

# CHAPTER I

## INTRODUCTION

### 1.1 Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is a leguminous crop widely cultivated in tropical and subtropical regions, particularly in Asia, including India, Thailand, Vietnam, the Philippines, Indonesia, and China. It is characterized by its short life cycle, typically maturing within 60–90 days after planting (DAP), depending on the variety, agroclimatic conditions, and management practices (Lawn and Ahn, 1985; Kim et al., 2015). Mungbean is relatively easy to cultivate, adaptable to various soil types and climatic conditions, and exhibits drought tolerance. Additionally, it possesses the ability to fix atmospheric nitrogen through symbiotic relationships with rhizobium bacteria in the soil. This nitrogen-fixing capability makes mungbean an ideal candidate for crop rotation systems and as a green manure crop to enhance soil fertility (Nair et al., 2013; Kim et al., 2015). This trait not only improves soil health but also contributes to sustainable agricultural practices by reducing input costs and environmental impacts.

In 2023, Thailand reported a mungbean cultivation area of 663,500 rai, with a total production of 101,825 tons. Compared to the previous year, this represented a 5.48% decrease in cultivation area and a 3.66% decline in production (Office of Agricultural Economics, 2022). Major mungbean-growing regions in Thailand include the provinces of Chai Nat, Phetchabun, and Khon Kaen, where the crop is integrated into diverse cropping systems to improve soil fertility and farmer livelihoods (Udomsak, 2008; Office of Agricultural Economics, 2022). In Thailand, popular mungbean varieties include Kamphaeng Saen (KPS) 2, Chai Nat (CN) 84-1, CN72, CN3, and Suranaree University of Technology (SUT) 1. Mungbean is typically cultivated during the rainy season, late rainy season, and dry season. Mungbean is a nutrient-dense crop, rich in protein, vitamins, and minerals, contributing to food security and nutritional health in resource-limited communities (Ganesan and Xu, 2017).

Mungbean is a crop significant in terms of economics and nutrition, serving as a valuable source of nutrition for food and feed. Its nutritional composition varies considerably depending on genotypes, environmental conditions, and cultivation practices (Skylas et al., 2017; Wang et al., 2021). These variations highlight the need for targeted breeding and cultivation strategies to optimize nutritional quality. The protein and carbohydrate content of mungbean seeds typically range from 20.00-30.00% and 60.00-70.00%, respectively (Somta et al., 2022). Due to its versatile nutritional profile, mungbean is able to be processed into a variety of food products, including mungbean flour, desserts, vermicelli, ice cream, and snacks (Bhatty et al., 2000). These products are popular in many Asian cuisines and contribute to the global demand for plant-based protein sources. Additionally, mungbean sprouts are a convenient and highly digestible form of consumption. Sprouts are particularly rich in dietary fiber and phytonutrients, including vitamin C, vitamin A, vitamin B1, vitamin B2, phytochemicals, and gamma-aminobutyric acid (GABA) (Randhir & Shetty, 2005). These nutrients make mungbean sprouts a functional food suitable for individuals of all ages and genders, offering health benefits such as improved digestion, enhanced immune function, and reduced oxidative stress. The nutritional and functional properties of mungbean, combined with its adaptability to diverse agroecological conditions, underscore its potential as a key crop for addressing global food security and nutritional challenges.

Mungbean is a vital agricultural crop, playing a significant role in sustainable food production systems. Ensuring sustainable mungbean production is critical to meet the increasing domestic demand for its consumption. However, domestic production capacity has been insufficient to fulfill this demand, leading to a reliance on imports. According to the Office of Agricultural Economics (2021), Thailand imported 36,385 tons of mungbean in 2021, while domestic consumption reached 109,446 tons during the same period. This import volume accounted for 33.24% of the annual consumption, highlighting the instability in the food supply chain and the need to enhance domestic production. Several factors contribute to the insufficient production of mungbean. These include: low average yield per unit area, often influenced by unpredictable weather conditions; deficiency in the availability of high-quality seeds, and varieties that are well-adapted to local agroclimatic conditions, which limits the potential for robust and consistent crop growth; high labor costs associated with harvesting, exacerbated by non-uniform maturation of the crop; and prevalent plant diseases, particularly powdery mildew (PM; caused by *Sphaerotheca phaseoli*) and Cercospora leaf spot (CLS; caused by *Cercospora canescens*). Tsou et al. (1979) reported that PM can cause yield losses of up to 40% if no disease management

practices are implemented. Similarly, Kelly et al. (2017) emphasized the economic impact of PM on mungbean production. Additionally, CLS can reduce mungbean yield up to 50% if it occurs after the flowering stage (Asian Vegetable Research and Development Center, 1974, 1975). Currently, there are limited mungbean varieties in Thailand that resistant to both diseases.

Effective management strategies for PM include increasing the plant spacing to improve air circulation and reduce humidity; environmental control measures to minimize conditions favorable for disease development; biological control using antagonistic fungi such as *Trichoderma* spp. for seeds and foliar application, which can reduce the accumulation and spread of the pathogen; and chemical control using fungicides such as triadimefon and triazoles (Khunti et al., 2005). However, the reliance on chemical treatments is not sustainable due to their environmental impact, high costs, and development of chemical resistant pathogen strains. An environmentally friendly and sustainable approach to disease management is the development and use of disease-resistant mungbean varieties through plant breeding programs. Resistant varieties can significantly reduce the need for chemical inputs, save labor, and lower cultivation costs while maintaining or improving yield potential.

Improving mungbean varieties for disease resistance can be achieved through various methods, such as conventional breeding and mutagenesis (Reddy et al., 1994; Wani et al., 2014; Javed et al., 2016). However, traditional plant breeding methods are time-consuming and slow to achieve success. Therefore, several molecular markers have been developed to enhance the efficiency of plant breeding programs, including the study of genetic diversity in plants and plant pathogens, as well as the selection of parental lines and hybrids using both qualitative (Fazio et al., 1999) and quantitative traits (Veldboom and Lee, 1994). Specifically, disease resistance genes have been utilized to develop disease-resistant plant varieties, accelerating the progress of plant breeding. The pyramiding of multiple disease resistance genes using marker-assisted gene pyramiding techniques can result in plant varieties with resistance to multiple pathogen races, making it more difficult for resistance to break down.

Mungbean varieties in Thailand, such as KPS2, CN72, CN84-1, and CN3, are known for their high yield potential but remain susceptible to PM and CLS (Chueakhunthod, 2019). Reports from Phruetthitthep et al. (2011) and Wongwarat et al. (2023) indicate that Thai-certified varieties, such as SUT1, KPS2, CN72, and CN84-1, are susceptible to PM and CLS. The integration of breeding programs focused on disease resistance, coupled with the adoption of well agronomic practices, is essential to ensure the increased availability of mungbean as a nutritious and sustainable legume

crop (War et al., 2017). To address this disease, there is a pressing need to develop new mungbean varieties with enhanced resistance to PM and CLS, along with high yield and stability. Recently, our laboratory has developed new disease resistant breeding lines with high yield potential, including lines P08, P12, P22, and P24 (Pookhamsak et al., unpublished data). These lines resulted from crosses between the CN84-1 variety and resistant double cross [(CN72×V4758) × (CN72×V4718)] × [(CN72×V4718) × (CN72×V4785)] which were developed through gene pyramiding methods. The resistant V4718, V4758, and V4785 lines were derived from India and obtained from the World Vegetable Center in Taiwan. The PM resistance genes in these lines are controlled by single dominant genes located at different loci on the chromosomes (non-allelic) and independently assorted (Khajudparn et al., 2009). Lines P08, P12, P22, and P24 were developed through backcrossing using the resistant donor parents and CN84-1 as recurrent parent, containing 3-4 resistance genes (2-3 genes for PM and 1 gene for CLS), providing resistance to both diseases and high yield potential resulted from cultivation trials conducted at the preliminary and standard trial levels during 2020–2022, these newly developed mungbean lines derived from backcrossing are eligible for subsequent evaluation through regional trial and farm trials.

This regional trial represents a critical step toward identifying mungbean cultivars that can enhance agricultural productivity and provide sustainable benefits to farmers. Building upon previous research, the present study conducts regional trials across diverse environmental conditions to rigorously evaluate the performance, adaptability, and disease resistance of newly developed lines. Understanding genotype × environment interaction (GEI) is fundamental in breeding programs that aim to develop cultivars with high yield potential and stable performance. GEI arises when different genotypes respond differently across environments, and a particularly important form is crossover interaction, where genotype rankings vary from one environment to another (Smith et al., 2001; Yan and Hunt, 2002). This implies that a genotype superior in one location may not retain its performance elsewhere, underscoring the need for multilocation testing.

To analyze GEI, various statistical methods have been developed, including regression coefficient analysis, summation of squared deviations from regression, additive main effects and multiplicative interaction (AMMI) models, and genotype plus genotype-by-environment interaction (GGE) biplot analysis. These approaches enable the identification of genotypes with either broad or specific adaptability, guiding the selection of stable and high-performing cultivars.

A key focus of this study is disease resistance, a trait highly influenced by environmental conditions. Disease development depends on the interaction of three essential components: a susceptible host plant, a virulent pathogen, and a conducive environment. In the absence or limitation of any one of these factors, disease incidence and severity are significantly reduced (Velásquez et al., 2018; Jiwuba et al., 2020). Therefore, breeding for disease resistance must consider the target environments in which the crop will grow. Regional trials are essential for evaluating the expression and stability of resistance traits, as the effectiveness of resistance genes can vary significantly depending on environmental conditions. The regional yield trials provide crucial data to support the recommendation of cultivars tailored to specific agro-ecological zones, while also identifying broadly adaptable lines. This approach ensures that selected genotypes meet both the productivity and resilience demands of diverse farming systems.

In addition to disease resistance and yield stability, nutritional content is also important, as mungbean is a significant food crop that provides high levels of carbohydrates and protein. Sprouts and microgreens are often more nutrient-dense than ungerminated seeds or mature vegetables, containing higher levels of vitamins, minerals, and bioactive compounds essential for healthy diets (Ebert, 2022). Microgreens are rich sources of vitamins such as vitamin C, minerals including copper and zinc, and phytochemicals (Zhang et al., 2021). Comparative analyses show that germinated seeds tend to have higher macronutrients (lipids, proteins, sugars, amino acids, minerals), while microgreens possess significantly higher concentrations of vitamins and polyphenols (Bhaswant et al., 2024). However, there is limited data on the nutritional composition of new mungbean genotypes. Therefore, the nutritional values of these mungbean genotypes must be rigorously assessed to ensure that breeding efforts address both quantity and quality. Evaluating the nutritional composition of seeds, sprouts, and microgreen is crucial, as it not only supports the development of value-added products but also facilitates the registration and certification of new varieties. By integrating nutritional profiling into breeding programs, researchers can develop varieties that meet both agronomic and dietary needs (Saltzman et al., 2013; Garcia et al., 2016; Bouis and Saltzman, 2017; Salsman et al., 2021), contributing to improved food security and addressing nutritional deficiencies in populations worldwide.

The development and dissemination of disease-resistant, high-yielding, and nutritionally enhanced mungbean varieties will enable farmers to increase production efficiency, reduce reliance on imports, and promote sustainable agricultural practices.

This holistic approach aligns with global efforts to enhance food security, improve nutritional outcomes, and ensure the long-term sustainability of agricultural systems. Leveraging advancements in plant breeding, agronomy, and nutritional science, stakeholders can foster a resilient and productive mungbean sector that meets the demands of a growing population while minimizing environmental impacts.

## 1.2 Objectives

1.2.1 To assess the potential of novel mungbean lines exhibiting resistance to PM and CLS diseases in regional yield trials.

1.2.2 To determine the yield stability and consistency of new mungbean lines (P08, P12, P22, and P24) based on yield performance and yield-related components compared to recurrent parent and check varieties.

1.2.3 To evaluate the nutritional composition of seeds, sprouts and microgreen from the newly developed mungbean lines recurrent parent and check varieties.

1.2.4 To characterize the morphological traits of sprouts and microgreen from the new mungbean lines compared to recurrent parent and check varieties.

## 1.3 Research hypotheses

1.3.1 The new mungbean lines resistant to PM and CLS demonstrated yield performance similar or superior to recurrent parent under diverse regional growing conditions at the regional yield trial level.

1.3.2 The new mungbean lines exhibited resistance to PM and CLS diseases in various environments, as confirmed through field condition evaluations.

1.3.3 The morphological and nutritional characteristics of seeds, sprouts, and microgreens from the new mungbean lines are comparable or exceeded those of existing varieties, with notable improvements in key nutritional and morphological traits.

1.3.4 Regional yield trials conducted across multiple locations within the target region provided critical insights into the adaptability, stability, and overall performance of the new mungbean lines, supporting evidence-based decisions for their commercial release and adoption by farmers.

## 1.4 Scopes of research

1.4.1 This study was divided into three experiments: 1) regional yield trial and stability evaluation through the GGE biplot analysis 2) nutritional and morphological characterization of seed and sprout and 3) nutritional and morphological characterization of microgreens.

1.4.2 The regional yield trials evaluation of eight Thai mungbean genotypes, consisting of four new mungbean lines (P08, P12, P22, and P24) compared to the recurrent parent (CN84-1) and check varieties (CN3, SUT1, and SUPER5). These genotypes exhibited distinct characteristics, such as large seed size, resistance to PM and CLS, high yield potential, and enhanced nutritional values. All mungbean genotypes were evaluated under the four different environments conditions for regional yield trials evaluation including Nakhon Ratchasima, Chai Nat, Phitsanulok, and Phetchabun, across rainy season and dry season during the years 2023-2024.

1.4.3 The nutritional and morphological characterization of seed and sprout were evaluated under control conditions. Eight mungbean genotypes were included in this experiment, comprising recurrent parent (CN84-1) and check varieties (CN3 and SUPER5) and five new mungbean lines (P08, P12, P22, P24, and D5).

1.4.4 The nutritional and morphological characterization of microgreens were evaluated under control conditions. Nine mungbean genotypes were used, comprising recurrent parent (CN84-1) and check varieties (CN3 and SUPER5) and six new mungbean lines (P08, P12, P22, P24, W5 and D5).

1.4.5 The assessment of nutritional components was performed through proximate analysis, including the determination of carbohydrates, crude protein, crude lipid, crude fiber, and ash content.

## 1.5 References

- Asian Vegetable Research and Development Center. (1974). Annual report 74(142). Shanhua, Taiwan, Republic of China.
- Asian Vegetable Research and Development Center. (1975). Annual report 74(69). Shanhua, Taiwan, Republic of China.
- Bhaswant, M., Miyazawa, T., Abe, C., Fukasawa, R., Higuchi, O., Nguyen Thi, M. T., & Miyazawa, T. (2024). Comparative analysis of macro- and micro-nutrients of *Perilla frutescens* var. *crispa* f. *viridis* microgreens and germinated seeds. *Food Chem.*, *455*, 139858. doi:10.1016/j.foodchem.2024.139858
- Bhatty, N., Gilani, A. H., & Ahmad, N. S. (2000). Nutritional value of mung bean (*Vigna radiata*) as effected by cooking and supplementation. *Arch. Latinoam. Nutr.*, *50*(4), 374-379.
- Bouis, H. E., & Saltzman, A. (2017). Improving nutrition through biofortification: a review of evidence from HarvestPlus, 2003 through 2016. *Glob Food Sec.*, *12*, 49-58. doi:10.1016/j.gfs.2017.01.009
- Chueakhunthod, W. (2019). *Development of mungbean breeding lines with improved resistance to Cercospora leaf spot and powdery mildew by molecular marker assisted gene pyramiding*. (Master's thesis), Suranaree University of Technology. Retrieved from <http://sutir.sut.ac.th:8080/jspui/handle/123456789/8383>
- Ebert, A. W. (2022). Sprouts and Microgreens-Novel Food Sources for Healthy Diets. *Plants (Basel)*, *11*(4). doi:10.3390/plants11040571
- Fazio, G., Stevens, M. R., & Scott, J. W. (1999). Identification of RAPD markers linked to fusarium crown and root rot resistance (Frl) in tomato. *Euphytica*, *105*(3), 205-210. doi:10.1023/A:1003497719705
- Ganesan, K., & Xu, B. (2017). A critical review on polyphenols and health benefits of black soybeans. *Nutrients*, *9*(5), 455. doi:10.3390/nu9050455
- Garcia, K., Doidy, J., Zimmermann, S. D., Wipf, D., & Courty, P. E. (2016). Take a trip through the plant and fungal transportome of Mycorrhiza. *Trends Plant Sci.*, *21*(11), 937-950. doi:10.1016/j.tplants.2016.07.010
- Javed, I., Ahsan, M., Ahmad, H. M., & Ali, Q. (2016). Role of mutation breeding to improve mungbean (*Vigna radiata* L. Wilczek) yield: an overview. *Nat. Sci.*, *14*, 63-77. doi:10.7537/marsnsj140116.09.
- Jiwuba, L., Danquah, A., Asante, I., Blay, E., Onyeka, J., Danquah, E., & Egesi, C. (2020). Genotype by environment interaction on resistance to cassava green mite associated traits and effects on yield performance of cassava genotypes in Nigeria. *Front. Plant Sci.*, *11*. doi:10.3389/fpls.2020.572200

- Kelly, L., White, J., Sharman, M., Brier, H., Williams, L., Grams, R., . . . Sparks, A. H. (2017). Mungbean and sorghum disease update. *Grains Research and Development Corporation Grains Research Update*.
- Khajudparn, P. (2009). *Characters associated with yield potential and development of molecular markers for powdery mildew resistance in mungbean*. (Doctoral dissertation). Suranaree University of Technology, Nakhon Ratchasima.
- Khunti, J., Bhoraniya, M., & Vora, V. (2005). Management of powdery mildew and Cercospora leaf spot of mungbean by some systemic fungicides. *Legume Res.*, 28(1), 65-67.
- Kim, S. K., Nair, R. M., Lee, J., & Lee, S. (2015). Genomic resources in mungbean for future breeding programs. *Front. Plant Sci.*, 6, 626. doi:10.3389/fpls.2015.00626
- Lawn, R. J., & Ahn, C. S. (1985). Mung bean (*Vigna radiata* (L.) Wilczek/*Vigna mungo* (L.) Hepper). In R. Summerfield & E. H. Roberts (Eds.), *Grain legume crops* (pp. 584–623). London Collins, United Kingdom: World Vegetable Center.
- Nair, R. M., Yang, R. Y., Easdown, W. J., Thavarajah, D., Thavarajah, P., Hughes, J. A., & Keatinge, J. D. H. (2013). Biofortification of mungbean (*Vigna radiata*) as a whole food to enhance human health. *J. Sci. Food Agric.*, 93(8), 1805-1813. doi:10.1002/jsfa.6110
- Office of Agricultural Economic. (2022). Mungbean. *J. Agric. Econ.*, 69, 58.
- Office of Agricultural Economics. (2021). *Mungbean*. Retrieved from <https://agriman.doe.go.th/home/news/2565/46bean.pdf>
- Phruetthitthep, C., Ngampongsai, S., Masari, A., Thanomsub, S., & Pengphol, S. (2011). Evaluation of mungbean varieties for resistance to powdery mildew disease. *Khon Kaen Agr. J.*, 39. Retrieved from <https://ag2.kku.ac.th/kaj/PDF.cfm?filename=331.pdf&id=604&keeptrack=6>
- Randhir, R., & Shetty, K. (2005). Developmental stimulation of total phenolics and related antioxidant activity in light-and dark-germinated corn by natural elicitors. *Process Biochem.*, 40(5), 1721-1732. doi:10.1016/j.procbio.2004.06.064
- Reddy, K. S., Pawar, S. E., & Bhatia, C. R. (1994). Inheritance of powdery mildew (*Erysiphe polygoni* DC) resistance in mungbean (*Vigna radiata* L. Wilczek). *Theor. Appl. Genet.*, 88(8), 945-948. doi:10.1007/BF00220800
- Salsman, E., Liu, Y., Hosseinirad, S. A., Kumar, A., Manthey, F., Elias, E., & Li, X. (2021). Assessment of genetic diversity and agronomic traits of durum wheat germplasm under drought environment of the Northern Great Plains. *Crop Sci.*, 61(2), 1194-1206. doi:10.1002/csc2.20449

- Saltzman, A., Birol, E., Bouis, H. E., Boy, E., De-Moura, F. F., Islam, Y., & Pfeiffer, W. H. (2013). Biofortification: progress toward a more nourishing future. *Glob Food Sec.*, *2*(1), 9-17. doi:10.1016/j.gfs.2012.12.003
- Skylas, D., Blanchard, C. L., & Quail, K. J. (2017). Variation in nutritional composition of Australian mungbean varieties. *J. Agric. Sci.*, *9*(5), 45-53. doi:10.5539/jas.v9n5p45
- Smith, A., Cullis, B., & Thompson, R. (2001). Analyzing variety by environment data using multiplicative mixed models and adjustments for spatial field trend. *Biometrics*, *57*(4), 1138-1147.
- Somta, P., Laosatit, K., Yuan, X., & Chen, X. (2022). Thirty years of mungbean genome research: where do we stand and what have we learned? *Front. Plant Sci.*, *13*. doi:10.3389/fpls.2022.944721
- Teferie, B. B., Admasu, M. A., & Damessa, G. G. (2020). Assessment and characterization of mung bean (*Vigna radiata*) bacterial brown spot in eastern Amhara, Ethiopia. *Afr. J. Agric. Res.*, *16*(5), 606-621. doi:10.5897/AJAR2019.14681
- Tsou, C. S., Hsu, M. S., Tan, S. T., & Park, H. G. (1979). The protein quality of mungbean and its improvement. *Acta Horticulturae*, *93*, 279-288. doi:10.17660/ActaHortic.1979.9.3.26
- Udomsak, B. (2008). *Mungbean disease in Thailand*. Retrieved from <http://lib.doa.go.th/multim/e-book/eb00083.pdf>
- Veldboom, L. R., & Lee, M. (1994). Molecular-marker-facilitated studies of morphological traits in maize. II: determination of QTLs for grain yield and yield components. *Theor. Appl. Genet.*, *89*(4), 451-458. doi:10.1007/BF00225380
- Velásquez, A. C., Castroverde, C. D. M., & He, S. Y. (2018). Plant-pathogen warfare under changing climate conditions. *Curr. Biol.*, *28*(10). doi:10.1016/j.cub.2018.03.054
- Wang, F., Huang, L., Yuan, X., Zhang, X., Guo, L., Xue, C., & Chen, X. (2021). Nutritional, phytochemical and antioxidant properties of 24 mung bean (*Vigna radiata* L.) genotypes. *Food. Prod. Process. Nutr.*, *3*(1), 1-12. doi:10.1186/s43014-021-00073-x
- Wani, M. R., Kozgar, M. I., Khan, S., Ahanger, M. A., & Ahmad, P. (2014). Induced mutagenesis for the improvement of pulse crops with special reference to mung bean: a review update. In P. Ahmad, M. R. Wani, M. M. Azooz, & L. S. P. Tran (Eds.), *Improvement of Crops in the Era of Climatic Changes: Volume 1* (pp. 247-288). New York, NY: Springer New York.
- War, A. R., Murugesan, S., Boddepalli, V. N., Srinivasan, R., & Nair, R. M. (2017). Mechanism of resistance in mungbean [*Vigna radiata* (L.) R. Wilczek var. radiata] to bruchids, *Callosobruchus* spp. (Coleoptera: Bruchidae). *Front. Plant Sci.*,

8, 1031. doi:10.3 389/fpls.2017.01031

- Wongwarat, T., Jomsangawong, A., & Phruetthitthep, C. (2023). Classification of powdery mildew resistance in mungbean (*Vigna radiata* (L.) Wilczek) using SSR markers. *Khon Kaen Agr. J.*, 445-451. Retrieved from <https://bit.ly/3C5inzM>
- Yan, W., & Hunt, L. A. (2002). *Biplot analysis of multi-environment trial data: quantitative genetics, genomics and plant breeding*. Wallingford UK: CABI Publishing.
- Zhang, Y., Xiao, Z., Ager, E., Kong, L., & Tan, L. (2021). Nutritional quality and health benefits of microgreens, a crop of modern agriculture. *J. Future Foods.*, 1(1), 58-66. doi:10.1016/j.jfutfo.2021.07.001