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RESEARCH ARTICLE

Integrative Breeding Assessment for Climate-Resilient Garden Pea: Harnessing Portable Genomics and Pheno-Plasticity

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ABSTRACT

Pea (*Pisum sativum*) is a globally significant legume crop cultivated for both human consumption and animal feed. Its adaptability to diverse environments, nutritional value, and genetic diversity make it a vital resource for food and nutritional security, particularly under the challenges posed by climate change. Pea crop growth is affected by climatic surroundings such as temperature, soil type, and moisture, with optimal germination occurring at 18–22 °C and best growth in slightly acidic soils. The crop faces threats from abiotic stresses like drought and heat, as well as biotic stresses such as pests and diseases. Breeding efforts focus on developing early maturing, high-yielding, and stress-resistant varieties, leveraging both morphological and molecular markers to enhance genetic diversity and accelerate selection. Advances in functional genomics and next-generation sequencing have facilitated the development of gene-based markers, enabling marker-assisted selection and high-resolution genetic maps. F1 hybrid seeds, produced by crossing pure lines, offer superior traits but require continuous maintenance and manual production, making them costly. The integration of genomic data and marker-assisted breeding holds promise for future improvements in pea productivity and resilience.

Key words: Gene pool, regional adaptation, molecular markers, hybrid development

INTRODUCTION

Peas are used both as a food source for humans and as animal feed. The garden pea (*Pisum sativum* var. sativum) is commonly consumed by people, either canned, dried, or fresh, while the field pea (*Pisum sativum* var. arvense) is mainly cultivated for animal feed, providing both biomass and flour (Rasskazova and Kirse-Ozolina, 2020; Sarri *et al*., 2024). Garden peas are annual crops cultivated globally during winter and early summer, depending on the region (Abdel-Hamid and Salem, 2021). Field peas, a winter season legume, are grown for animal and human nutrition and are valued for their protein, micronutrients such as B vitamins, vitamin A, folic acid, calcium, zinc, and iron, and complex carbohydrates. They are low in fat, with composition varying among cultivars (Asen *et al*., 2023; Do Carmo *et al*., 2020; Golovko *et al*., 2023; Rasskazova and Kirse-Ozolina, 2020; Wu *et al*., 2023). Field peas contain more tryptophan and lysine than cereals and many trypsin inhibitors (5–20%) than soy, making them a nutritious option (Golovko *et al*., 2023).

Many polyphenolics, specifically flavonoids, are also present in field pea, which contributes to its potential as a functional food or health product (Rasskazova and Kirse-Ozolina, 2020; Wu *et al*., 2023). Their protein content typically ranges from 21.3% to 32.9%, making them an important plant-based protein source. Starch is the main carbohydrate, accounting for 36.9–49.0% of seed dry weight, with resistant starch making up 2.1–6.3%, which supports dietary functionality and metabolic health. Soluble sugars (5.3–8.7%) affect taste and energy content. Dietary fiber ranges from 14% to 26%, mostly insoluble (10–15%), with soluble fiber between 2% and 9%. Starch quality is defined by an amylose content of 20.7–33.7%, important for processing, digestibility, and resistant starch formation. Lipid content is low (1.2–2.4%), and ash content (indicating minerals) is 2.3–3.4% (Table 1) (Dahl *et al*., 2012).

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Table 1: List of nutritional contents present in garden pea seeds with concentration in %.

Content	Concentrations (%)
Protein	21.3-32.9
Ash	2.3-3.4
Soluble sugar	5.3-8.7
Starch	36.9-49
Amylose	20.7-33.7
Resistant starch	2.1-6.3
Soluble fiber	2-9
Insoluble fiber	10-15
Dietary fiber	14-26
Lipids	1.2-2.4

Field peas benefited from crop rotations due to their nitrogen-fixing ability. Europe leads global production (30%), followed by North America (24%) and Asia (20%) (FAO, 2023), cultivated on about 7.0 million hectares worldwide (FAOSTAT, 2024). East Africa and West Asia are centers of origin have diversity, and the Mediterranean and South Asia are secondary centers (Semba *et al.*, 2021; Parihar *et al.*, 2022).

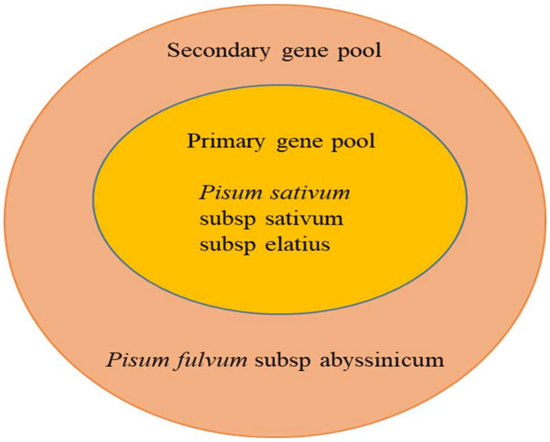

Fig. 1: Primary and secondary gene pools of the genus Pisum.

The genus Pisum mainly includes three species: *P. sativum* (with subspecies sativum, elatius), *P. fulvum*, and *P. abyssinicum*. The widely accepted classification by Maxted and Ambrose (2001) now includes Vavilovia formosa as a fourth species. The primary gene pool consists of *P. sativum* and wild *P. sativum* ssp. elatius; the secondary pool is *P. fulvum*; and the tertiary pool is Vavilovia formosa, the closest species to the Fabeae tribe, valued for breeding. Gepts and Papa (2003) introduced a quaternary gene pool, incorporating biotechnological advances like plant transformation and genomics, allowing access to genes from sexually incompatible wild species and synthetic sequences (Fig 1) (Suma *et al.*, 2025).

Gene banks hold extensive pea germplasm collections, reflecting diversity in biological status, geography, and phenotypic characters. The introgression of modern alleles by crossing various genetic possessions, such as newly introduced and locally adapted cultivars, boosts genetic diversity and trait preselection, crucial for meaningful phenotypic variation. Breeders and geneticists aim to improve pea's endurance to abiotic and biotic stresses, quality, and yield using genomics tools alongside traditional breeding (Abdel-Hamid and Salem, 2021). Pea was pivotal in early genetic studies, notably by Gregor Mendel in the 1850s (Smykal, 2014). Mendel selected Pisum sativum for its distinct heritable traits, rapid growth, and ability to self- or cross-pollinate. He analyzed seven traits, laying the foundation for genetics (Bateson, 1902; Weldon, 1902, Fisher, 1936). Modern plant breeding and genomics continue to build on Mendel's principles. The germplasm of pea consisted of 98,000 accessions globally, including landraces (38%), wild relatives (2%), breeding lines (13%), mutant stock (2%), and commercial varieties (34%) (Fig 2). Wild species accessions are minimal: *Pisum fulvum* (0.46%), Pisum. ssp. Elatius (0.42%), *Pisum sativum* ssp. sativum (1.2%), and *Pisum abyssinicum* (0.36%).

Table 2: List of genes/markers for given traits in the pea plant

Trait	Gene/Marker	Type	References
Pea seed borne mosaic virus resistance	sbm-1, GS185 (RFLP)	RFLP	(Timmerman-Vaughan *et al.*, 1993)
Bean yellow mosaic virus resistance	mo, Pgm-p (isozyme), P252 (RFLP)	Isozyme, RFLP	(Weeden *et al.*, 1984)
Ascochyta blight resistance	QTL Af& I (LG I); p227, p105 (RFLP LG IV); p236 (RFLP LG VI)	QTL, RFLP	(Dirlewanger *et al.*, 1994)
Fusarium wilt resistance	Fw, H19, Y14, Y15 (RAPD); p254, p248, p227, p10μ (RFLP)	RAPD, RFLP	(Dirlewanger *et al.*, 1994)
Powdery mildew resistance	er-1, p236 (RFLP), PD10650 (RAPD to SCAR)	RFLP, RAPD/SCAR	(Dirlewanger *et al.*, 1994)
Powdery mildew resistance	er-2	SCAR, 3 AFLP primers	(Tiwari *et al.*, 1998)
Powdery mildew resistance	er-1, Sc-OPO-181200, Sc-OPE-161600	SCAR	(Frew *et al.*, 2002)
Mycosphaerella pinodes resistance	mp, ccta2 (SSR), cccc1 (SSR), acct1 (SSR)	SSR	(Dita *et al.*, 2006)
Powdery mildew resistance	er1, er2, er3	MAS	(Ghafoor and McPhee, 2012)
Pea enation mosaic virus (PEMV) resistance	En	EST, MAS, RAPD, SSR, STS, TRAP	(Jain *et al.*, 2013)
Ascochyta blight resistance	abI-IV-2.1	SNP	(Jha *et al.*, 2017)
Mycosphaerella blight resistance	QTLs	SNP	(Gali *et al.*, 2018)
Ascochyta blight resistance	QTLs	SNP	(Carpenter *et al.*, 2018)
Fusarium root rot resistance	Fsp-Ps 2.1, Ps900203	SNP	(Coyne *et al.*, 2019)

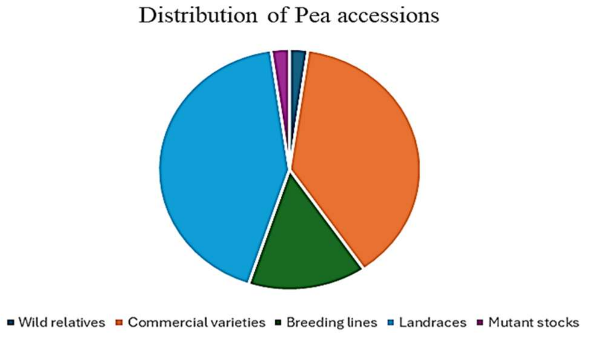

Fig. 2: Distribution of pea accessions among wild relatives, commercial varieties, breeding lines, landraces, and mutant stock.

Impact of Heavy Metal Pollution on Plant Growth and Use as Biomonitors

The escalating burden of ecological pollution factors, specifically poisonous metal ions in water, air, and soil, has been extensively documented over recent decades as a consequence of widespread and often uncontrolled human activities. These pollutants have been shown to exert severe environmental stress, adversely affecting the developmental stages and yield in crop plants, especially those that have significant nutritive value for humans and livestock (Lyanguzova, 1999; Mishra and Choudhuri, 1999). Tracheophytes, including legume crops, exhibit heightened sensitivity to heavy metals, often responding at minor levels that are needed to prompt effects in humans and animals. As a result, these plants are increasingly recognized as valuable indicators of environmental pollution and can serve as biomonitors to track and assess pollutant concentrations. It was demonstrated that Pisum sativum is among the plant species suitable for such biomonitoring purposes (Abdel-Hamid, 2000). Furthermore, it was reported that pea crops can be watered with yeast containing industrial bilge water, maintaining good germination, and growth performance, highlighting their resilience and potential utility in polluted environments (Aissani *et al*., 2019).

Optimal Environmental and Agronomic Conditions for Pea Cultivation

Pea cultivation is highly dependent on specific temperature and soil conditions to achieve optimal germination and growth. A temperature range of 18–22 °C is required for high germination rates, though peas can initiate germination at lower temperatures of 4–5 °C and exhibit moderate frost tolerance. However, germination percentages decline significantly when temperatures exceed 25 °C. Peas are flexible towards various types of soil but perform poorly in heavy clay soils. The most favorable growth is observed in soils pH ranges from 6.0 to 7.5, which are a little neutral to acidic. Prior to planting, the addition of organic matter or compost is recommended to enhance soil fertility, structure, and overall properties. Soil preparation depends upon the preceding plant and field types; if the previous crop provided substantial organic matter, the soil should be plowed twice in vertical directions, followed by two disking to achieve the desired structure.

Sowing methods vary according to environmental conditions and regional practices. In the Northern Hemisphere, double sowing (sprouting) is typically employed when planting occurs from late September to early October. Seeds are sown either manually or mechanically, with recommended row spacing (60cm) and plant spacing (25cm). Irrigation is maintained until the seed germinates and shoot emergence occurs. Alternatively, seeds can be planted in soils with adequate moisture, either from prior irrigation or rainfall, which facilitates germination without damaging the seed coat. In heavy soils, the hard seed coat can restrict aeration and nutrient absorption, potentially leading to yellowing and death of seedlings (Abdel-Hamid and Salem, 2021).

Climate Change and Its Impact on Field Pea Productivity

Climate change, marked by rising global temperatures and a heightened frequency of extreme weather events including erratic rainfall, heat waves, droughts, and floods represents a major threat to global agricultural productivity and food security (Vijai *et al*., 2023; Wu *et al*., 2023). The anticipated increase in the global population to over 10 billion within the next 50 years will intensify the demand for greater agricultural output, even as environmental conditions become increasingly challenging (Lam, 2025). India's field pea-growing regions are characterized by a broad range of edapho-climatic conditions (Das *et al*., 2019), complicating efforts to breed cultivars with wide adaptability (Biswas *et al*., 2021; Nadarajan and Gupta, 2010). Adverse climate effects on field pea productivity have been documented at national scales in countries such as Italy, Australia, Ethiopia, China, and Mediterranean climate regions (Sadras and Dreccer, 2015; Annicchiarico *et al*., 2017; Dreccer *et al*., 2018).

Research indicates that field pea productivity declines when the maximum ambient temperature during flowering exceeds 25°C (Sadras *et al*., 2013), highlighting its lower heat tolerance compared to other winter legumes such as chickpeas and lentils (Dreccer *et al*., 2018; Kumari *et al*., 2021). Elevated temperatures accelerate crop development, reducing the time available for resource utilization in grain formation and development (Iglesias-García *et al*., 2017; Sparks *et al*., 2005). In contrast, low temperatures can severely disrupt physiological processes and plant development. The "plasticity" and "stability" of crops and genotypes across diverse environments are critical for adaptation, with appropriate phenology serving as a key trait to minimize exposure to climatic stresses and maximize productivity in specific environments (Cotrina Cabello *et al*., 2023; Singhal *et al*., 2017). Eco-phenological models are essential tools for identifying crops and genotypes best suited to particular growing conditions (Fig 3) (Rötter *et al*., 2018).

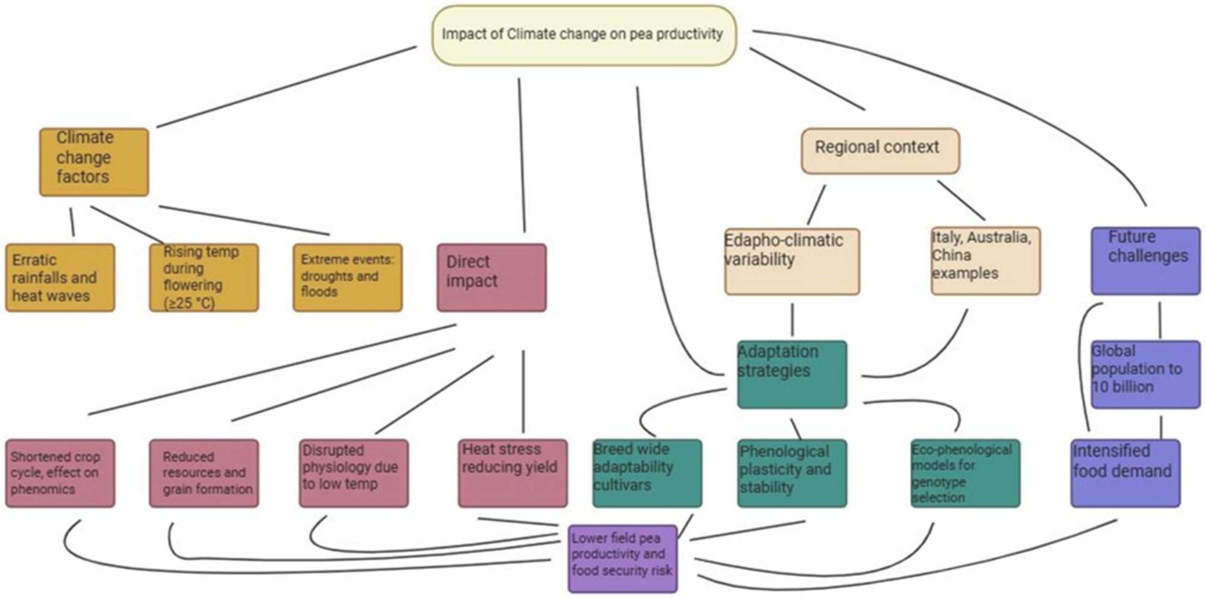

Fig. 3: Describe the impact of climate change in the regional context and extreme events like droughts, rainfall, heat waves, and low temperatures etc. on resource utilization and grain formation in pea plants.

Legume Vegetables and Their Role in Food Security

The bean vegetables, encompassing wild, orphan crops, and domesticated, from the Fabaceae family, are vital sources of essential amino acids, protein, and minerals, playing a crucial role in addressing nutrition and food security amid the challenges of changed climatic conditions (Laosatit *et al*., 2022; Priyadarsini *et al*., 2024). Amongst these, pea (*Pisum sativum* L. subsp. hortense) is a significant winter legume cultivated globally for its soft greenish seeds and pods. Peas are consumed in canned, processed, and fresh forms and are recognized as good sources of vitamin K, protein, vitamins, fiber, minerals, folic acid, and ascorbic acids (Rana *et al*., 2021; Sharma *et al*., 2020).

Cultivation, Yield, and Stress Challenges

Garden pea cultivation is feasible in cold, subtropical, and mild tropical zones. However, rising temperatures and other abiotic factors negatively impact both quality and yield, thus reducing crop productivity for growers. Additionally, biotic and abiotic stresses, including infestations by pea weevil and aphid, as well as diseases such as ascochyta blight and powdery mildew, cause substantial crop demises (Fikere *et al*., 2010; Teshome *et al*., 2014).

Breeding for Resilience and Genetic Diversity

The development of resistant and high-yielding cultivars under changing climate is a prerequisite for plant breeders to fulfill the food demand of the increasing population globally. Genetic diversity is a fundamental requirement to develop the desired traits in crop plants (Kiran *et al*., 2024). Exploring and utilizing the genetic diversity present in pea genotypes is essential to widen the basis of genetic and accelerate the breeding programs for high-yielding and climate-resistant varieties. The remarkable morphological and genetic diversity within pea germplasm offers valuable resources for successful breeding programs aimed at enhancing crop resilience and productivity.

Abiotic and Biotic Stresses in Vegetable Crops

Vegetable crops are subject to numerous biotic and abiotic stresses that adversely damage their development and productivity, particularly caused by climate change and global warming (Pandey *et al*., 2015). Abiotic stress factors such as salinity, heat, and drought, when acting together, are more detrimental to crop growth and production than any single stress factor acting alone during different vegetative stages (Mittler, 2006; Prasad *et al*., 2011). The abiotic stress also influences the prevalence and impact of weeds, insects, and pathogens (Ziska *et al*., 2010; Peters *et al*., 2014). Future projections suggest that pests may pose an even greater threat to crop production (Duveiller *et al*., 2007). Environmental stress conditions alter the organ functions and mechanisms of resistance in plants that directly affect pest-plant interactions (Scherm and Coakley, 2003). For example, there is competition between weeds and crops for water under drought conditions (Valerio *et al*., 2013).

Breeding Objectives and Pest Resistance in Pea

Early maturity and high productivity are key goals in pea breeding. Early ripening gives farmers a competitive advantage, often resulting in higher market prices at the start of the season. Pod characteristics like the size of pods and seeds are crucial quality traits that influence the market value of peas. Breeding programs focus on developing disease-resistant genotypes, targeting major diseases such as structural, pea-borne, and yellow mosaic virus, powdery mildew, and Fusarium wilt (Shubha *et al*., 2019). Additionally, breeding efforts aim to enhance resistance to pests, including leaf miners, weevils, and aphids. Frost sensitivity is another key concern, and breeding for frost resistance is an important goal to mitigate environmental stress. Peas are cultivated for various end uses, including freezing, canning, processing, and fresh consumption (Paul and Southgate, 1988; Hedley, 2001).

Morphological and Molecular Characterization in Pea Breeding

Characterization and identification of phenotypical characters are needed for recognizing superior germplasm and incorporating desirable traits from elite genotypes into breeding programs. Phenotypical characters encompass quantitative and qualitative parameters; nevertheless, reliance solely on phenotypical variation for estimating genetic variability among genotypes is limited due to its low polymorphism and high sensitivity to environmental influences (Voichita *et al*., 2011). As molecular markers are not affected by environmental factors, they can be used for the analysis of the diversity of germplasm. SSR markers are particularly valuable because of their co-dominant nature, high reproducibility, multi-allelic status, and extensive polymorphism (Singh and Singh, 2015). Earlier studies have also advocated SSR markers for assessing genetic variation in pea genotypes. Therefore, a collective approach utilizing both morphological and molecular markers enhances the estimation of complete variation within pea germplasm, facilitating the efficient use of markers in breeding programs (Taran *et al*., 2005 Nasiri *et al*., 2009).

Global Genetic Diversity and Marker-Assisted Selection

A substantial allelic variation in Pisum sativum has been identified in Asia and Africa, with numerous plant genetic resources maintained worldwide. These collections include wild and primitive varieties, disease-resistant cultivars, lines with breeding lines, structural mutations, and targeted genotypes (Zong *et al*., 2008). The identification of phenotypical and agronomic characters associated with resistance to abiotic and biotic stresses in cultivars increases the value of germplasm (Ghafoor *et al*., 2005; Ceyhan and Avci, 2015). The financial significance of pea populations is linked to phenotype, nutritional quality of seed, agronomic performance, and other characteristics. Effective use of native plant material demands comprehensive information about genotypic diversity relevant to economic traits (Singh *et al*., 2019). Morphological traits assist breeders in developing improved preservation techniques and maximizing the market-driven exploitation of pea germplasm. However, as these parameters are environmentally affected (Ceyhan and Avci, 2015), breeders require secure genetic markers for accurate germplasm characterization. Molecular markers, such as AFLP and RAPD, have been successfully used to estimate diversity in pea populations (Hanci, 2019). The identification of RAPD and AFLP markers linked to resistance against Fusarium wilt, which are appropriate for marker-assisted selection (MAS) in pea variety development programs. Molecular breeding merged with classical breeding to accelerate trait-focused selection that manifests late in crop ontogeny, such as resistance to diseases, lodging resistance, and seed characteristics. For example, the isozyme marker alcohol dehydrogenase (Adh1) has been associated with resistance to pea enation virus, while PCR markers derived from cDNA-AFLP fragments have been cultivated for defense against pea seed-borne mosaic virus and SSR markers for powdery mildew resistance (McClendon *et al*., 2002; Ambrose, 2008). Quantitative trait loci (QTLs) for resistance to lodging have also been stated, further supporting the application of molecular tools in pea improvement.

Genetic Linkage and Molecular Mapping in Pea

Vilmorin and Bateson, 1911 reported the genetic linkage in pea as a documented example for the first time, and Wellensiek, 1925 constructed the initial genetic map. During the 20th century, genetic-maps of pea were refined to include seven linkage groups (LGs), corresponding to the pea karyotype. These maps were further developed using RAPD and RFLP markers, as detailed in Table 2 (Aubert *et al*., 2006; Bordat *et al*., 2011). More recently, the accessibility of pea expressed sequence tag (EST) databases has enabled the formulation and alignment of abundant gene-derived markers throughout *Pisum sativum*. The innovation in next generation sequencing (NGS) technologies has facilitated the identification of a large number of single nucleotide polymorphism (SNP) sites (Zhernakov *et al*., 2017). The utilization of the SRAP (sequence-related amplified polymorphism) methodology for linkage mapping in *P. sativum* (Guindon *et a*l., 2016). Multiple studies (Jing *et al*., 2010; Ellis, 2011; Smykal *et al*., 2011) have positioned *P. abyssinicum* between *P. fulvum* and *P. sativum* ssp. elatius, with supplementary branches identified within planted pea, further enriching the understanding of pea genetic architecture.

Advances in Molecular Markers and Marker-Assisted Selection in Pea Breeding

Modern pea breeding efforts have accelerated over the last decade, with an increasing adoption of PCR-based markers to detect polymorphisms, thereby enabling the development of detailed molecular maps for various pea traits. Marker-assisted selection (MAS) allows breeders to combine favorable gene variants for desirable characteristics, enhancing the efficiency and precision of breeding efforts (Collard and Mackill, 2008; Bohra *et al*., 2014). Numerous pea linkage maps incorporating genetic marker sequences have been documented extensively (Ellis *et al*., 1992; Dirlewanger *et al*., 1994; Weeden *et al*., 1998), supporting the characterization of quantitative trait loci (QTLs) associated with seed mass and verdant seed pigmentation (Timmerman-Vaughan *et al*., 1997). A range of genetic marker types were utilized, including restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), sequence tagged sites (STS), and simple sequence repeats (SSR)(Sreedevi *et al*., 2009; Hanci, 2019).

Researchers have pinpointed DNA markers linked to recessive alleles that provide resistance against key pea pathogens, including seed-transmitted mosaic virus (PSbMV) strain P-1 and powdery mildew (Timmerman-Vaughan *et al*., 1993; Timmerman-Vaughan *et al*., 1994). The integration of advanced molecular markers and MAS, along with progress in omic technologies, holds significant promise for the development of improved pea cultivars (Vignesh *et al*., 2011). Advancements in high-throughput sequencing tools have intensified the momentum of pea genetic investigations. Although whole-genome sequencing of Pisum remains incomplete, transcriptome studies have provided valuable insights for creating nucleotide-based genetic markers and constructing ultra-precise genetic maps (Gali *et al*., 2019).

Functional Genomics and Marker Development in Pea

The discipline investigates genomic/transcriptomic features, with emphasis on transcribing genes, translating mRNA, controlling expression, and protein binding networks (Gibson and Muse, 2009; Pevsner, 2009). Next-generation sequencing (NGS) advancements have driven the creation and positioning of many gene-linked molecular markers in pea, alongside the discovery of extensive single nucleotide polymorphism (SNP) locations throughout the Pisum species, enabling precise genetic map assembly (Bordat *et al*., 2011; Tayeh *et al*., 2015; Yang *et al*., 2015; Boutet *et al*., 2016; Ma *et al*., 2017; Zhernakov *et al*., 2017). In *Pisum sativum*, expressed sequence tags (ESTs) offer valuable tools for gene discovery and marker development (Zhuang *et al*., 2013). High-throughput NGS technology rapidly optimizes SSRs derived from expressed sequences, vital for genomic-assisted breeding, linkage analysis, and alignment studies across *P. sativum* varieties.

Genomic Data Integration and Marker Databases

Extensive genetic and genomic data gathered for vital crops offers a stable foundation enabling marker-assisted selection (MAS) and genomics-assisted breeding (GAB) for better yields (Bohra *et al*., 2014). The effectiveness of genetic and genomic resources depends on the ability to integrate various types of data efficiently. Although several marker databases exist, many lack the capacity to provide large quantities of data in an accessible format. The Pea Marker Database (PMD) addresses this need by consolidating data on pea gene-based markers into a single, user-friendly database (Kulaeva *et al*., 2017; Tayeh *et al*., 2015). PMD includes 2 forms: PMD-1, containing approximately 2,484 DNA-based markers, their placement across chromosome linkage clusters, and corresponding transcript sequences; and PMD-2, an current adaptation with 15,944 pea genetic markers, offering advanced features and improved accessibility for marker development and gene mapping.

F1 Hybrid Seeds and Their Importance in Agriculture

F1 hybrid seeds are among the most expensive genotypes in agricultural markets and are produced by crossing two pure lines, resulting in offspring with superior traits. The hybridization process involves mutual fertilization, leading to genetic development and the manifestation of desirable characteristics. Developing a pure line through conventional breeding is a lengthy process, often taking 7–8 years, and may involve several previous crossings to establish the required traits before hybridization. The F1 hybrid is specifically created by crossing two pure lines to achieve targeted qualities (Sagar and Chandra, 1977; Singh *et al*., 2017).

Advantages and Challenges of Hybrid Breeding

Strict scientific breeding programs have enabled the enhancement of native plant qualities and the integration of new desirable traits into hybrids. F1 hybrids typically exhibit vigor, high yield, quality, and standardization, including tolerance for salt, drought, resistance to diseases, and early maturing. Uniform development in timing, structure, and bulk suits hybrids to mechanized reaping. However, maintaining pure lines for continuous F1 hybrid seed production is essential, as these lines must be preserved each year to ensure consistent hybrid seed supply. The production of hybrid seed is costly, primarily due to the annual manual labor required for hybridization and seed collection (Sagar and Chandra, 1977; Singh *et al*., 2017).

Economic and Genetic Implications

Hybrid seed production often involves manual cross-pollination to prevent self-pollination, ensuring that only the desired hybrid traits are expressed. Seeds are collected manually to maximize productivity. While growers benefit from the superior traits of hybrids, breeders also gain financial rewards, as only the original breeder possesses the pure lines needed to produce the hybrid. Seeds harvested from F1 hybrids do not retain the same characteristics in subsequent generations, with yield typically decreasing by at least 50% in the F2 generation. Therefore, Exclusively through pure-line hybridization can the original hybrid variety be recreated, safeguarding the breeder's investment and intellectual property (Sagar and Chandra, 1977; Singh *et al*., 2017).

Conclusion

Pea remains a cornerstone of global agriculture, valued for its nutritional benefits and adaptability.

Continuous efforts in breeding, supported by advances in genomics and molecular marker technology, are essential for addressing the challenges posed by climate change, pests, and diseases. The use of F1 hybrids, combined with robust genetic and genomic resources, enables the development of high-yielding, resilient pea varieties. Maintaining and expanding genetic diversity, along with the integration of modern breeding techniques, will be crucial for ensuring sustainable pea production and food security in the coming decades.

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