) which contribute to the phenotypic expression of quantitatively inherited traits. These markers allow selection of genotypes possessing positive QTL prior to field evaluation. For example, Pilet<sup>17</sup> identified flanking DNA markers for three quantitative trait loci (QTL) contributing to *Aphanomyces* root rot tolerance. These and related markers are being used in both private and public breeding programs to identify superior genotypes.

### Breeding

Pea is a self-pollinated diploid ( $2n=14$ ,  $x=7$ ) annual crop and has been the subject of controlled hybridization and selection for decades. Modern breeding programs typically use either a bulk population, pedigree selection or a combination of these two procedures. The bulk population method has the advantage of easy population maintenance and delayed selection until the  $F_4$  or  $F_5$  when selections are near homozygosity and breed true. A disadvantage of the bulk procedure is that certain genotypes may be lost reducing the range of variation present for selection. The pedigree method maintains a wider range of the variation initially present and allows specific undesirable genotypes to be removed from the population. However, it is much more time consuming, labor intensive and requires that individual plants be separated for close observation and data collection. A disadvantage to wide plant spacing is that data collected may not be representative of growth in a solid stand<sup>18</sup>. There are several methods for population improvement in pea<sup>18</sup>. Biparental mating or backcrossing followed by selection has been successful in transferring disease resistance from landraces and wild germplasm into adapted legume germplasm<sup>7</sup>. Male sterility is present in *Pisum* germplasm; however, due to limitations associated with cross pollination in the male sterile parent, development of hybrid cultivars has not been successful. Recurrent selection though time consuming and laborious in self-pollinated crops has been used to pyramid favorable alleles for disease resistance<sup>19</sup>. Specific crossing designs such as the diallel and top cross are commonly used to combine various traits and to determine combining ability among parental types<sup>20</sup>.

Mutation breeding has been used worldwide for improvement of grain legumes through increased genetic variation and creation of novel alleles. Several pea cultivars resulting from mutagenesis have been released with improvements including increased yield, lodging resistance (*afila* leaf trait), larger seed, increased protein concentration and modified maturity.<sup>21</sup> Mutation breeding of pea has been centered in many European countries including Sweden, the Netherlands, Germany, Italy as well as several eastern European countries and Russia<sup>22</sup>.

Conventional breeding methods have been successful in improving pea germplasm toward development of superior cultivars. However, results of many genetic studies have revealed that improvement of several important agronomic

characters in pea is difficult and may not be possible using conventional procedures. Development of modern DNA technology (i.e. DNA markers) and biotechnological approaches (gene transformation) will aid cultivar development and provide additional methods to realize full production potential. Marker assisted selection (MAS) aids selection in plant breeding and is based on pre-existing DNA sequences located near a gene of interest. This method should not be confused with genetic engineering or gene technology which involves the introduction of foreign genes from unrelated species. MAS uses DNA markers tightly linked to genes of interest to predict their presence (and absence) in individual progeny. These markers can be identified consistently under lab conditions while phenotypic selection for many traits in pea is difficult and time consuming due to inconsistent environmental conditions. Several co-dominant markers allow plant breeders to identify heterozygous individuals and allow effective selection in early generations when large numbers of individual progeny must be evaluated. Detailed genetic maps have been generated for pea placing many genes of interest on individual linkage groups and associating them with DNA markers using a variety of molecular techniques<sup>23</sup>. The diversity of procedures employed to develop the markers currently available limits the application of MAS in breeding programs. Optimum application of MAS requires that markers be 1) tightly linked to the trait of interest, 2) based on one or few technologies and 3) co-dominant to allow selection in early generations. Advances in biotechnology have opened many opportunities for plant breeders to accomplish program goals and objectives which were not possible with conventional breeding. DNA manipulation and successful transformation of plant cells has allowed genetic recombination beyond the boundary of sexually compatible species. In addition to providing new methods of accomplishing applied goals, genetic transformation allows geneticists to study specific genes of interest in greater detail. Gene technology involves isolation and cloning a gene of interest and insertion of that gene into the nuclear genome of the desired target plant such that it is stably expressed and heritable in subsequent generations. Several techniques have been developed to introduce genes into plant cells including transfer through modified *Agrobacterium tumefaciens* strains, direct transfer using biolistic procedures and electroporation of intact cells and protoplasts. Transformation using *A. tumefaciens* is widely used among the grain legumes for gene transfer<sup>24,25</sup>.

Genetic variation for improvement of several economically important traits in pea is inadequate at best and, in many cases, absent from available germplasm. Therefore, natural resistance must be introduced from sexually incompatible species. These traits include insect resistance, reduced concentration of antinutritional factors, improved seed composition and resistance to several soil-borne fungal pathogens. Additionally, herbicide resistance has been transferred to many crops providing producers with additional options for weed control. Genetic transformation has met with mixed reception in the marketplace and media resulting in many potentially improved cultivars being held back from release. Genetically modified crop species including peas with improved characteristics that benefit the consumer may improve consumer acceptance of this technology in the long run.

## Conclusion

Dry pea continues to be an important crop worldwide both for food and feed and as a rotational crop with cereals. Its long crop history and advantages for genetic study have resulted in significant understanding of inheritance and improvements in production and seed quality. The pea plant has been transformed in recent years from a long vine, conventional plant type with leaflets to a more modern semi-dwarf, lodging-resistant type with stiff stems and tendrils. These changes have improved crop quality and reduced foliar disease incidence without loss in productivity. Genetic resistance to many pea pathogens is controlled by single genes which have allowed breeders and geneticists to minimize yield loss. However, resistance to the most important fungal pathogens is still difficult due to their multigenic control and significant environmental influence. Construction of detailed genetic maps including single gene traits and QTL will provide additional tools to identify progeny containing desirable alleles early in the breeding process and ideally reduce the time from initial hybridization to cultivar release. *Pisum* germplasm is genetically diverse which has allowed breeders to overcome many production constraints; however, resistance to some fungal pathogens and insects is not available in sexually compatible germplasm. This absence of desired genetic variation has caused researchers to seek alternative methods to create useful variation including mutagenesis and gene technology approaches to overcome production constraints through access to genetic information in distantly related and unrelated species. These technologies will advance genetic study and understanding in pea and plant genetics as a whole, opening opportunities for crop improvement not currently possible.

## References

- Zohary, D. and Hopf, M. 1973. Domestication of pulses in the old world. *Science* **182**:887-894.
- Smartt, J. and Hymowitz, T. 1985. Domestication and evolution of grain legumes. In: Summerfield, R.J. and Roberts, E.H. (eds.). *Grain Legume Crops*, London: Collins Professional and Teck Books. p. 37-72.
- Marx, G.A. 1977. Classification, Genetics and Breeding. In: Sutcliffe, J.F. and Pate, (eds.). *Physiology of the Garden Pea*. New York, New York: Academic Press. p. 21-44.
- FAO (2002). <http://apps.fao.org/cgi-bin/nph-db.pl?subset=agriculture>.
- Muehlbauer, F.J., Short, R.W., and Kraft, J.M. 1983. Description and culture of dry peas. *Agricultural Research Service, Agricultural Reviews and Manuals, Western Series, No. 37*. p. 92.
- Miller, P., Brandt, W., Slinkard, A., McDonald, C., Derksen, D., and Waddington, J. 1998. New crop types for diversifying and extending spring wheat rotations in the Brown and Dark Brown soil zones of Saskatchewan. Project Rep. Agric. Agri-Food Can., Swift Current, SK.
- Muehlbauer, F.J. 1992. Use of introduced germplasm in cool-season food legume cultivar development. In: Shands, H.L. and Weisner, L.E. (eds.). *Use of Plant Introductions in Cultivar Development, Part 2. Crop Science Society of America Special Publication Number 20*. p. 49-73.
- McPhee, K.E. and Muehlbauer, F.J. 2002. Registration of 'Lifter' green dry pea. *Crop Sci.* **42**(4):1377-8.
- McPhee, K.E. and Muehlbauer, F.J. 2002. Registration of 'Franklin' green dry pea. *Crop Sci.* **42**(4):1378.

- <sup>10</sup> Kraft, J.M. and Pflieger, F.L. 2001. Compendium of pea diseases and pests, second edition. American Phytopathological Society, St. Paul, Minnesota. p. 67.
- <sup>11</sup> Hardie, D.C., Collie, H., Clement, S.L., and Elberson, L.R. 1999. Field evaluations of wild peas against pea weevil, 1994 and 1996. *Arthr. Man. Tests* **24**:433-435.
- <sup>12</sup> Nouri-Ghanbalani, G., Auld, D.L., O’Keeffe, L.E., and Campbell, A.R. 1978. Inheritance of resistance to the adult pea leaf weevil in Austrian winter peas. *Crop Sci.* **18** :858-860.
- <sup>13</sup> Mendel, G. 1866. Experiments in plant hybridization (1865). *Versuche uber Pflanzen-hybriden. Verhandlungen des naturforschenden Vereines in Brunn, Bd. IV fur das Jahr 1865. Abhandlungen.* p. 3- 47.
- <sup>14</sup> Goldberg, F.B. 1965. Afila, a new mutation in pea (*Pisum sativum* L.). *Boletin Genetica, Instituto de Fitotecnia Castelar, Argentina,* pp. 27-28.
- <sup>15</sup> McPhee, K.E. and Muehlbauer, F.J. 1999. Variation for biomass and residue production by dry pea. *Field Crops Res.* **62**:203-212.
- <sup>16</sup> McPhee, K.E. and Muehlbauer, F.J. 2001. Biomass production and related characters in the core collection of *Pisum* germplasm. *Gen. Res. and Crop Evol.* **48**:195-203.
- <sup>17</sup> Pilet-Nayel, M.L., Muehlbauer, F.J., McGee, R.J., McGee, J.M., Barranger, A., and Coyne, C.J. 2002. Quantitative trait loci for partial resistance to *Aphanomyces* root rot in pea. *Theor. and App. Gen.* (in press).
- <sup>18</sup> Muehlbauer, F.J., Redden, R.J., Nassib, A.M., Robertson, L.D., and Smithson, J.B. 1988. Population improvement in pulse crops: an assessment of methods and techniques. In: Summerfield, R.J. (ed.). *World Crops: Cool Season Food Legumes.* Kluwer Academic Publishers. p. 943-966.
- <sup>19</sup> Lewis, M.E. and Gritton, E.T. 1992. Use of one cycle of recurrent selection per year for increasing resistance to *Aphanomyces* root rot in peas. *J. Amer. Soc. Agron.* **117**(4):638-642.
- <sup>20</sup> Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* **9**:462-493.
- <sup>21</sup> Micke, A. 1988. Genetic improvement of food legumes in developing countries by mutation induction. In: Summerfield, R.J. (ed.). *World Crops: Cool season food legumes.* Dordrecht: Kluwer Academic Publishers. p. 1030-1047.
- <sup>22</sup> Micke, A. 1988. Genetic improvement of grain legumes using induced mutations: an overview. In: *Improvement of Grain Legume Production Using Induced Mutations.* Vienna: International Atomic Energy Agency. p. 1-51.
- <sup>23</sup> Weeden, N. F., Ellis, T.H.N., Timmerman-Vaughan, G.M., Swiecicki, W.K., Rozov, S.M., and Berdnikov, V.A. 1998. A consensus linkage map for *Pisum sativum*. *Pisum Genetics* **30**:1-4.
- <sup>24</sup> Schroeder, H.E., Schotz, A.H., Wardley-Richardson, T., Spencer, D., and Higgins, T.J.V. 1993. Transformation and regeneration of two cultivars of pea (*Pisum sativum* L.). *Pl. Phys.* **101**:751-757.
- <sup>25</sup> Krishnamurthy, K.V., Suhasini, K., Sagare, A.P., Meixner, M., de Kathen, A., Pickardt, T., and Schieder, O. 2000. Agrobacterium mediated transformation of chickpea (*Cicer arietinum* L.) embryo axes. *Pl. Cell Rep.* **19**:235-240.

**Table 1.** World production of grain legumes in 2001 (FAO, 2002).

Crop	Species	Production	Harvested Area
		(Mt)	(hectares)
Common bean	<i>Phaseolus vulgaris</i>	16,248,219	23,126,705
Field pea	<i>Pisum sativum</i>	10,288,096	6,120,723
Chickpea	<i>Cicer arietinum</i>	6,001,781	8,523,168
Lentil	<i>Lens culinaris</i>	3,388,954	3,685,361
Field bean	<i>Vicia faba</i>	3,276,158	2,257,984
Cowpea	<i>Vigna unguiculata</i>	3,041,680	9,955,672
Pigeon pea	<i>Cajanus cajan</i>	2,925,980	3,833,415
Lupin	<i>Lupinus spp.</i>	1,685,952	1,370,203
Vetch	<i>Vicia spp.</i>	974,121	1,030,832
Total		51,536,655	65,318,922

**Table 2.** Dry pea production in 2001 for the ten countries with the greatest production (FAO, 2002).

Country	Production	Harvested Area
	(Mt)	(hectares)
Canada	2,175,400	1,396,600
France	1,595,000	395,000
China	1,150,000	750,000
Russian Federation	1,000,000	575,000
India	700,000	700,000
Ukraine	595,000	301,000
Germany	557,495	164,000
Australia	410,000	315,000
United Kingdom	312,500	102,400
United States	200,000	88,506
World total	10,288,096	6,120,723

**Table 3.** Biotic stress agents constraining US dry pea production.

Biotic Stress	Causal Organism	Resistance Mechanism
<b>Disease</b>		
Fusarium root rot	<i>Fusarium solani</i>	Polygenic
Aphanomyces root rot	<i>Aphanomyces euteiches</i>	Polygenic
Fusarium wilt	<i>Fusarium oxysporum</i> <i>f.sp. pisi</i> Race <sup>1, 2, 5, 6</sup>	Fw, Fwn, Fwf
Pea enation mosaic virus		En
Pea streak virus		Not defined
Bean leaf roll virus		lr
Pea seed-borne mosaic virus		sbm-1, sbm-2, sbm-3
Powdery mildew	<i>Erysiphe pisi</i>	er-1
Downy mildew	<i>Peronospora pisi</i>	Not defined
Ascochyta blight	<i>Phoma medicaginis</i> , <i>Mycosphaerella pinodes</i> <i>var. pinodella</i> , and <i>Ascochyta pisi</i>	Polygenic
<b>Nematodes</b>		
Pea cyst nematode	<i>Heterodoera</i> <i>goettingiana</i>	NA
Root-knot nematode	<i>Meloidogyne spp.</i>	NA
Root-lesion nematode	<i>Pratylenchus penetrans</i>	NA
<b>Insects</b>		
Pea leaf weevil	<i>Sitona lineatus</i>	NA
Pea seed weevil	<i>Bruchus pisorum</i>	Not defined
Pea aphid	<i>Acyrthosiphon pisum</i>	NA
Loopers	<i>Autographa californica</i> (Speyer) <i>Anagrapha</i> <i>falcifera</i> (Kirby)	NA

<sup>1</sup> PNW = Pacific Northwest; UMW = Upper Midwest