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# Yield Adaptability and Stability in Field Pea Genotypes Using AMMI, GGE, and GYT Biplot Analyses

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**Abstract:** Pea (*Pisum sativum* L.) is a vital leguminous crop farmed worldwide. Pea plays an essential role in China's crop rotation system, but the major restrictions to its cultivation are stability and low yield. Breeding for promising cultivars with a significantly high yield will impact the sustainability of pea production. Additionally, diverse environment trials are crucial in determining the best genotype. The new cultivar "Yunwan 52" was developed by hybridization and subsequently evaluated through yield trials among six pea genotypes across 14 environments during the 2016–2018 growing seasons. The results showed that the average yield of "Yunwan 52" for all tested environments was 2.64 t ha$^{-1}$ compared to the control cultivar (Yunwan 18, 1.83 t ha$^{-1}$). Analysis of AMMI variance showed significant differences ($p < 0.01$) between genotypes, environments, and their interaction. Based on the GGE biplot, some genotypes possessed wide and narrow adaptability to environments, such as Yunwan 52 was considered the most stable and ideal gen-otype across all tested environments. GYT biplot analysis also revealed that this realized cultivar was a superior and stable genotype that can be identified visually by combining all characters in breeding programs. Yunwan 52 distinguishes with purple blossoms and seed coat peas. It is possible to infer that the newly released cultivar "Yunwan 52" has outstanding yield performance and wide adaptability to multiple environmental conditions (resilience to abiotic stress). It will contribute to developing nutritional pea genotypes and increase pea production in irrigated areas.

**Keywords:** pea; G × E interaction; stability; AMMI; GGE biplot; GYT biplot; seed yield; abiotic stress

**Citation:** Yang, X.; Soliman, A.A.; Hu, C.; Yang, F.; Lv, M.; Yu, H.; Wang, Y.; Zheng, A.; Dai, Z.; Li, Q.; et al. Yield Adaptability and Stability in Field Pea Genotypes Using AMMI, GGE, and GYT Biplot Analyses. *Agriculture* **2023**, *13*, 1962. https://doi.org/10.3390/agriculture13101962

Academic Editors:
Evangelia Stavridou,
Panagiotis Madesis and
Irini Nianiou-Obeidat

Received: 4 September 2023
Revised: 1 October 2023
Accepted: 2 October 2023
Published: 8 October 2023

## 1. Introduction

Pea (*Pisum sativum* L.) is one of the prevalent cool-season legumes farmed worldwide and originated in Western Asia and Mediterranean coastal regions. Pea has been domesticated and cultivated for over 6000 years [1]. Moreover, its classification is the fourth most important among legume crops [2]. It plays a vital role in soil amelioration, crop rotation, crop structure adjustment, and sustainable agricultural development based on its wide adaptability and high nitrogen fixation ability, according to Macwilliam et al. [3] and Smykal et al. [4]. Many studies have shown that the pea is rich in nutrients such as protein, amino acid, vitamin, and mineral elements. These rich nutrition compounds in pea are easy to digest and absorb, making them a super an excellent food, vegetable, and feed crop, reported by Cui et al. [5] and Wang et al. [6]. China plays a vital role in the world's pea production and is considered the world's largest producer. The harvested area and production in 2020 were 2.3 million ha and 12.7 million tons, respectively [7]. More importantly, the National Crop Gene Bank of China (NCGC) preserved over 7000 pea germplasm resources, and over 70% of them are unique to China [8]. In the last four years, the pea varieties reached 242 in China, and "Yunnan province" produced 72 varieties of them (National Bureau of Statistics (NBS): https://www.stats.gov.cn/, accessed on 19 September 2023).

"Yunnan" province is located down the latitude plateau and has different environmental conditions suitable for pea growth and production. Thus, winter and semi-winter types of pea varieties are widely planted. As one of the leading pea-producing areas in China, the harvested area in the "Yunnan" province reached 300,000 ha, representing 13.4% of China's total production, followed by Sichuan, Gansu, and Hebei provinces [9]. In recent years, farmers' demand for new varieties of peas has increased due to the use of palatable foods, and the peas crop is distinguished by its short growing periods and managed efficiently [10]. Climate change effects (abiotic stress) are one of the most common problems that face pea production and seriously affect its production efficiency, followed by biotic stress (foliar diseases). Thus, climate change, such as global warming, is one of the most important obstacles that pea production is facing for planting legume crops, as reported by Bénézit et al. [11] Xiao et al. [12] Cernay et al. [13] Ghafoor and Mcphee [14]. Therefore, one of the techniques to stimulate the pea's expansion and production is breeding pea cultivars suitable for different needs and environments. The new breeding skills improved through the last period, providing world pea production opportunities.

The pea genotypes with purple pigment, e.g., purple flowers, pods, and seed coats, had been proven to contain more anthocyanin and flavones [15], which benefitted human health greatly [16]. The pea cultivar represented by purple or red can be used as potted flowers, flower beds, and leisure agriculture theme parks in landscape architecture [17]. Few studies on purple peas have been reported in China, and fewer pea varieties with purple flowers, purple pods, or purple seed coats have been bred, so the exploration and utilization of the purple pea germplasm need to be explored further.

For a long time, the main objectives of pea breeding focused on improving root rot and powdery mildew control, according to Fondevilla and Rubiales [18] and Zhukov et al. [19]. Enhancing pea cultivars with improved yield and quality features is necessary due to the economic strength of the pea. The ultimate goal of plant breeders is to develop novel commercial cultivars that can effectively acclimatize to a vast array of environmental circumstances. There is a need to enhance the genotypes' stability and yield by using multiple genotypes under different environmental situations to tolerate abiotic stress [20,21]. The grain yield of each genotype is consistently influenced by genotypes (G), environment (E), and their interaction (GEI) [22,23]. Comprehending GEI characteristics, especially locations, is essential in plant breeding efforts because a substantial GEI might control the ability to identify and choose superior genotypes effectively if compared to introducing new crops and strategies for developing the cultivars [7,24]. Pattern analysis is one of the statistical techniques recently drawn attention, in addition to the combined analysis of variance, which measures and identifies the effectiveness [25,26]. For example, the Additive Main Effects and Multiplicative Interaction (AMMI model) explains the GEI in several conditions, as reported by Scavo et al. [27] through using the variance analysis and the Interaction Principal Components (IPCA) as similarly identified by Kilic [28], Mohammadi et al. [29] and Yan [30].

The interaction degree between G and E can be analyzed using graphical stability methods (GGE biplot), which also help define stable and high-yield genotypes in various conditions. GGE biplot (the main genotypic effect plus GE interaction) methodology attracted the attention of plant breeders for analyzing data at multi-environment trials. Therefore, as a result, this research method is suitable for the final part of a breeding program, which is completed by cultivar release, allowing the identification of the highest yields in varied conditions. It uses a graphical presentation of the interaction estimates GGE using the biplot technique, according to Yan and Kang [23] and Akinwale et al. [31], for genotype selection utilizing multiple environments evaluation, such as the "which-won-where" pattern, mean performance, and genotypes stability, ability to discriminate and environment's representativeness (ideal genotype, as well as mega environments) [32].

The genotype by yield*trait biplot (GYT) was designed by Yan and Frégeau-Reid [33] to supply valuable information for evaluating genotypes on several characters. It is determined by the breeder's use of a graphical method to select and rank genotypes, which displays character forms based on general gains over yield by trait combinations, based on findings by Elfanah et al. [34] and Mohammadi [35]. This model of GYT calculates by multiplication of the mean genotype of the seed yield by other traits if the highest value is desired and divided if the lowest value is desired. So, the key and essential trait is yield, and additional characteristics become important when combined with a high yield.

This study aimed to (1) produce new promising pea cultivars with high yield potential, good quality (purple blossoms and seed coat peas), wide adaptability to a broad range of abiotic stress, and improve crop productivity in the irrigation area; (2) estimate GEI and identify the new cultivar with stable and higher yield; (3) determine the discerning ability of the environments; (4) using a genotype by yield*trait (GYT) biplot to detect which traits are related to seed yield; and (5) Evaluate the relationship between environments.

## 2. Materials and Methods

### 2.1. Plant Materials

The pea cultivar "Yunwan 52" was created by hybridization between "Yunwan 1" as a female parent and "L2157" as a male parent. "Yunwan 1" was developed by the Food Crops Research Institute of Yunnan Academy of Agricultural Sciences in 2009. This variety was registered under the variety right No.: CAN 20080356.5 in 2015 to be China's first released pea variety for protection authorization. It distinguished of a white flower (Figure 1a), shallow green seed coat, green cotyledon, oval-elongated seed shape (Figure 1b), erect plant and without tendrils (Figure 1c), in addition to a little cellulose in its soft leaflets which gives it good edible quality [36]. The leaf color and shade of anthocyanin pigment at the axil of "Yunwan 1" are green and without anthocyanin pigment, respectively.

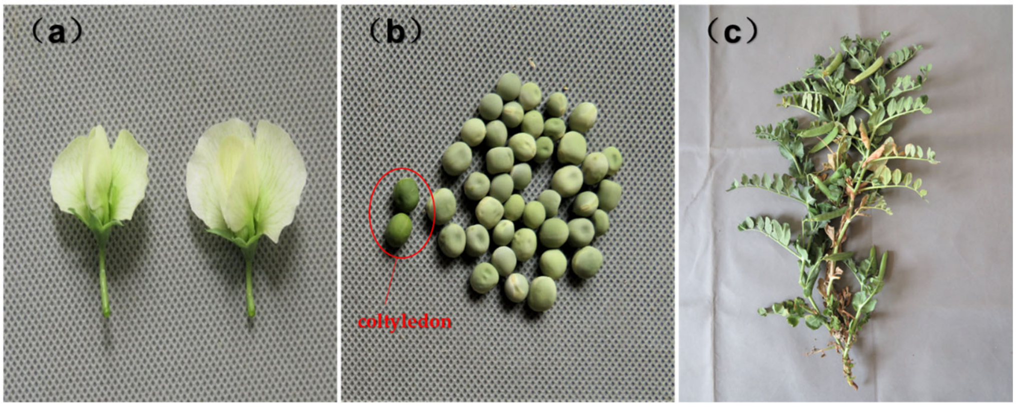

**Figure 1.** The agronomic traits of the female parent "Yunwan 1" (white flower (**a**), green seed coat, and green cotyledon (**b**), erect plant and without tendrils (**c**)).

The "L2157", which was introduced in Australia in 2004, has grown for four consecutive years of adaptability identification tests. It is a stable genotype with purple flowers and seed coat, orange cotyledon, irregular seed shape (Figure 2a,b), semi-erect plant, and whole tendrils (Figure 2c). The leaf color and shade of anthocyanin pigment at the axil of L2157 are green and with rich anthocyanin pigment, respectively.

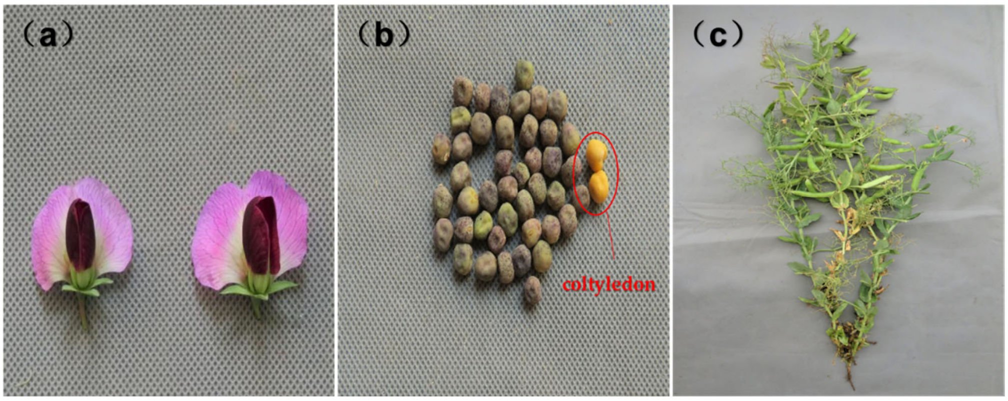

**Figure 2.** The agronomic traits of the male parent "L2157" (purple flowers and seed coat, orange cotyledon (**a**,**b**), semi-erect plant, and whole tendrils (**c**)).

### 2.2. Breeding Process

In October 2008, the "Yunwan 1" and "L2157" genotypes were sown in a field that was isolated under a free insect cage at the Modern Agricultural Scientific Research and Demonstration base in Songming (25°21′14″ N, 103°6′44″ E; 1910 m altitude), which the Yunnan Academy of Agricultural Sciences operates. Artificial hybridization was performed at the initial flowering stage of the parents in January 2009. The operation method was as follows: these not-yet-open flowers from the female parent were chosen, and we performed artificial removal of the stamens to ensure that the pollen did not spread on their stigmas. Then, the pollen was collected from the male parent, artificially pollinated those flowers, and removed stamens within 2 h. The hybrid material was numbered W09(84), labeled (traditional breeding method), and the hybrid seeds were harvested in April 2009.

From 2009 to 2011, the F1-F2 generations identification and pedigree method were carried out in the selective nursery test. In 2011–2014, the superior and stable lines were selected and numbered as W09(84)-1 from F3-F5 generations, then the lines comparison and resistance identification test in addition to the multi-site experiments were carried out from 2014–2016 and 2016–2018, respectively (Figure 3). The "Yunwan 52" was examined and approved for registering as a non-major crop variety with the GPD Pea (2021) 530032 registration number.

### 2.3. Multi-Site Experiments

Field experiments were conducted in the 2016–2017 and 2017–2018 growing seasons at seven locations (14 environments), including Baoshan, Songming, Lijiang, Qujing, Yaoan, Yuxi, and Zhaotong. These locations are mainly pea production areas and cover or are distributed in the whole Yunnan province. Additionally, the site altitude ranges from 1650 to 2363 m above sea level (Figure 4), showing differences in the environmental conditions. To describe the locations, geographical and soil characteristics are shown in Table 1. The locations' differences characterize the environments under study; maximum air temperatures ranged from around 20 °C in Lijiang to 25 °C in Baoshan and Yuxi sites in the studied growing season. On the contrary, the minimum temperature averaged around −0.05 °C for Zhaotong to 5 °C in Boshan and Yuxi. In addition to the differences among locations of total precipitation i.e., the Lijiang site recorded the lowest rainfall (0.26 and 0.19 mm, respectively) in the 2016–2017 and 2017–2018 seasons. Meanwhile, Baoshan and Songming sites recorded 0.5 mm in the 2016–2017 season. Besides, soil textures differ from loam soil with a high capacity to retain water to sandy loam soil with a water deficit capacity (e.g., abiotic stress).

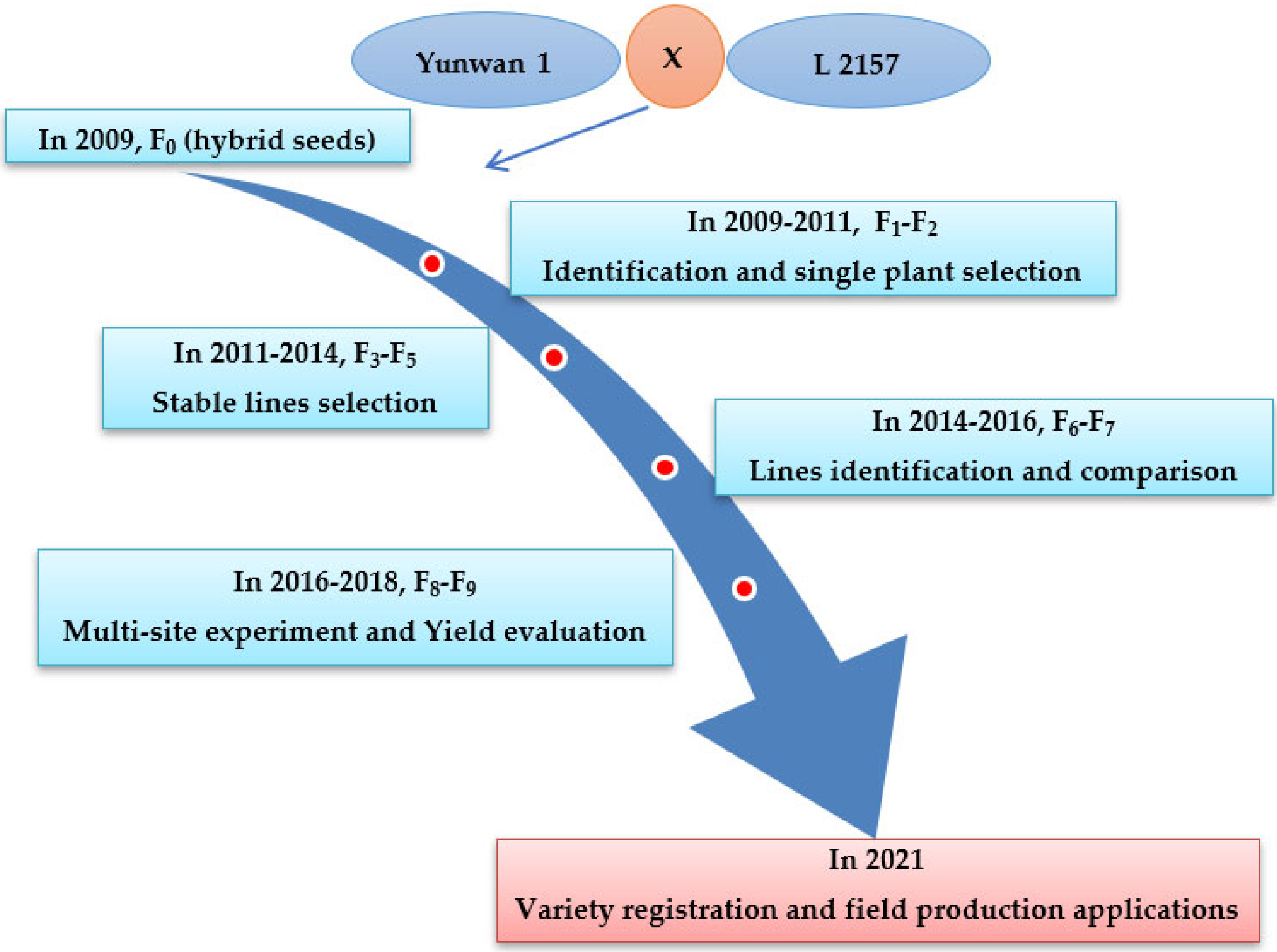

**Figure 3.** Breeding process of the "Yunwan 52".

During October, in both seasons, six pea genotypes consisting of Yunwan 52 (the released cultivar), Baofeng 2, Yuwan 1, Yunwan 50, Yunwan 51, and Yunwan 18 (as a check cultivar) were grown in a local crop management practice and harvested on April of the following year. In each experiment, the plot sizes were 20.0 $m^2$, including 18 rows. The spacing between rows was 30 cm and 10 cm among plants, arranged in a randomized complete block design in three replications. Data were collected as an average of ten individual guarded plants chosen randomly from each plot. The studied characters (at harvest time) included plant height (PH, cm), which can be measured from the soil surface to the longest stem in the plant, no. of primary branches (NPB) on the main stem, seeds/plant (SP), and seeded pods/plant (SPP) which can be observed and counted by visual observation. Furthermore, pods length (PL, cm) using vernier digital caliper, 100-seed weight (SW, g), and seed yield (t $ha^{-1}$) transformed from the yield in plot size 20.0 $m^2$ to t $ha^{-1}$ were also evaluated.

**Table 1.** Geographic coordinates, agro-climatic conditions, soil characteristics for each field site, and fertilizing amount for the field pea growing season.

| Trials Sites | Latitude (N) | Longitude (E) | Air Temperature (°C) | | | | Total Precipitation (mm) | | Soil Texture | Previous Crop |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | 2016–2017 | | 2017–2018 | | 2016–2017 | 2017–2018 | | |
| | | | Min | Max | Min | Max | | | | |
| Baoshan | 25°10′43″ | 99°12′16″ | 5.61 | 24.97 | 5.82 | 25.07 | 0.55 | 0.27 | Sandy Loam | Maize |
| Songming | 25°21′14″ | 103°6′44″ | 4.21 | 23.04 | 1.60 | 23.16 | 0.52 | 0.39 | Red Loam | Rice |

**Table 1.** *Cont.*

| Trials Sites | Latitude (N) | Longitude (E) | Air Temperature (°C) |  |  |  | Total Precipitation (mm) |  | Soil Texture | Previous Crop |
|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  | 2016–2017 |  | 2017–2018 |  | 2016–2017 | 2017–2018 |  |  |
|  |  |  | Min | Max | Min | Max |  |  |  |  |
| Lijiang | 26°48′13″ | 100°57′16″ | 2.21 | 20.99 | 1.41 | 20.83 | 0.26 | 0.19 | Sandy Loam | Maize |
| Qujing | 25°55′24″ | 103°86′14″ | 3.09 | 23.68 | 0.98 | 23.77 | 0.48 | 0.48 | Red Loam | Maize |
| Yaoan | 25°31′13″ | 101°13′27″ | 3.94 | 23.87 | 3.32 | 24.21 | 0.31 | 0.23 | Loam | Maize |
| Yuxi | 24°16′52″ | 102°29′50″ | 7.00 | 24.62 | 4.87 | 25.09 | 0.38 | 0.27 | Loam | Maize |
| Zhaotong | 27°40′15″ | 103°45′24″ | −0.03 | 22.19 | −0.09 | 21.97 | 0.43 | 0.48 | Loam | Chili |
| Fertilizer amount; 450 kg $ha^{-1}$ of calcium superphosphate and 225 kg $ha^{-1}$ of potassium sulfate |  |  |  |  |  |  |  |  |  |  |

Copernicus Climate Change Service (C3S) (2017): ERA5: Fifth generation of ECMWF atmospheric reanalyses of the global climate. Copernicus Climate Change Service Climate Data Store (CDS), (date of access), https://cds.climate.copernicus.eu/cdsapp#!/home, accessed on 1 January 2020.

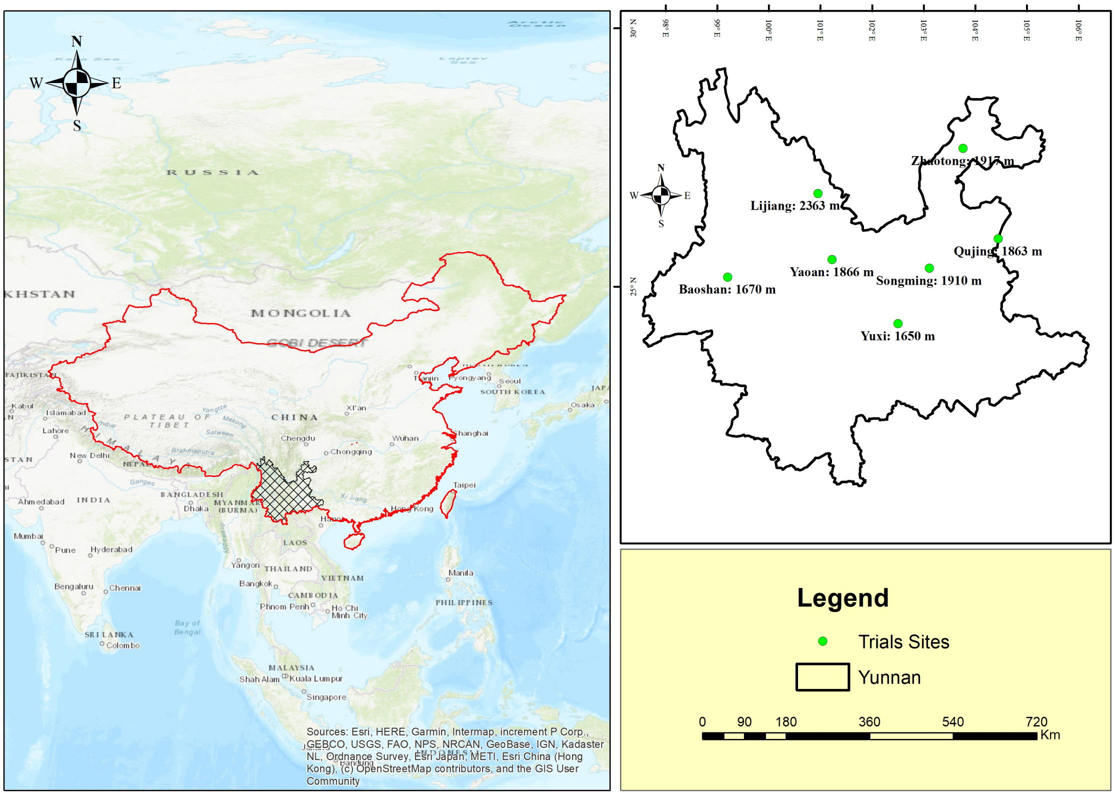

**Figure 4.** Maps over the study area and green dots refer to trial sites with the altitude of the growing field pea.

### 2.4. Statistical Analysis

The collected data were subjected to analysis of variance (ANOVA) for each season and location separately. A combined analysis of variance was performed after verifying the homogeneity of error mean squares across seasons by Levene's test [37]. Each location × season combination was utilized as an environment, giving 14 environments. RCBDs analysis of variance was first computed for each environment to assess differences between genotypes. In addition, the coefficient of variation (CV%) was calculated for each environment. Then, analysis of variance for the AMMI model was carried out to estimate the main effects of the six genotypes and the 14 environments and their interaction and dividing the genotypes by environment interaction to principal component analysis, e.g., IPCA 1 and IPCA 2.

The main genotypic effect plus genotype by environment interaction (GGE biplot) graphical analysis of seed yield for six pea genotypes across fourteen environments proposed by Yan et al. [38,39] was computed. The data visualization to represent the winner and superior genotypes in the figure, such as which-won-where and mega environment, mean performance vs. stability (the genotype rank), and ideal genotypes and environments.

The genotype by yield*trait (GYT) biplots based on seed yield and other trait combinations data was computed according to Yan and Frégeau-Reid [33]. The 19th Edition of the GenStat (VSN International Ltd., Hemel Hempstead, UK) was used to analyze all subjected data, i.e., AMMI, GGE, and GYT biplots. Furthermore, before the data analysis, the trait combinations data of GYT were normalized to convert them into unitless trait values as follows:

$$Yij = \frac{\left(Tij - \overline{T}j\right)}{Sj} \tag{1}$$

where $Yij$ value of standardized genotype $i$ for yield-trait combination $j$, $Tij$ is the original value of genotype $i$ for yield-trait combination $j$, $\overline{T}j$ genotype mean $i$ for yield-trait combination $j$, and $Sj$ is the standard deviation for yield-trait combination $j$, according to the GenStat 19th edition.

## 3. Results

The new pea variety "Yunwan 52" was released by hybridization, followed by the pedigree breeding method after nine generations (between 2009 and 2018). The new cultivar, "Yunwan 52", exhibited purple flowers and seed coat, green cotyledon, irregular seed shape (Figure 5a,b), green leaf with clear anthocyanin pigment at the axil, erect plant and semi-tendrils (Figure 5c) that were synthesized with the characteristics of the "Yunwan 1" and "L2157".

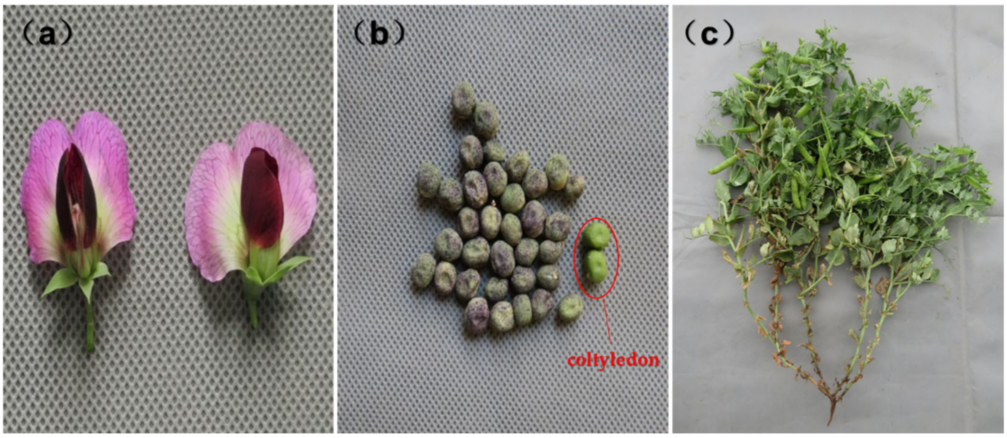

**Figure 5.** The agronomic traits of the "Yunwan 52" (purple flowers and seed coat, green cotyledon, irregular seed shape (**a**,**b**), erect plant and semi-tendrils (**c**)).

### 3.1. Mean Performance

The mean performance for seed yield of six pea genotypes in fourteen environments (seven location*two years) and Coefficient of Variation (CV%) are presented in Table 2, where mean comparisons for these traits were made according to the least significant difference (LSD) test at $p \leq 0.01$.

The presented data showed that the mean seed yield of six genotypes ranged from (2.64 a) to (1.83 d) t ha$^{-1}$ with an environmental average of 2.13 t ha$^{-1}$. Moreover, the highest average seed yield was (2.64 a) t ha$^{-1}$ for the genotype Yunwan 52, which is epistasis in most of the environment and exhibited 43.92% yield advantage compared with the control (the genotype Yunwan 18) recorded (1.83 d) t ha$^{-1}$.

Among the fourteen environments (seven locations * two years), the environmental mean ranged from (3.34 a) t ha$^{-1}$ in E13 to (0.78 h) t ha$^{-1}$ in E4. Moreover, the highest average seed yield was in E13 (Yuxi 2018), whereas the lowest value was in E4 (Songming 2017).

**Table 2.** Mean performance for seed yield (ton $ha^{-1}$) of six field pea genotypes under fourteen environments.

| | **E1** | **E2** | **E3** | **E4** | **E5** | **E6** | **E7** | **E8** | **E9** | **E10** | **E11** | **E12** | **E13** | **E14** | **G. Mean** | **Check (%)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Yunwan 52 | 2.03 b * | 2.62 a | 2.71 a | 1.27 a | 2.57 a | 2.63 ab | 1.86 a | 2.21 b | 3.19 a | 2.38 ab | 3.72 a | 2.79 ab | 3.68 a | 3.26 b | 2.64 a | 43.92 |
| Baofeng 2 | 2.36 a | 2.08 ab | 2.24 ab | 0.20 c | 2.02 ab | 1.85 b | 1.67 abc | 2.99 a | 1.64 b | 2.23 abc | 0.28 d | 3.22 a | 3.38 ab | 3.96 a | 2.15 b | 17.24 |
| Yuwan 1 | 1.43 d | 1.98 ab | 2.53 ab | 1.22 a | 1.44 b | 2.71 a | 1.76 ab | 2.41 b | 1.45 b | 2.47 a | 1.61 bc | 1.61 d | 3.48 a | 3.10 bc | 2.09 bc | 13.75 |
| Yunwan 50 | 1.52 cd | 1.71 b | 2.06 b | 0.56 b | 2.72 a | 2.45 ab | 1.34 bc | 2.39 b | 0.94 c | 2.17 bc | 1.81 b | 3.07 a | 3.28 ab | 2.66 cd | 2.05 bc | 11.73 |
| Yunwan 51 | 1.08 e | 2.04 ab | 2.57 ab | 0.67 b | 1.94 ab | 2.58 ab | 1.28 c | 3.18 a | 1.68 b | 2.09 c | 1.36 c | 1.95 cd | 3.35 ab | 2.26 d | 2.00 c | 9.27 |
| Yunwan 18 | 1.76 c | 1.98 ab | 2.44 ab | 0.74 b | 1.99 ab | 1.97 ab | 1.53 abc | 2.17 b | 1.70 b | 2.31 abc | 0.29 d | 2.41 bc | 2.88 b | 1.51 e | 1.83 d | 00 |
| Env. Mean | 1.70 fg | 2.07 e | 2.42 cd | 0.78 h | 2.11 e | 2.37 cd | 1.57 fg | 2.56 c | 1.77 f | 2.27 de | 1.51 g | 2.51 c | 3.34 a | 2.79 b | 2.13 | |
| CV% | 5.9 | 15.5 | 9.9 | 12.2 | 15.1 | 13.4 | 10.7 | 7.5 | 8.2 | 4.5 | 8.1 | 8.4 | 6.2 | 8.3 | 10 | |

* There is no discernible difference between the mean values for each attribute in the same column with the same lowercase letter; CV, Coefficient of Variation; Env. Mean, Environmental mean; G. mean, Genotype mean; E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

### *3.2. AMMI Analyses of Variance*

Combining the AMMI model's analysis of variation for seed yield across six pea genotypes and fourteen environments is presented in Table 3. Data revealed that there is a significance ($p < 0.01$) between genotype (G), environments (E), and the interaction between them (GEI). The proportion of main effects in genotype, environment, and interaction accounted for 9.20%, 55.48%, and 30.57, respectively, of the total variation of the treatments, indicating that the assorted and high differences among environments caused most of the variation in seed yield.

**Table 3.** Analyses of variance for AMMI model for yield (t ha$^{-1}$) of six pea genotypes across fourteen environments.

| Source | d.f. | S.S. | M.S. | Explained SS % |
|---|---|---|---|---|
| Total | 251 | 169.64 | 0.676 | |
| Genotypes (G) | 5 | 15.61 | 3.121 ** | 9.20 |
| Environments (E) | 13 | 94.12 | 7.24 ** | 55.48 |
| Interactions (GE) | 65 | 51.86 | 0.798 ** | 30.57 |
| IPCA 1 | 17 | 23.8 | 1.4 ** | 45.89 |
| IPCA 2 | 15 | 11.24 | 0.75 ** | 21.67 |
| Residuals | 33 | 16.82 | 0.51 ** | 32.43 |
| Error | 140 | 6.33 | 0.045 | |

** significant at 0.05 and 0.01, respectively.

The AMMI model clearly showed the presence of the GEI when separated between the first two interaction principal component axes (IPCA) as they were significant in predictive assessment. The IPCA1 and IPCA2 recorded 45.89 and 21.67 total GEI variation, respectively, and significant ($p < 0.01$) differences in all variation sources. Using the first two PCAs, we could clarify the maximum interaction of GE reported by Biswas et al. [40], Fikere et al. [41], and Verma et al. [42].

### *3.3. GGE-Biplot Analysis for Seed Yield*

#### 3.3.1. GGE biplot analysis "Which-Won-Where"

GGE biplot of "Which-Won-Where" for seed yield (t ha$^{-1}$) of six genotypes across fourteen environments is located in Figure 6. "Which-Won-Where" exposed the identification of higher genotypes and respective environments for planting such genotypes. The results clarify that PC1 and PC2 recorded 51.09% and 22.92% of the total variation (74.01%) of seed yield, respectively. The identification of mega-environments achieved by separating the scatter plot into parts. The winner's genotypes are located on the peaks of the polygon, starting from the origin and extending toward the outer edges. Accordingly, fourteen environments fell into two sectors (Mega Environment), i.e., Baoshan (E1 and E8), Yaoan (E12), and Zhaotong (E14) fell into one Mega Environment (ME1). Whereas all the other ten environments fell into another sector, ME2 involves Lijiang (E2 and E9), Qujing (E3 and E10), Songming (E4 and E11), Yoan (E5), Yuxi (E6 and E13), and Zhaotong (E7). The genotypes sited on the peaks of the polygon are the most responsive; subsequently, the genotype Baofeng 2 was the winner in ME1, and Yunwan 52 considered the winner in ME2, which contains ten environments. So, the ideal and best genotype is Yunwan 52, which exhibited the highest seed yield among the ten environments within the specified sector.

#### 3.3.2. "Vector" View of GGE Biplot of the Environment

Estimating the environment's pattern by the "Vector" view of the environment's GGE biplot is presented in Figure 7. The environments E1, E12, and E14 have an acute angle (<90°) (positively correlated). On the contrary, environments E8 and E6 have an obtuse angle (negatively correlated).

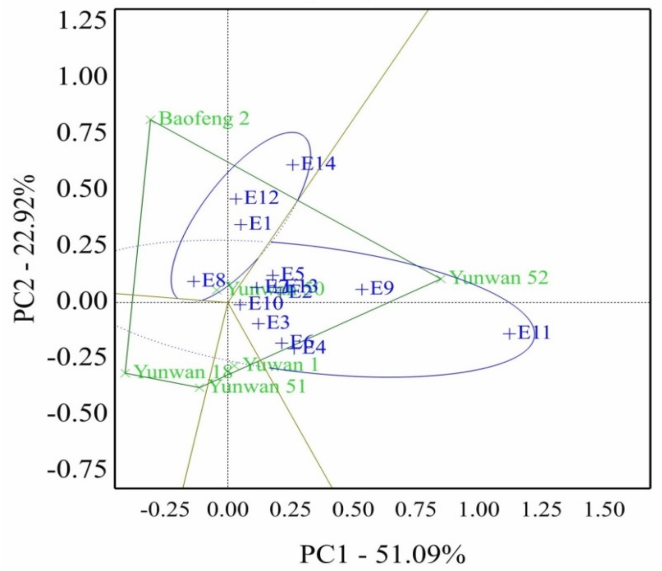

**Figure 6.** GGE biplot of Which-Won-Where" pattern for seed yield (t ha$^{-1}$) of six pea genotypes across fourteen environments. E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

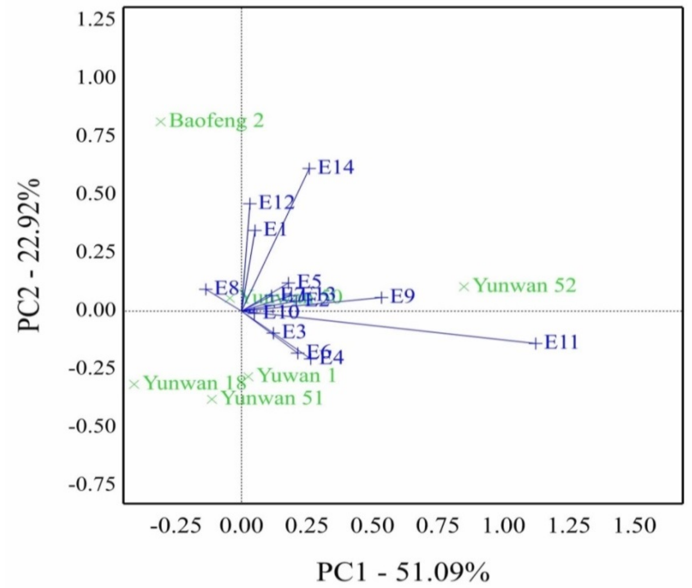

**Figure 7.** GGE biplot of Vector view for the environment for seed yield (t ha$^{-1}$) of six pea genotypes across fourteen environments. E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

### 3.3.3. GGE Biplot Mean Performance and Stability of Genotypes (Mean vs. Stability)

The average environment coordination (AEC) method evaluated the mean vs. stability according to Yan et al. [43], Yan and Hunt [44], and Yan and Rajcan [45]. An average environment in this method is definite by the PC1 and PC2 average scores of all fourteen environments, symbolized by a small circle (Figure 8). The genotype Yunwan 52 recorded a high yield and shorter projections, and Baofeng 2 showed a more extended projection onto the AEA ordinate.

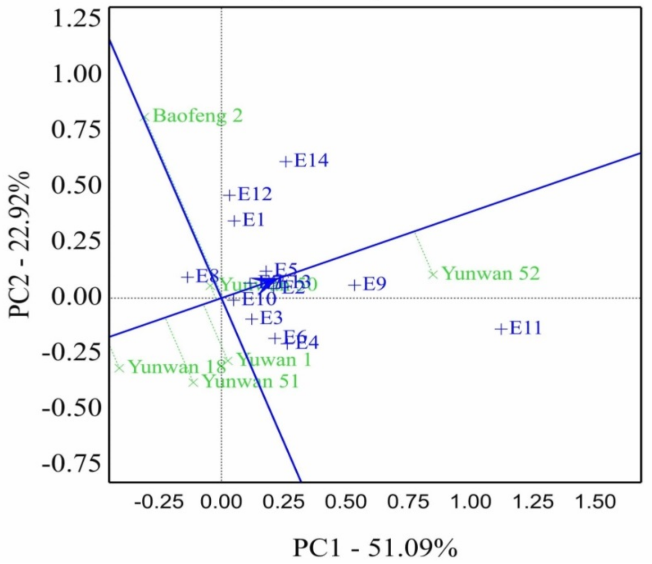

**Figure 8.** GGE biplot, mean performance vs. stability for seed yield (t $ha^{-1}$) of six pea genotypes across an average environment. E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

### 3.3.4. GGE Biplot, Ideal Genotypes for Seed Yield (t $ha^{-1}$)

The best genotype should be stable and have the highest mean performance (best performance in all environments). It can be characterized by having a high vector length, which indicates high-yielding genotypes, and showing zero genotype-environment interaction (GEI), as illustrated by an arrow pointing towards it (Figure 9). Figure 9 shows that the Yunwan 52 genotype has superior higher yielding ability and stability characteristics than other genotypes. Moreover, any genotypes from the next to the last concentric circle may be desirable to undesirable (Yunwan 18) genotypes. Plant breeding programs aim to select superior genotypes in target environments [46].

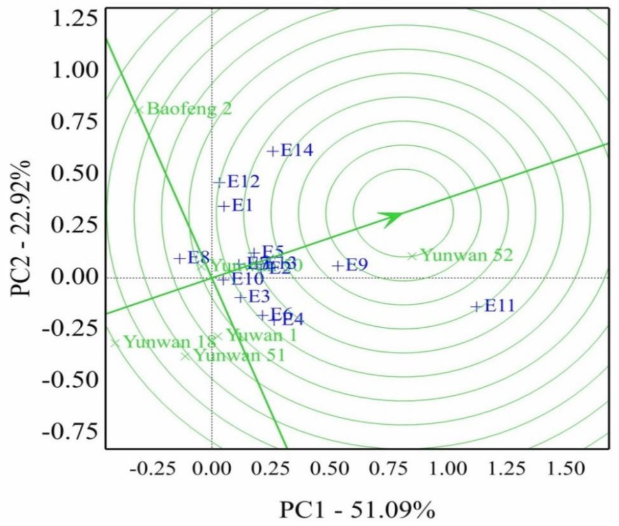

**Figure 9.** GGE biplot, ideal genotypes for seed yield (t $ha^{-1}$) of six pea genotypes across fourteen environments. E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

#### 3.3.5. GGE Biplot, IDEAL Environments for Seed Yield (t ha$^{-1}$)

The perfect environment is shown by an arrow directing to it (Figure 10). Therefore, E11 (Songming 2018), which falls into the center of the concentric circles, is the ideal environment. The desirable environment was E9 (Lijiang 2018); on the other hand, the undesirable environment was E8 (Baoshan 2018).

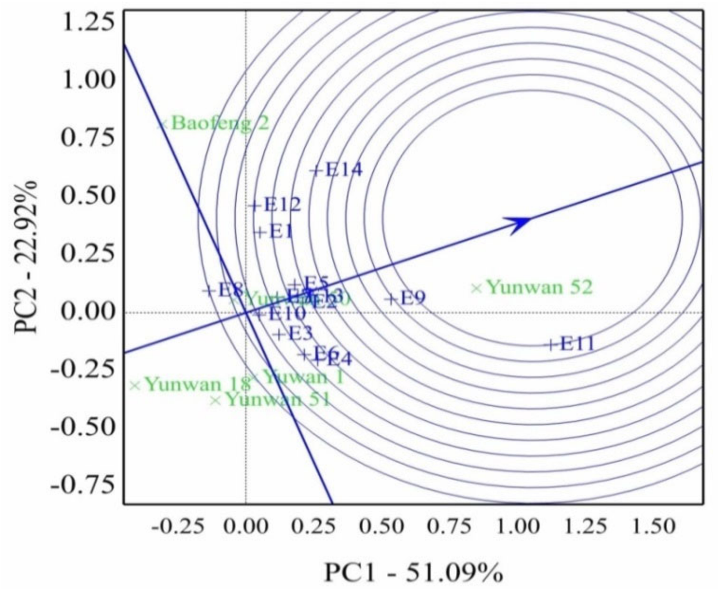

**Figure 10.** GGE biplot, ideal environment for seed yield (t ha$^{-1}$) of six pea genotypes across fourteen environments. E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

### *3.4. Genotype by Yield*Trait (GYT) Biplot Analysis*

#### 3.4.1. Genotype by Yield*Trait (GYT) Biplot “Which-Won-Where”

The pooled seed yield means of genotypes by all combination traits (GY*T) evaluated under fourteen environments for six pea genotypes are explained in Figure 11. It shows that the first and second principal components of the GYT biplot accounted for 72.26% and 24.70% of the total variation (96.96%) of seed yield, respectively. The GYT biplot separates into three distinct sectors, including the genotype Yunwan 52, the winner of the polygon vertexes for SY*NPB, SP, SW, PL, and SY/SPP combinations. This result shows that Yunwan 52 has the best-combined seed yield with the other traits. While genotype Yunwan 50 is located on another vertex sector and is called a winner for SY*PH. Moreover, the genotype Yunwan 18 did not exhibit proper results in combining traits.

#### 3.4.2. Genotype by Yield*Trait (GYT) Biplot “Means vs. Stability”

The effect of GYT on the “means vs. stability” ranking of genotypes is shown in Figure 12. The view of Average Tester Coordination (ATC) was used in this research to compare genotypes based on GYT records. The horizontal line with one arrow refers to the combination’s stability line and the evaluation based on this line of genotypes (ATC blue line with arrow). Also, the vertical line on ATC evaluates the genotype’s superiority (over the grand mean). Regarding mean performance and stability, genotype Yunwan 52 exhibited superior characteristics to Yunwan 50; however, genotype Yunwan 18 had the lowest performance of the GYT pattern of biplots.

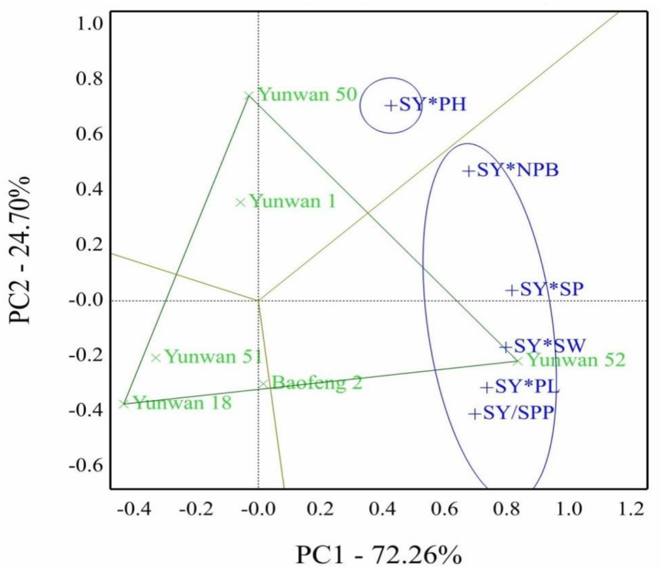

**Figure 11.** Which_Won_Where" pattern view of the genotype by yield*trait profile (GYT) biplot. SY, Seed yield; PH, Plant height; NPB, No. of primary branches; SP, Seeds/plant; SPP, Seeded pods/plant; PL, Pods length cm; SW, 100_seed weight.

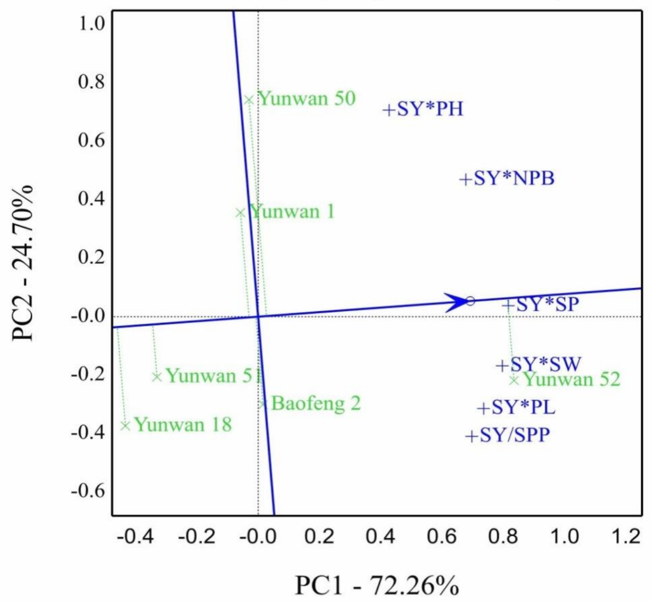

**Figure 12.** Mean vs. stability view of the genotype by yield*trait profile (GYT) biplot. SY, Seed yield; PH, Plant height; NPB, No. of primary branches; SP, Seeds/plant; SPP, Seeded pods/plant; PL, Pods length cm; SW, 100_seed weight.

### *3.5. Simple Correlation Coefficients*

Simple correlation coefficients among the studied environments are presented in Figure 13. Environments revealed various trends of associations among themselves. The graph showed strong positive correlation between the following environments: environment (E4) and each of environments (E6, 11, 7, 10, 3, 2 and 9); environment (E6) with environments (E11 and 13); environment (E11) with environments (E2, 9 and 13); environment (E7) with environments (E10, 2, 9, 1 and 14); environment (E10) with environments (E2 and 9); environment (E2) with environments (E9); environment (E1) with environments (E12 and 14); environment (E5) with environments (E12) and environment (E13) with environments (E14). This strong correlation suggested the similarity of the environments.

However, strong negative correlations were observed between environment (E4) and each of the environments (E12 and 8); environment (E6) with environments (E1 and 12); environment (E10) with environment (E8) and among environment (E12) with environment (E3). These results may be due to the dissimilarity of the environments. Meanwhile, the magnitude of the correlation coefficients among other traits was insignificant. The findings were consistent with the results obtained by Ghaffari et al. [47].

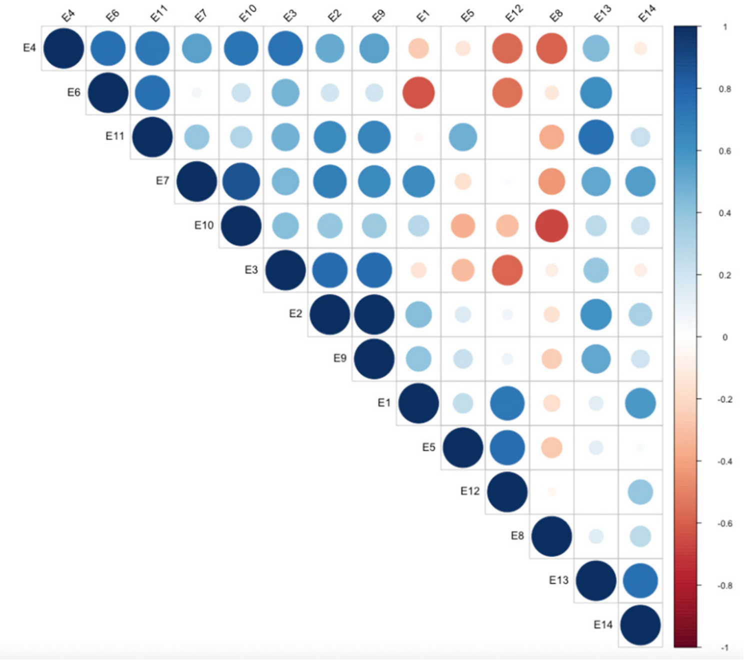

**Figure 13.** The Pearson correlation coefficients among the studied environments. E1, Baoshan 2017; E2, Lijiang 2017; E3, Qujing 2017; E4, Songming 2017; E5, Yaoan 2017; E6, Yuxi 2017; E7, Zhaotong 2017; E8, Baoshan 2018; E9, Lijiang 2018; E10, Qujing 2018; E11, Songming 2018; E12, Yaoan 2018; E13, Yuxi 2018; E14, Zhaotong 2018.

## 4. Discussion

In this study, the new pea variety "Yunwan 52" was bred through sexual hybridization, and the pedigree breeding method could inherit the characteristics of the "Yunwan 1" and "L2157". The growth habit and leaf type combined the characteristics of its parents that showed erect plant and semi-tendrils. These traits gave the "Yunwan 52" good performance for lodging-resistance and sprawling in field production applications, even though the lodging-resistance is not as good as its male "L2157,". L2157 disclosed semi-erect and whole-tendrils, making it easier for plants to hold to each other using tendrils [48]. The flower and seed coat color of "Yunwan 52" was as in the male "L2157" and showed purple (recorded a little in China), which had good nutritional and ornamental value. However, some studies reported that the purple pea is rich in anthocyanin and had unique nutritional value compared with the common pea [15]. Nevertheless, we did not measure the anthocyanin in this study; nonetheless, further study on the determination of anthocyanin in peas will provide great significance in developing the nutritional value and healthcare function of a purple pea.

Historically, the primary breeding goals in peas have predominantly revolved around enhancing resistance to biotic stress factors, such as root rot, rust, and powdery mildew, as described previously by Yang et al. [2]. The utilization of diverse germplasms as parental sources and the execution of comprehensive cross-breeding processes to incorporate main gene features conducted under favorable conditions will contribute to evaluating many breeding genotypes for abiotic stress tolerance, hence aiding in yield testing [49]. Climate diversity in Yunnan presents a new challenge for developing a new and high yield stability of leguminous crops compared with wheat, rape, and other crops in the same growing season. Furthermore, the productivity of peas, similar to several other leguminous crops, is regarded as unstable due to significant internal variability in yield compared to non-leguminous crops [50]. Therefore, to enhance the value of peas as a crop for farmers, it is imperative to identify pea varieties that exhibit high yield and stability for tolerance to abiotic stress. Estimating the yield and stability of "Yunwan 52" and other genotypes, multi-site experiments were carried out at mainly pea production area of Yunnan province in two seasons from 2016–2018.

The observed data in mean performance showed that Yunwan 52 has epistasis in most environments, followed by Baofeng 2 compared with the control variety (Yunwan 18) and the other genotypes. These differences between genotypes may be due to ge-netic variation informed by Bocianowski et al. [51]. The locations in Lijiang and Song-ming have the lowest seed yields, where high altitudes (2363 m and 1910 m, respec-tively) (Figure 4) and relatively low temperatures caused late maturity and high lodg-ing of pea genotypes. In reality, climate and soil conditions are not the only factors that determine high yield but also ideal management in research stations, including fertili-zation, actual field preparation, sowing and harvesting time, appropriate irrigation, and also the vital factor for high pea yield and production is actual control of weeds, pests, and foliar diseases. These variances in yield may also indicate remarkable GEI between these environments with the results of previously published reports by Yang et al. [52]. So, we made more effort to reduce the variances in these factors, like using pesticides for pests and controlling weeds and foliar diseases to estimate the yield be-side the different environments.

Pea breeders have the obstacle of environmental influences during attempts to introduce a novel genotype. So, they depend on various trials to realize this goal, as previously reported by Yan [53]. Breeders use AMMI and GGE methods to identify these targets and rely on principal component analyses (PCA), which suggested by Gabriel [54]. Therefore, the differences between them are that AMMI defines the GE interaction to split it into PCA1, PCA 2, and PCAn. Consequently, it is exposed in the ANOVA Table 3, but GGE evaluates the PCA from G + GE for the studied trait and shows it in graphical representation as similarly identified by Scavo et al. [27], Yan et al. [39], and Yan [55]. The significance between genotype (G), environments (E), and the interaction in between indicates that the effect of environment on the seed yield of pea genotypes and the examination of important genotypes across different environments enabled us to identify the nature and extent of (G × E). These features cannot be realized using conventional combined analysis of variance found by Horn et al. [56] and Thungo et al. [57].

GGE biplot analysis is one of the appropriate methods that plant breeders have improved dramatically for analyzing multi-environment trial data approved by Sandhyakishore et al. [26], Yan et al. [39], and Olanrewaju et al. [58]. The mega-environments in the GGE biplot of "Which-Won-Where" were identified by separating the scatter plot into sectors, and winners' genotypes are sited on the peaks of the polygon. These findings agree with those reported by Sandhyakishore et al. [26] and Filio et al. [59]. The cultivar Banfeng 2 was the winner in ME1, suitable for planting in the Baoshan, Yaoan, and Zhaotong areas, whereas Yunwan 52 was the winner in ME2, which contains ten environments (Figure 6). In addition, all studied environments were distributed to represent most of Yunnan's province, and the differences between environments in ME1 may be referred to as altitude (site height from sea level) and sandy loam soil of Baoshan (E1 and E8). Specifically, Zhaotong (E14) in the north of Yunnan province had a low-temperature climate during the pea growing season (Table 1). Meanwhile, ME2 consists of Lijiang (E2 and E9), Qujing (E3 and E10), Songming (E4 and E11), Yoan (E5), Yuxi (E6 and E13), and Zhaotong (E7) tend to be higher than ME1 based on the altitude. However, the soil texture differs from red loam to loam. Moreover, the temperature average throughout ME2 is higher than the average of ME1. Some lines were painted to link the test environments to the origin of the biplot as environment vectors to compare the relationship between environments. The angle that falls among the two environments refers to their correlation found by Dehghani et al. [60] and Kendal [61]. A broad, obtuse angle among environments indicates high cross-over genotype x environment interaction, according to Yan et al. [62] and Yan and Tinker [63]. Furthermore, as a pea breeder, the recommendation is to plant the winner genotype Yunwan 52 in most locations (climate-resilient cultivar).

The genotypes' mean performance and stability (Mean vs. Stability) of the average environment axis (AEA) is shown by a single arrow passing through the origin of the biplot and intersecting with the average environment, depicted as a little circle. The arrow refers to genotypes with higher mean performance and the perpendicular line to AEA. It passes through the origin biplot, which refers to higher performance variability or less stability in both directions (grand mean), as reported by Shim et al. [64]. Yunwan 52 recorded a high yield and short projections, indicating the stability of this cultivar over environments, whereas Baofeng 2 had more extended projections, indicating a high instability.

The ideal genotype is Yunwan 52, which has the best performance in all environments (superior yield potential and stability comparison to the other genotypes), which falls into the concentric circles of the center according to Yan et al. [39] and Rakshit et al. [65]. On the other hand, when evaluating the environment by the GGE biplot, the essential parameters are discrimination and representativeness. An optimal environment should have elevated PC1 scores, indicating increased discriminatory power for genotypes based on the primary genotypic effect and minimal (absolute) PC2 values, which better refers to the overall representation of environments. An environment near the ideal environment is desirable, and a direction far from the ideal environment is undesirable. Thus, concentric circles were drawn using the ideal environment in the middle to assist the distance between other environments and the ideal environment, as reported by Yan et al. [38] and Yan and Rajcan [45]. Based on that, E11 (Songming 2018) is the ideal environment. An efficient test location is essential in plant breeding because it represents G×E and the target environments for releasing the genotypes, as found by Yan et al. [46].

The GY*T biplot method is suggested by Yan and Frégeau-Reid [33] and is an applicable method for selecting a genotype by evaluating multiple traits. It has been described as inclusive and practical, which orders genotypes according to their ranks in grouping with target traits and graphical levels with their respective strengths and weaknesses in different plants, as reported by Yan [55]. The GYT biplot is more advantageous to use in breeding research if the selection of genotypes is created on one trait. The results of the GYT biplot refer to the strong correlation amongst all combinations of yield-traits; these various combinations of yield-trait come out as positively correlated or uncorrelated, according to Sofi et al. [66,67]. This advantage prevented the selection of false positive genotypes that caused more suitable selection. Therefore, a composition between seed yield and each constituted trait is desirable concerning high yield. Thus, the desired genotypes were superior, and the breeder used selection methods based on their seed yield and other trait combinations, as recorded by Elfanah et al. [34]. The result shows that the Yunwan 52 is the best genotype for seed yield and associated traits, while Yunwan 50 is located on another vertex sector winner for SY*PH according to the biplot "Which-won-where." Also, it is the best mean performance in the effect of GYT on the "means vs. stability".

## 5. Conclusions

The newly released "Yunwan 52" cultivar has outstanding yield performance, wide adaptability, and resilience to abiotic stress. Purple blossoms and seed coat peas, green cotyledon, green leaf with rich anthocyanin pigment at the axil, erect plant, and semi-tendrils distinguish it.

The data conclusion revealed that the GGE biplot clarified that specific genotypes have both broad and limited environmental adaptability, whereas the field pea Yunwan 52 is the stable and ideal genotype based on the GGE biplot across all tested environments. The applied genotype by yield*trait (GYT) biplot in this article offers a new method of genotyping based on multiple traits. This method is inclusive and effective since genotypes are categorized based on their level in combination yield with different traits, simultaneously showing the genotypes' strengths and weaknesses.

This study showed that the genotype Yunwan 52 was selected as the superior genotype and released a new variety of the best mean performance and stability according to the GYT biplot. This cultivar will boost improvements in pea yield in irrigation areas and may be adapted to similar conditions in other parts of the world, proving constructive for farmers to increase their income.

**Author Contributions:** Conceptualization, X.Y. and Y.H.; methodology, X.Y. and Y.H.; software, A.A.S. and H.Y.; validation, X.Y., A.A.S. and Y.H.; formal analysis, X.Y., Q.L., A.A.S. and H.Y.; investigation, X.Y., F.Y., M.L., J.Y. and L.W.; data curation, X.Y., C.H., Q.L. and M.L.; writing—original draft preparation, A.A.S., H.Y., M.L., C.H., W.N. and Y.H.; writing—review and editing, M.L., A.A.S., A.Z. and Z.D.; visualization, X.Y., Y.H. and A.A.S.; supervision, Y.W., Y.T. and Y.Z.; project administration, Y.H. and L.W.; funding acquisition, Y.H. and L.W. All authors have read and agreed to the published version of the manuscript.

**Funding:** This research was supported by the Yunnan Province Science and Technology Department (202202AE090003; 202302AE090011) and the International Plan of Talented Young Scientist Program (Egypt-19-046).

**Institutional Review Board Statement:** Not applicable.

**Informed Consent Statement:** Not applicable.

**Data Availability Statement:** The datasets used and/or analyzed during the current study are available from the corresponding author upon reasonable request.

**Acknowledgments:** The authors are highly thankful to Ahmed M. S. Elfanah, Researcher, Field Crops Research Institute, Agricultural Research Center, Giza, Egypt, for helping in the statistical analysis.

**Conflicts of Interest:** The authors declare no conflict of interest.

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