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*Article*

# Dissecting the Genotype × Environment Interaction for Potato Tuber Yield and Components

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**Abstract:** In the Mediterranean Basin, potato (*Solanum tuberosum* L.) is a major staple crop, the yield performance of which can vary dramatically based on pedo-climatic conditions and genotype. Hence, dissecting the genotype × environment interaction (GEI) in this region is mandatory for the setup of high-yielding and stable potato genotypes, also considering its importance for local potato breeding and the development of protected geographical identifications. Therefore, this research evaluated the marketable tuber yield (MY) and several yield components of five potato genotypes (Arizona, Generosa, Levante, Paradiso, and Vogue) over 4 years (2019, 2020, 2021, and 2022) and three locations in Sicily (Southern Italy) by additive main effects and multiplicative interactions (AMMI) and genotype main effects + genotype × environment interaction (GGE) biplot analyses. From combined ANOVA emerged a high significance of GEI, with the environment that provided the most considerable extent of variation for the most of the productive traits. The AMMI and GGE analyses identified Arizona as the best leading genotype in the studied area by virtue of its high productivity (44.5 t ha$^{-1}$ of mean MY) coupled with stability, followed by Generosa (46.5 t ha$^{-1}$). Ideal environments (location × year) were highly dependent on the productive trait, but most of them belonged to Acireale, characterized by fertile soils. According to our results, this approach could be recommended for breeding programs and commercial cultivation in the studied regions, along with the setup of potato protected geographical identifications.

**Keywords:** *Solanum tuberosum*; stability analysis; AMMI; GGE biplot; yield; yield components



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## 1. Introduction

The potato (*Solanum tuberosum* L.) is recognized as the fourth-highest crop in terms of global production quantity, with about 359 million tons of tubers deriving from 16.5 million hectares [1]. Its present use is mainly focused on human nutrition in the form of both fresh produce consumption and various industrially processed versions. Potatoes, in fact, provide a lot of energy and are an excellent source of carbohydrates (starch and free sugars), good-quality proteins, and numerous minerals and antioxidants [2,3]. Thanks to the potato's remarkable ability to adapt to the elements of the climate, it is grown on all continents, in developed and developing countries, at different altitudes (from the plains to the mountains), and at different times of the year. It is a staple food in the Mediterranean Basin, where the surface area dedicated to this crop is ~3 million hectares with an overall production of 28 Mt of tubers [1]. In this area, it is cultivated not only in the usual cycle (spring–summer) but also in a winter–spring cycle (from November–January to March–early June) for early production, especially in several coastal countries such as southern Italy, Tunisia, Egypt, Cyprus, Israel, Lebanon and Turkey [4–6].

The large variability in tuber yield is a consequence of a multitude of factors, namely genotype, soil properties, climate, and agronomic management [4,5,7–11]. In a given environment, a cultivar provides a maximum yield when it is well-adapted to the prevailing climate conditions and belongs to a maturity class that matches the available number of growing days. Stable and high-yielding cultivars are recommended for cultivation, however tuber yield traits of cultivars can vary from environment to environment and within a location for different growing seasons. The basic cause of low stability is a wide occurrence of genotype × environment interaction (GEI). GEI is a complex phenomenon involving agroecological, climatic, and agronomic conditions, as well as all the physiological and genetic factors that determine plant growth and development [12]. It results in the inconsistent performance of genotypes across environments, caused either by differential responses of the same set of genes to changes in the environment or by the expression of different sets of genes in different environments [13]. In order to prepare high-yielding and stable genotypes, genotype × environment interaction (GEI) is one of the most important and complicated issues for breeding programs [14]. Therefore, stability and adaptation studies across multi-environmental trials (METs) are imperative, also considering that most of the traits of agronomic importance are hereditary quantitative. Tuber yield, for instance, which is a character that presents continuous distribution, has polygenic inheritance and is highly influenced by variations in the environment [15]. The farmers or growers need cultivars that show high performance for yield and other essential agronomic traits and are stable, i.e., perform well over both different environmental conditions and years. Usefulness in dissecting the GEI is not only related to the development of widely adapted and stable genotypes across environments, but also to the improvement of yield traits of existing cultivars under conditions that positively influence such traits [16].

Several statistical techniques have been developed to study the GEI effects, measure stability, and facilitate varietal recommendations in METs. In addition to linear mixed models (LMMs) [17], two actual methods are widely used to dissect the GEI: the additive main effects and multiplicative interaction (AMMI) analysis and the genotype main effect plus genotype × environment interaction (GGE) biplot analysis [14,18]. AMMI and GGE analyses for yield traits stability have been studied in several crops including maize [19], rice [20], sugarcane [21], sorghum [22], Bambara groundnut [23], etc. In potatoes, AMMI analysis was used for cultivar recommendation in Peru on purple-pulp colored genotypes [24] and in Poland on post-registration series cultivars [25]; the GGE biplot analysis was performed on Russet Burbank, Umatilla Russet, and Cal White cultivars in Canada [26] and eight potato genotypes in Ethiopia [27]. The only study in which AMMI and GGE analysis has been conducted simultaneously was realized in Kenya to estimate the magnitude of GEI for potato tuber yield and bacterial wilt resistance in 42 breeding families [28]. However, this research was mainly focused on bacterial wilt resistance. To the best of our knowledge, although the GEI on potato tuber yield was partially investigated in previous research [26,27,29,30], a systematic study on potato yield by AMMI and GGE biplot analyses is lacking. Furthermore, there is a need to incorporate the GEI into local potato breeding programs for the setup of Protected Geographical Identifications. In a given geographical area, this could be useful to identify well-adapted and stable potato genotypes with productive characteristics that comply with quality standards, with the goal of better matching the needs of farmers and distinct market demands. For this reason, the present study aimed to investigate the GEI and determine the most stable and productive potato genotypes (five) over four seasons and three locations in Sicily based on AMMI and GGE analysis.

## 2. Materials and Methods

### *2.1. Study Sites*

The present experiment was performed throughout three locations sited in Sicily (Southern Italy) on the southeast foothills of Mount Etna, an area traditionally devoted to potato cultivation: Acireale (37°60′ N 15°16′ E, 80 m a.s.l.), Giarre (37°74′ N 15°18′ E, 50 m a.s.l.), and Mascali (37°77′ N 15°11′ E, 60 m a.s.l.). According to the USDA soil classification [31], the soils over the three locations are Typic Xerochrepts type, with sandy texture and low water field capacity. Under a chemical point of view, in Acireale the soil had higher organic matter and macro (P, N, K, Ca, and Mg) and micro (Zn, Cu, and Mn) element contents, as well as a higher cation exchange capacity than Giarre and Mascali; in Giarre, the soil stood out for the high amount of both Fe and exchangeable Na. Table 1 shows the detailed physical and chemical characteristics of the −30 cm soil layer of the three locations under study, carried out in accordance with the procedures approved by the Italian Society of Soil Science [32]. The experimental trials last four growing seasons from 2019 to 2022, hereafter referred to as Season I, Season II, Season III, and Season IV. The zone has a typical Mediterranean climate, with mild–wet winters, springs with low rainfall and raising temperatures, and with most rainfall falling during the autumn–early winter period, which allows the growth of the winter–spring cycle potato.

**Table 1.** Description of soil characteristics (−30 cm depth) of the three locations under study.

| Soil Characteristic | Unit of Measurement | Acireale | Giarre | Mascali |
|---|---|---|---|---|
| Sand | % | 82 | 85 | 90 |
| Silt | % | 14 | 11 | 7 |
| Clay | % | 4 | 4 | 3 |
| Organic matter | % | 4.9 | 2.5 | 2.4 |
| C/N | / | 9.5 | 8.9 | 10.7 |
| Total N | % | 0.30 | 0.16 | 0.13 |
| $P_2O_5$ available | ppm | 428 | 236 | 149 |
| $K_2O$ exchangeable | ppm | 1193 | 723 | 672 |
| pH | / | 7.3 | 7.4 | 7.4 |
| Electrical conductivity | mS cm$^{-1}$ | 1.96 | 2.26 | 0.60 |
| Cation exchange capacity | meq 100 g$^{-1}$ | 20.2 | 12.5 | 11.9 |
| Ca exchangeable | meq 100 g$^{-1}$ | 13.0 | 7.2 | 8.0 |
| Mg exchangeable | meq 100 g$^{-1}$ | 3.8 | 1.9 | 2.2 |
| Na exchangeable | meq 100 g$^{-1}$ | 0.8 | 1.9 | 0.3 |
| K exchangeable | meq 100 g$^{-1}$ | 2.5 | 1.5 | 1.4 |
| Zn | ppm | 57 | 8 | 6 |
| Cu | ppm | 30 | 8 | 19 |
| Fe | ppm | 103 | 110 | 78 |
| Mn | ppm | 30 | 11 | 10 |

### *2.2. Genotypes*

Five potato genotypes—namely Arizona, Generosa, Levante, Paradiso, and Vogue (hereafter referred to as G1, G2, G3, G4, and G5, respectively)—were evaluated in this study. Except for Arizona, developed in 2009, the other genotypes are new cultivars recently introduced (between 2015 and 2018), never evaluated in the studied area, and whose pedigrees have been taken from van Berloo et al. [33]. Arizona (UK 150-19D22 × Mascotte) and Generosa are AB cooking type (based on the European Association for Potato Research cooking classification) cultivars with a medium-to-late cycle, high vigor, and low resistance to common scab. Levante (AR 01-3218 × Almera) is a B cooking type featuring excellent organoleptic characteristics with a medium-to-late cycle and high vigor, and high tolerance to late blight and potato cyst nematodes (PCN) 1 and 4. Paradiso (Rodeo × Valor) is a B cooking type characterized by very large tubers and high tolerance to late blight. Vogue (Marabel × Amorosa) is an AB cooking type characterized by high tuberification and tuber-enlargement speed, with medium vigor and high tolerance to common scab and PCNs 1 and 4. All cultivars are Dutch and high yielding, skin and flesh yellow colored, oval and long-oval shape tubers, and are potentially suitable for the early potato market.

### *2.3. Design and Agronomic Management*

The experimental design used at each location was a 3.75 × 4.5 m randomized block with three replications. Each block consisted of five genotypes (Arizona, Generosa, Levante, Paradiso, and Vogue), i.e., six rows each consisting of 90 plants at 5.3 plants m$^{-2}$ (0.25 m × 0.75 m). The external rows and two plants of each row-end were considered as the border. Planting was done by hand in the first week of December throughout the four growing seasons, using disease-free and certified A-class sprouted seed tubers. Agronomic management (tillage, fertilization, irrigation, and weed control) was carried out as per recommendations for the local farming practices and with uniformity criteria across the three locations. In detail, a 30 cm depth plowing followed by harrowing in October was performed, together with a fertilization program consisting of a pre-planting application of an NPK synthetic fertilizer at the dose of 50-80-120 kg ha$^{-1}$ of N (as ammonium nitrate), $P_2O_5$ (as double perfosphate), and $K_2O$ (as potassium sulphate), respectively, plus a further 70 kg ha$^{-1}$ application of N (as ammonium nitrate) as top dressing. About 70 mm, 100 mm, 50 mm, and 120 mm of irrigation water were provided by furrow irrigation to fully satisfy crop water requirements in seasons I II, III, and IV, respectively.

### *2.4. Yield and Yield Components*

Potato yield and yield components were determined for each location and all growing seasons by manually harvesting tubers at about 120 days after planting (DAP), i.e., when the leaves and stems were bleached and dried, from 52 plants from the central rows of each plot. Initially, tubers were classified as marketable (unitary weight > 20 g) and unmarketable (unitary weight < 20 g, or deformed, green, and diseased), with each category counted and weighed separately. Only marketable tubers were used to determine marketable yield (MY), the number of marketable tubers per plant (NMTP), and the average marketable tuber weight (AMTW). Based on the measurement of the transverse diameter, marketable tubers were also distributed into three dimensional classes: <40 mm, 40–60 mm, and >60 mm. Then, the percentage incidence of each size class on the overall marketable production was calculated as caliber tubers (CT). Discarded production (unmarketable tuber, UT) was determined as the % weight of unmarketable tubers of the total tuber yield (marketable + unmarketable). A representative sample of marketable tubers—at least fifty tubers per replicate for each genotype and location—was washed and dried at 65 °C up to a constant weight to evaluate dry matter content. Tuber specific gravity (TSG) was determined from a sample weight of 5 kg by calculating the quotient weight in air divided by the weight in air minus the weight in water [34].

### *2.5. Weather Description*

In each location, meteorological measurements (rainfall and minimum and maximum air temperatures) were recorded daily using a data logger (CR21, Campbell Scientific, Logan, UT, USA) positioned about 20 m from the experimental fields. The growing degree days (GDD) were also calculated with the formula GDD = $[(T_{max} - T_{min})/2] - T_{base}$, where $T_{max}$ and $T_{min}$ are the daily maximum and minimum air temperatures, respectively, and $T_{base}$ is the temperature below which the crop growth does not progress, which is 7 °C. The three locations under study showed different climatic characteristics. Considering the months in which the growing season (December–May) takes place during the 10-year period 2013–2022, Acireale was characterized by the lowest average minimum and maximum temperatures (10.1 and 16.5 °C, respectively) and accumulated GDDs (1152), whereas Mascali showed the highest values (11.0 and 17.5 °C, and 1322, respectively). The temperature differences between Acireale and Mascali were more marked in March, with monthly accumulated GDD values of 166 and 199, respectively. Regarding rainfall, the lowest fell in Acireale (831 mm) and the highest in Giarre (1040 mm). Over the three locations, about 80% of rainfall was concentrated during the December–March period.

With regard to the weather conditions during the experimental field trials across the three locations (Figure 1), compared to the 10-year period, there emerged:

- higher minimum and maximum temperatures in March (+1.4 and +0.9 °C in Acireale, +1.1 and +0.9 °C in Giarre, +1.1 and +0.9 °C in Mascali) in Season I;
- lower rainfall throughout the growing season (612 vs. 831 mm in Acireale, 732 vs. 1040 in Giarre, and 702 vs. 960 in Mascali) in Season II, but a high concentration in March when rainfall was 41%, 37%, and 34% of the total for the growing season in Acireale, Giarre, and Mascali, respectively;

- higher rainfall (1150 vs. 831 mm in Acireale, 1176 vs. 1040 mm in Giarre, and 1206 vs. 960 mm in Mascali) in Season III, mostly concentrated in December and March, as well as higher minimum and maximum temperatures in April and May, which led to a strong increase of accumulated GDD (+171 in Acireale, +193 in Giarre, and +194 in Mascali, respectively);
- lower minimum and maximum temperatures in March and lower rainfall (by about half) throughout the growing season across the three locations in Season IV.

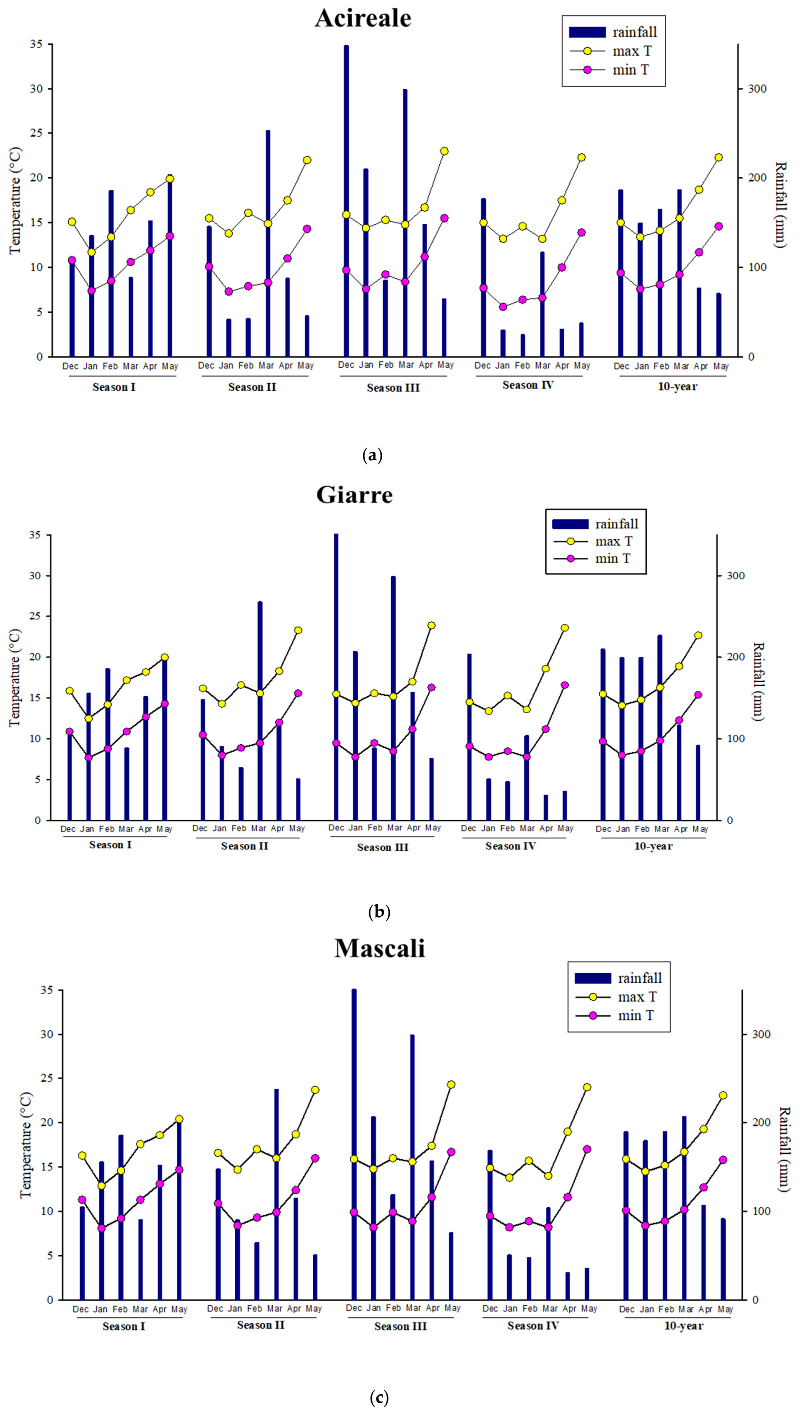


**Figure 1.** Monthly rainfall, average minima and maxima monthly air temperatures, and 10-year (2013–2022) climatic trend in Acireale (**a**), Giarre (**b**), and Mascali (**c**) throughout Season I (2018–2019), Season II (2019–2020), Season III (2020–2021), and Season IV (2021–2022).

However, the variations in weather conditions between the seasons were more pronounced in Acireale, where there was a greater variation in the accumulated GDD throughout the growing seasons, essentially due to the greater variation in the average minimum temperatures.

### 2.6. Statistical Analysis

The quantitative traits under study were statistically analyzed following a three-stage procedure consisting of an ANOVA followed by two multivariate models, i.e., AMMI and GGE biplot analysis, both based on the singular value decomposition (SVD). The ANOVA was adopted to estimate the variations among genotypes, environments, and GEI using CoStat® version 6.003 (CoHort Software, Monterey, CA, USA). For the purpose of this study and to simplify the estimation of variance components, location × year contributions were considered to be environments, consistent with Affleck et al. [26] and Gedif and Yigzaw [27]. The ANOVA was firstly computed for individual environments to check the genotype effect in each environment and then combined to check the GEI, considering both the environments and genotypes as fixed factors. One-way ANOVAs were also applied to pooled data of both environments and genotypes to test the significance of each variable. Before ANOVA and in accordance with Lombardo et al. [35], percentage data (UT and CT) and NMTP data were Bliss- and square-root transformed, respectively, to obtain normalized distribution. Homogeneity of variance and normality were respectively verified with the Bartlett and Shapiro–Wilk tests. Differences between means were assessed using Fisher's protected least significant difference (LSD) test at the 95% probability level.

Once the significance of the GEI was assessed, it was further elucidated through stability analysis to graphically generate biplots. In the AMMI model, combining additive and multiplicative parameters into a single analysis, the GEI is divided into interaction principal component (IPC) scores and residual values according to the equation described by Zobel et al. [36]. In detail, the AMMI firstly involves an ANOVA to analyze the genotype and environment main effects without the interaction and, then, a principal component analysis to standardized residuals that include the experimental error and the effect of the GEI. The GGE model absorbs the main effects of genotype plus the GEI into the multiplicative component and uses the SVD of the first two principal components (PCs) [18,37]. The GGE biplot is based on the sites regression (SREG) linear-bilinear model indicated by Crossa et al. [38]. Model equations of AMMI and GGE are reported in Scavo et al. [39]. Moreover, following Scavo et al. [39], the results of the AMMI and GGE analyses were graphically displayed via five biplot patterns with scaling = 0, centering = 2, and environment-focused partitioning (SVP = 2): AMMI1 (IPC1 scores vs. trait main effect), AMMI2 (IPC1 vs. IPC2), "which-won-where" (mega-environment analysis), "ranking genotypes" (genotype evaluation), and "ranking environments" (environment evaluation). The PBTools version 1.4 (IRRI, Los Baños, Laguna, Philippines) software was used to perform AMMI and GGE analysis.

## 3. Results and Discussion

With the aim of identifying productive and stable potato genotypes under diverse environmental conditions in Sicily, in this work, a multi-environmental trial was performed considering five potato genotypes, three locations, and four growing seasons. Overall, 12 environments resulting from the combination of three locations × four growing seasons were considered. In particular, a three-stage approach was employed. It started with a combined ANOVA on pooled data to estimate the variance contribution of genotype and environment and to test the significance of GEI. Then, stability analysis was conducted by AMMI and GGE biplot analysis to elucidate and partition the GEI, graphically observe the interrelationships among tested genotypes and environments, recognize mega-environments (if any) within the studied area, and rank the genotypes and environments for each yield trait.

### 3.1. Combined ANOVA

From the ANOVA emerged that the main effects of genotype and environment were a significant source of variation ($p \leq 0.001$) for all productive traits (Table 2). MY, NMTP, AMTW, and CT 40–60 mm showed the most considerable extent of variation due to environment, which respectively accounted for 68.8%, 85.9%, 54.9%, and 70.2% of the total variation (G + E + GEI + blocks). This is not surprising since quantitative traits are well known to be closely dependent on environmental conditions [20,21,40]. On the contrary, genotype was the largest source of variation for TSG (77.9%), CT < 40 mm (47.3%), and CT > 60 mm (60.8%) (Table 2). Potato's TSG, in fact, is closely correlated to dry matter content [34], which in turn is highly genotype-dependent. Partitioning the environment into predictable (location) and unpredictable (year) variance components (Table S1), the three-way ANOVA (L × Y × G) showed that all interaction effects were significant at the 99% probability level, in accordance with Movahedi et al. [41], and that year was the most important source of variation for productive traits, except for UT. This indicated the higher influence of weather conditions than soil characteristics on potato yield. An opposite trend was found by Gedif and Yigzaw [27] in mid-high-altitude areas of Ethiopia. Specifically, in our study, the differences in weather conditions recorded between seasons were higher than those between locations in the same season (Figure 1). Weather influences potato yield and productive characteristics throughout all the phenological stages. For instance, tuber yield integrates development, total growth, and partitioning processes, and each of these processes is differently affected by temperature [42].

Regardless of environments, one-way ANOVAs indicated that Generosa showed the highest MY (46.5 t ha$^{-1}$), followed by Arizona (44.5 t ha$^{-1}$) (Table 2). For Arizona, MY can be attributed to NMTP (on average 7.4), while for Generosa it was mainly due to AMTW (137.9 g). This finding agreed with Lombardo et al. [34], who also reported high Arizona yields due to NMTP in a similar environment. On the contrary, Levante showed the lowest MY (35.7 t ha$^{-1}$), due to the lowest AMTW (99.5 g) mainly caused by the highest percentage of small caliber tubers (18.2% of <40 mm tubers) and by the greatest UT (2.3%).

Pooling over genotypes (Table 2), E4 had the greatest MY (54.7 t ha$^{-1}$), followed by E5 (49.2 t ha$^{-1}$), which showed also the highest TSG (1059.8 kg m$^{-3}$) and CT > 60 mm (36.5%). E10, despite the greatest AMTW (185.2 g) and a high percentage of 40–60 mm and >60 mm CTs, showed a very low MY (34.0 t ha$^{-1}$) due to the lowest NMTP (3.6), like E2 and E6 which both had low MYs. The highest NMTP was found in E1 (11.0), which at the same time showed the lowest AMTW (77.8 g) and the greatest CT < 40 mm percentage (24.8%). The poor NMTP of E2, E6, and E10 (i.e., Season II) may be attributable to the very low rainfall in January and February 2020 (also considering that irrigation was performed from March), which coincides with the phase of tuber differentiation. Indeed, NMTP is highly dependent on environmental conditions and water availability, among others, which play a key role during the critical period around tuberization [43]. According to the previous study on tuber quality characteristics [39], the variance magnitudes of the environment explained the differentiated performances of genotypes between environments, indicating a higher influence of seasonal climatic conditions than location. Although it had a low contribution to total variation, as also reported by Khan et al. [23], the GEI was highly significant ($p \leq 0.001$) for MY and yield components, so further analysis was justified.

**Table 2.** Joint analysis of variance (ANOVA, *F*-values) of five potato genotypes (G) and 12 environments (E) for marketable yield (MY, t ha$^{-1}$), unmarketable tubers (UT, %), number of marketable tubers plant$^{-1}$ (NMTP), average marketable tuber weight (AMTW, g), tuber specific gravity (TSG, kg m$^{-3}$), and caliber tubers (CT, %).

| Source of Variation | | MY | NMTP | AMTW | UT | TSG | CT < 40 mm | CT 40–60 mm | CT > 60 mm |
|---|---|---|---|---|---|---|---|---|---|
| G | Arizona | 44.5 (2.0) b | 7.4 (0.5) a | 122.5 (5.1) c | 1.3 (0.3) b | 1048.2 (1.0) c | 9.3 (1.5) bc | 70.9 (2.2) bc | 19.8 (1.9) bc |
| | Generosa | 46.5 (2.4) a | 6.9 (0.4) bc | 137.9 (6.7) a | 1.034 (0.2) b | 1055.7 (1.1) b | 9.8 (1.5) b | 72.6 (2.4) b | 17.6 (2.5) c |
| | Levante | 35.7 (1.6) d | 7.3 (0.5) ab | 99.5 (3.9) e | 2.3 (0.84) a | 1062.2 (1.1) a | 18.2 (1.7) a | 76.1 (1.7) a | 5.7 (1.3) d |
| | Paradiso | 41.5 (1.8) c | 6.5 (0.4) c | 128.4 (5.5) b | 1.5 (0.3) b | 1049.3 (1.2) c | 6.3 (0.9) d | 69.8 (1.9) c | 23.9 (1.9) a |
| | Vogue | 40.0 (2.1) c | 6.8 (0.4) bc | 115.9 (5.7) d | 2.9 (0.7) a | 1049.4 (1.1) c | 8.5 (1.1) cd | 71.1 (2.6) bc | 20.4 (2.8) b |
| E | E1 | 43.4 (1.7) c | 11.0 (0.4) a | 77.8 (4.0) f | 2.2 (0.6) bc | 1057.6 (1.5) ab | 24.8 (3.2) a | 57.6 (3.1) f | 17.5 (2.5) cd |
| | E2 | 23.7 (1.3) g | 3.9 (0.2) hi | 123.6 (7.4) d | 2.3 (0.6) ab | 1054.4 (2.1) cde | 5.2 (1.5) e | 72.4 (2.7) cd | 22.4 (3.7) bc |
| | E3 | 39.8 (2.9) de | 7.3 (0.6) ef | 101.5 (3.3) e | 4.6 (1.6) a | 1050.4 (0.9) f | 9.6 (1.1) d | 75.2 (1.1) bc | 15.1 (1.5) d |
| | E4 | 54.7 (2.8) a | 8.1 (0.2) cd | 127.5 (5.9) cd | 1.1 (0.3) ef | 1051.7 (1.8) ef | 13.3 (1.6) b | 61.8 (3.5) f | 24.9 (3.5) b |
| | E5 | 49.2 (2.7) b | 6.9 (0.4) ef | 134.3 (3.1) bc | 0.6 (0.21) fg | 1059.8 (1.3) a | 3.6 (0.9) e | 59.7 (2.9) f | 36.6 (3.1) a |
| | E6 | 33.3 (1.7) f | 4.5 (0.2) h | 139.8 (6.7) b | 2.5 (0.6) ab | 1056.1 (1.9) bc | 2.6 (1.1) f | 87.3 (1.5) a | 10.1 (2.1) e |
| | E7 | 38.8 (1.5) e | 6.2 (0.5) g | 123.1 (5.8) d | 1.4 (0.3) cde | 1050.5 (2.3) f | 11.9 (1.7) bcd | 84.8 (1.3) a | 3.2 (1.2) f |
| | E8 | 47.1 (2.9) b | 8.8 (0.4) bc | 101.6 (43) e | 2.0 (0.5) bcd | 1052.8 (2.0) def | 11.3 (1.1) cd | 66.6 (3.5) e | 22.1 (3.9) bc |
| | E9 | 47.1 (2.2) b | 9.1 (0.3) b | 98.0 (3.5) e | 0.6 (0.2) fg | 1054.7 (2.1) cd | 14.6 (2.5) b | 73.5 (1.6) cd | 11.9 (2.8) e |
| | E10 | 34.0 (1.4) f | 3.6 (0.2) i | 185.2 (8.0) a | 0.5 (0.2) g | 1052.9 (2.8) def | 3.3 (1.6) f | 77.9 (2.5) b | 18.8 (2.7) bc |
| | E11 | 47.1 (4.1) b | 7.5 (0.4) de | 118.6 (8.0) d | 1.2 (0.3) def | 1043.3 (2.1) g | 13.0 (1.7) bc | 78.1 (1.4) b | 8.9 (2.0) e |
| | E12 | 42.0 (3.8) cd | 6.7 (0.3) fg | 119.1 (10.2) d | 1.7 (0.5) cde | 1051.2 (2.5) f | 11.9 (2.1) bcd | 69.8 (3.5) de | 18.2 (5.1) cd |
| ANOVA | G [a] | 41.1 *** | 5.1 *** | 49.4 *** | 10.0 *** | 85.1 *** | 57.5 *** | 5.9 *** | 70.3 *** |
| | E [b] | 70.0 *** | 71.87 *** | 70.6 *** | 10.2 *** | 17.7 *** | 56.4 *** | 35.5 *** | 34.3 *** |
| | G × E [c] | 18.2 *** | 4.1 *** | 7.5 *** | 5.5 *** | 4.7 *** | 6.3 *** | 6.5 *** | 8.4 *** |
| | Blocks [d] | 1.0 ns | 2.6 ns | 1.1 ns | 1.0 ns | 1.8 ns | 1.1 ns | 2.7 ns | 2.7 ns |

Values are means with SEM (standard error of the mean, $n$ = 36 for G, $n$ = 15 for E) in brackets. Values within a column with different letters indicate significant differences ($p \leq 0.05$) using the LSD test. [a] 4 d.f.; [b] 11 d.f.; [c] 44 d.f.; [d] 2 d.f.; *** and ns indicate significant effect at $p \leq 0.001$ and not significant, respectively.

### 3.2. Stability Analysis

AMMI and GGE analyses divided the GEI sum of squares into IPCs (Table S2) and PCs (Table S3) to unfold the variance components. Both multivariate models were significant for potato yield and yield-related traits, except for CT < 40 mm and CT > 60 mm (Table 3), which therefore were not further analyzed. About AMMI, the cumulative contribution of IPC1 and IPC2 captured 70.2% of the GEI sum of squares for MY, 82.4% for UT, 80.4% for NMTP, 72.2% for AMTW, 75.1% for TSG, and 73.7% for CT 40–60 mm. Similarly, the first two PCs explained 67.5% of the GEI sum of squares for MY, 76.8% for UT, 77.7% for NMTP, 78.6% for AMTW, 87.2% for TSG, and 69.9% for CT 40–60 mm in the GGE model. These percentages demonstrated the validity of the AMMI and GGE models in representing the GEI in the present study. In fact, Thangavel et al. [44] asserted that an IPCA1 + IPCA2 cumulative variation > 66% is a reliable interpretation of the GEI for the AMMI models, while according to Yang et al. [45] a PC1 + PC2 variation > 60% is desirable for GGE. GEI interactions were graphically represented through five biplot patterns.

**Table 3.** Additive main effects and multiplicative interaction (AMMI) and G + GE (GGE) analyses in potato yield and yield components.

| | Marketable Yield | | | N. of Marketable Tubers Plant$^{-1}$ | | | Average Marketable Tuber Weight | | | Unmarketable Tubers | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | SS | MS | SS% of GEI | SS | MS | SS% of GEI | SS | MS | SS% of GEI | SS | MS | SS% of GEI |
| **AMMI analysis** | | | | | | | | | | | | |
| IPC1 [a] | 3414.4 | 243.9 *** | 42.0 | 69.1 | 4.9 *** | 57.8 | 14471.7 | 1033.6 ** | 43.4 | 769.1 | 54.9 ** | 62.0 |
| IPC2 [b] | 2294.3 | 191.1 *** | 28.2 | 27.1 | 2.1 *** | 22.6 | 9612.1 | 801.0 ** | 28.8 | 252.7 | 21.1 * | 20.4 |
| IPC3 [c] | 1806.4 | 180.6 *** | 22.2 | 18.1 | 1.7 *** | 15.1 | 7052.6 | 705.3 * | 21.2 | 135.6 | 13.6 ns | 10.9 |
| **GGE analysis** | | | | | | | | | | | | |
| PC1 [a] | 4177.4 | 298.4 *** | 42.7 | 70.9 | 5.1 *** | 53.1 | 27903.2 | 1993.1 ** | 52.3 | 798.7 | 57.0 ** | 55.3 |
| PC2 [b] | 2429.3 | 202.5 *** | 24.8 | 32.8 | 2.6 *** | 24.6 | 14039.1 | 1169.9 ** | 26.3 | 310.6 | 25.9 * | 21.5 |
| PC3 [c] | 2186.0 | 218.5 *** | 22.3 | 24.1 | 2.3 *** | 18.0 | 8337.3 | 833.6 * | 15.6 | 215.5 | 21.5 ns | 14.9 |
| | **Tuber specific gravity** | | | **Caliber tubers < 40 mm** | | | **Caliber tubers 40–60 mm** | | | **Caliber tubers > 60 mm** | | |
| | **SS** | **MS** | **SS% of GEI** | **SS** | **MS** | **SS% of GEI** | **SS** | **MS** | **SS% of GEI** | **SS** | **MS** | **SS% of GEI** |
| **AMMI analysis** | | | | | | | | | | | | |
| IPC1 [a] | 973.4 | 69.5 *** | 47.0 | 1284.2 | 91.6 ns | 51.1 | 1435.0 | 102.4 *** | 47.6 | 3606.6 | 257.5 ns | 52.4 |
| IPC2 [b] | 581.2 | 48.4 *** | 28.1 | 623.9 | 52.0 ns | 24.8 | 785.7 | 65.5 *** | 26.1 | 1416.4 | 118.0 ns | 20.6 |
| IPC3 [c] | 337.4 | 33.6 *** | 16.3 | 481.9 | 48.2 ns | 19.2 | 620.6 | 62.1 *** | 20.6 | 971.0 | 97.0 ns | 14.1 |
| **GGE analysis** | | | | | | | | | | | | |
| PC1 [a] | 3820.4 | 272.9 *** | 69.9 | 2948.4 | 210.6 ns | 63.9 | 1490.2 | 106.4 *** | 45.6 | 6388.5 | 456.2 ns | 53.0 |
| PC2 [b] | 947.0 | 78.8 *** | 17.3 | 975.6 | 81.3 ns | 21.2 | 794.2 | 66.2 *** | 24.3 | 3353.7 | 279.5 ns | 27.8 |
| PC3 [c] | 443.5 | 44.4 *** | 8.1 | 541.1 | 54.0 ns | 11.7 | 661.1 | 66.1 *** | 20.2 | 1415.5 | 141.5 ns | 11.7 |

[a] 14 d.f.; [b] 12 d.f.; [c] 10 d.f.; Notes: IPC: interaction principal component; SS: sum of squares; MS: mean square; SS% of GEI: variance proportion of genotype × environment interaction; ***, **, * and ns indicate significant effect at $p \leq 0.001$, $p \leq 0.01$, $p \leq 0.05$ and not significant, respectively.

3.2.1. AMMI Analysis

According to the $F_R$ test [46], the model better describing the GEI in this study is AMMI3, except for UT, since the IPC3 was the last component with significant residue (Table 3). However, the AMMI2 model was selected to explain the GEI effect because it always provided a total variation greater than 70%. Through the AMMI1 biplot shown in Figure 2, it is possible to identify superior genotypes (i.e., those with IPC1 scores nearing zero and above-average mean values) across the environments. At the same time, environments with IPC1 scores close to zero have a low interaction effect, thus ensuring good performances for all genotypes (Table S2). Overall, results obtained in the AMMI1 biplots are in line with the combined ANOVA, and highlighted G1 (Arizona) and G2 (Generosa) as the superior genotypes for potato production throughout the studied environments. In particular, G2 showed the highest MY and AMTW, although it was very unstable, as well as high CT 40–60 mm and TSG, and low UT. G1 was preferred for MY because it showed above-average values and an IPC1 score near zero, in addition to high and stable AMTW and low UT. G3 (Levante) was the superior genotype for TSG and NMTP. It is a new cultivar recently introduced on the market, so no scientific literature is available. However, the Romagnoli F.lli Spa (https://www.romagnolipatate.it; Bologna, Italy; accessed on 29 October 2021) reports similar values of dry matter. Except for AMTW, G5 (Vogue) had below-average main effects and was the most unstable; hence, it was not suitable in the studied area. In addition, G5 and G3 showed the highest UT, even though they were highly influenced by the environment (large IPC1 scores).

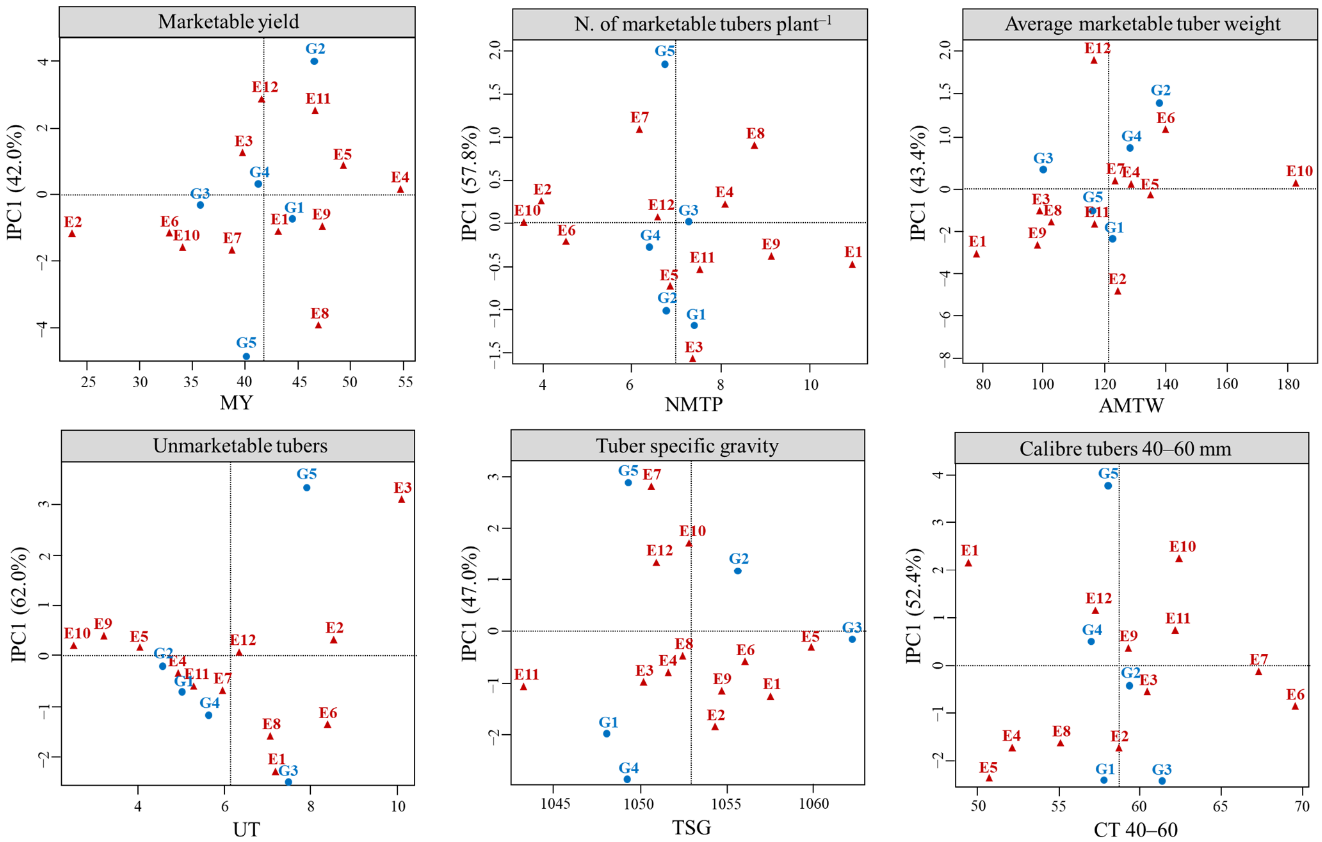


**Figure 2.** 'AMMI 1' biplot showing the mean trait effect and the first interaction principal component (IPC1) of five potato genotypes (G) over 12 environments (E). The biplots were constructed with scaling = 0, centering = 2, and SVP = 2. G1: Arizona; G2: Generosa; G3: Levante; G4: Paradiso; G5: Vogue; E1–E4: Acireale (seasons I to IV); E5–E8: Giarre (seasons I to IV); E9–E12: Mascali (seasons I to IV).

Regarding environments, E4 and E5 were the most favorable ones for MY, allowing both high performances and low interactive effects, while the lowest MY occurred in Season

II (E2, E6, and E10). Seasons I and II (E1, E2, E5, E6, and E9) allowed also the highest TSG values, with E5 showing the greatest stability. Except for 2022 (E4), Acireale had above-average UT, whereas E9 and E10 had the lowest UT for all genotypes. E10 and E1 showed, respectively, the highest and the lowest performance for AMTW. Moreover, except for Season IV (E8), Giarre allowed a high AMTW, likely due to a twofold reason: one is that, compared to Acireale, during April–May (the period of tuber growth) Giarre experienced higher minima and maxima air temperatures which are known to favor (to some extent) the development of tubers; the other reason may be related to the higher soil total N, available $P_2O_5$ and exchangeable $K_2O$ of Giarre than Mascali.

The AMMI2 biplot (Figure 3) was more accurate to extract the GEI variation since it captured a higher portion of variance than AMMI1. This statement is corroborated by the reports of Shahriari et al. [47] and Tena et al. [21]. The vertical and horizontal lines that passed through the origin (0, 0) divide the biplot into four sectors. Similar to the "which-won-where" GGE biplot, genotypes far from the origin are considered winning genotypes in the environments that fall in that sector [23]. In this study, G1 wins in E1, E2, and E9 for MY, mainly due to AMTW; G2 wins in E12 for MY, AMTW, and TSG; G3 wins in E2, E4, E9, and E11 for TSG; the same genotype wins in E2, E5, and E6 for CT 40–60 mm; G5 wins in E6, E7, E8, and E10 for MY. AMMI analysis is increasingly used for the evaluation of genotypes in multi-environmental trials, often reporting specific adaptations as in the present study [19,23]. The distance from the biplot origin controls the extent of GEI. Except for G3 and G4 in MY, G4 and G5 in AMTW, and G3 in TSG, all genotypes were far from the origin, hence they are more sensitive to the GEI and therefore specifically adapted to environments [48]. Considering that the three locations under study are close together, the fact that G3 and G4 show lower productive performances than G1 and G2 but high stability for all yield-related traits means that they could be introduced in the studied area. Neither for MY nor yield-related traits, genotypes clustered together, meaning that they did not behave similarly across the environments. Furthermore, except for UT and NMTP, E12 had a long vector; this indicated that it elicited strong interactive forces. On the contrary, environments with IPC1 scores near zero had small interaction effects, which indicated that all genotypes performed well in them, thus indicating they are favorable environments for all genotypes under study [20]. From the angle between the vectors of environment and genotype is possibly highlighting the type and degree of correlation, keeping in mind that it always points in the direction of a positive interaction. In this study, G2 positively correlated to E12 for all traits unless UT and CT 40–60 mm, G5 positively correlated to E8 unless UT, TSG, and CT 40–60 mm, and G4 negatively correlated to E9 unless NMTP and CT 40–60 mm (Figure 3). Regarding correlations between environments, E12 positively correlated to E4 and E11 for MY, UT, AMTW, and only E4 for NMTP, since they formed an acute angle. In the cases of obtuse and right angles, there is a negative correlation and no correlation, respectively [23,40]. Here, no clear correlations between environments and no environment clusters were observed.

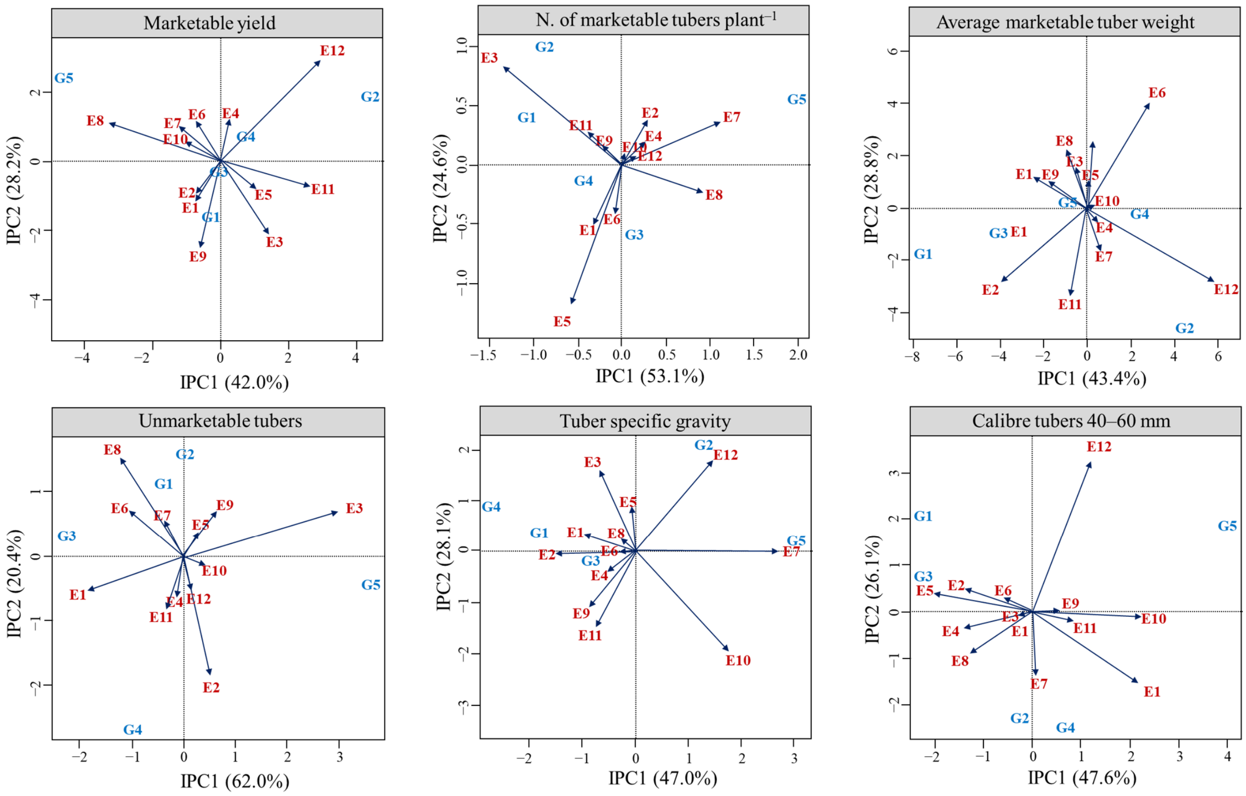


**Figure 3.** 'AMMI 2' biplot showing the first two interaction principal components (IPC1 and IPC2) effects of five potato genotypes (G) over 12 environments (E). The biplots were constructed with scaling = 0, centering = 2, and SVP = 2. G1: Arizona; G2: Generosa; G3: Levante; G4: Paradiso; G5: Vogue; E1–E4: Acireale (seasons I to IV); E5–E8: Giarre (seasons I to IV); E9–E12: Mascali (seasons I to IV).

### 3.2.2. GGE Analysis

The results from GGE were similar to those obtained from AMMI and combined ANOVA. A "which-won-where" biplot was constructed for each trait to explore the possible existence of mega-environments within the studied region and to identify winning genotypes in each mega-environment (Figure 4). In this biplot, a polygon is drawn joining the genotypes that are located farthest from the origin, containing all other genotypes within the polygon area. Each side of the polygon is crossed by a perpendicular line that divides the biplot into sectors. Vertex genotypes are the best performers in the environments encompassed within the sector (mega-environment) and, oppositely, vertex genotypes placed in a sector where there are no environments are treated as poor genotypes for all tested environments [21,40]. Here, in line with the AMMI2 biplot, no clear differentiation of mega-environments with similar characteristics was found, but results were closely dependent on the specific yield trait. For MY, three mega-environments have been identified: one encompassing E4, E5, E11, and E12 with G2 as the winning genotype, another encompassing E1, E2, E3, E9, and E10 with G1 as the winning genotype, and the last mega-environment comprising E7 and E8 with G5 at the vertex. G1 was also the winning genotype for NMTP in a mega-environment encompassing E1, E3, E9, and E11, as well as for AMTW in a mega-environment including E1, E2, and E9. The fact that G1 was the winning genotype for yield and other yield-related traits in Acireale in three out of four seasons (E1, E2, E3) may indicate that Arizona is able to optimally use soil fertility, given the higher soil nutrient element and organic matter levels of Acireale, thus suggesting its introduction in zones with high soil inputs. About AMTW, most environments (E4, E5, E6, E7, E8, E10, and E12) were encompassed in a mega-environment with G2 as the winner. At the same time, G1 and G2 were at the vertex in a sector with only E8 for UT; therefore, they are genotypes with low UT in the studied region. For TSG, excluding E7, all environments formed a mega-environment with G3 positioned at the vertex, in accordance with what was observed in AMMI2.

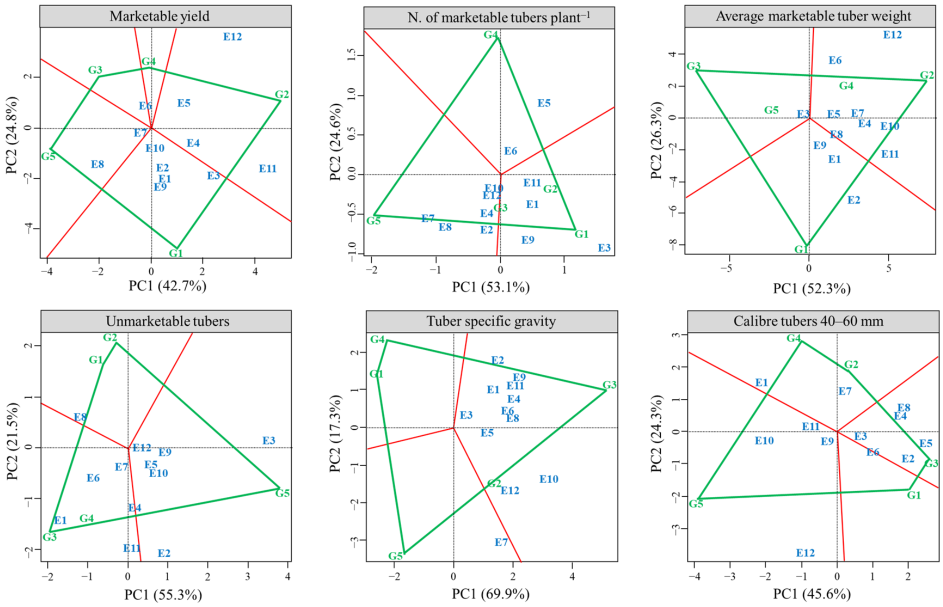


**Figure 4.** Polygon view of the GGE biplot illustrating the "which-won-where" analysis of five potato genotypes (G) over 12 environments (E). The biplots were constructed with scaling = 0, centering = 2, and SVP = 2. G1: Arizona; G2: Generosa; G3: Levante; G4: Paradiso; G5: Vogue; E1–E4: Acireale (seasons I to IV); E5–E8: Giarre (seasons I to IV); E9–E12: Mascali (seasons I to IV).

Figure 5 shows the "ranking genotypes" biplots, which compare the genotypes to an ideal genotype located at the center of the concentric circles. An ideal genotype has high performance coupled with high stability across environments [18,37]. In accordance with Rakshit et al. [22], the biplot was created by environment-focused partitioning of data (SPV = 2) without scaling to study the interrelationships among test environments. The average environment coordination (AEC) method was employed, in which an average environment axis (AEA) passes through the biplot origin and the average environment, represented on the AEA at the center of concentric circles [37]. Genotypes on the right side of AEC abscissa are above-average performers, whereas those on the left side underperform the overall mean. Moreover, the lower the length of the projection of a genotype, the more stable it is. From this study, it can be stated that G2 and G1 were close to the ideal genotype for productive components, despite a low stability of G2 for MY (Figure 5). They are also the worst genotypes for UT, which is an undesirable trait of potatoes. Cadersa et al. [29], Gedif and Yigzaw [27], and Muthoni et al. [28] reported similar findings for potato yield in Mauritius, Ethiopia, and Kenya, respectively. Summarizing, G1 (Arizona) is a variety specially bred for the South European and North African markets, and it is no coincidence that it can be noted as the best leading genotype in the studied area by virtue of its high productivity, as a consequence of both yield components and high stability. G2 (Generosa), despite the highest MY due to AMTW, can be considered less suitable than G1 because of the lower stability than G1. In addition, G3 was confirmed as the superior genotype for TSG; this, coupled with an MY stability (despite not being very high), suggests its introduction into the studied area for protected geographical identifications. Indeed, the choice of superior genotypes for protected geographical identifications needs the genotypes' assessment over diverse environments in a specific region.

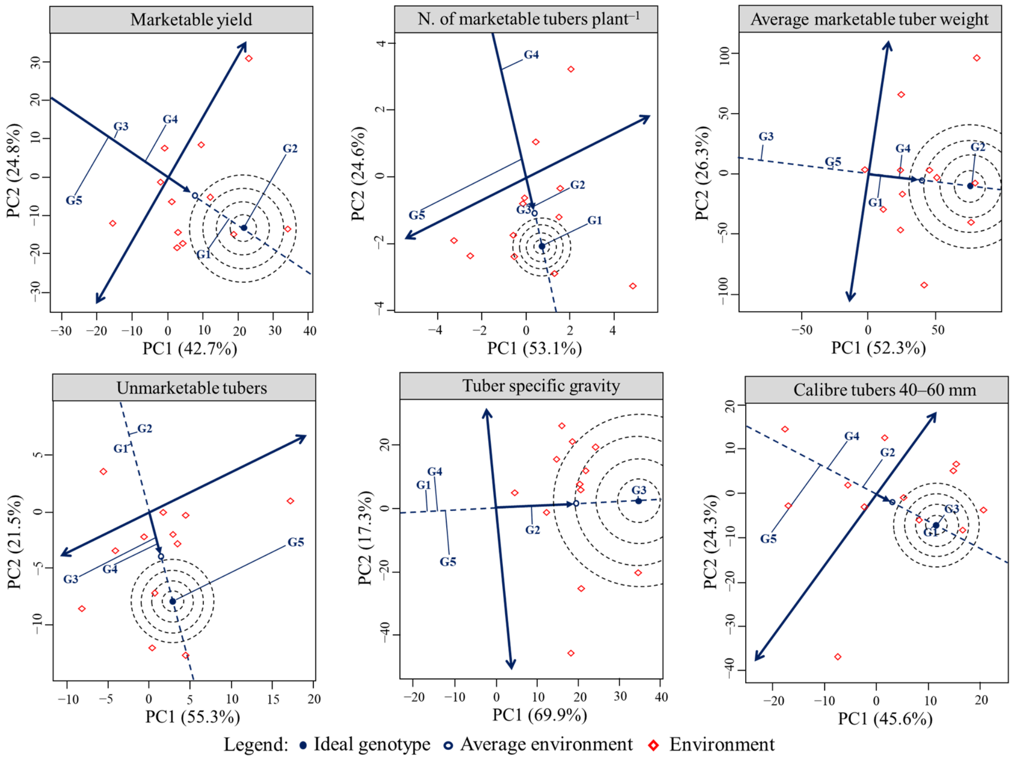


**Figure 5.** 'Ranking genotypes' GGE biplots illustrating the performance of five potato genotypes (G) over 12 environments (E) in comparison to an ideal genotype. The biplots were constructed with scaling = 0, centering = 2, and SVP = 2. G1: Arizona; G2: Generosa; G3: Levante; G4: Paradiso; G5: Vogue; E1–E4: Acireale (seasons I to IV); E5–E8: Giarre (seasons I to IV); E9–E12: Mascali (seasons I to IV).

Like in Figure 5, Figure 6 shows the "ranking environments" biplots, which help in evaluating the environments with respect to an ideal environment. Similarly to the ideal genotype, the ideal environment, a crucial element in multi-environmental trials, has the highest discriminativeness (power of genotype discrimination, visualized through the length of environment vectors, i.e., high PC1 scores) and the lowest representativeness (representativeness of all other environments, visualized through a small angle with the AEA, i.e., zero PC2 scores) [18]. Hence, a desirable environment should be near the ideal environment, thus having both high PC1 and low PC2 scores (Table S3), graphically represented by long vectors that form a short angle with the AEA (Figure 6). In this study, E4 for MY, E5 for UT and TSG, E1 for NMTP, E10 (followed by E4) for AMTW, and E3 for CT 40–60 mm were recorded as the most suitable environments for the studied potato genotypes in Sicily. It could be noted that the majority of ideal environments in terms of yield and yield components belong to Acireale, likely due to higher soil fertility (Table 1). A similar approach was used by Rakshit et al. [22] in sorghum by Khan et al. [23] in Bambara groundnut and by Gedif and Yigzaw [27] for potatoes in Ethiopia.

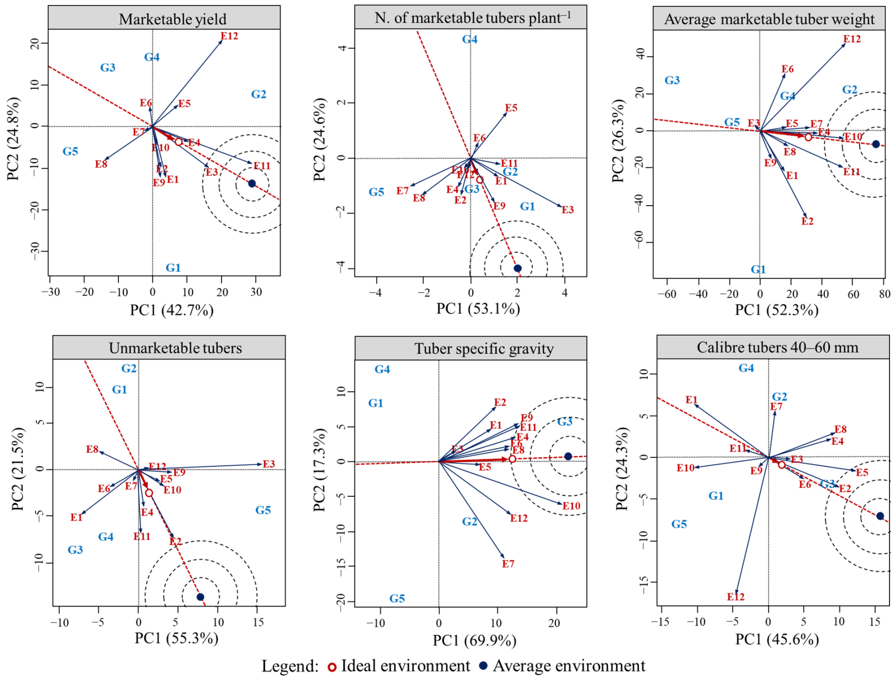

**Figure 6.** 'Ranking environments' GGE biplots showing the performance of 12 environments (E) and five potato genotypes (G) in comparison to an ideal environment. The biplots were constructed with scaling = 0, centering = 2, and SVP = 2. G1: Arizona; G2: Generosa; G3: Levante; G4: Paradiso; G5: Vogue; E1–E4: Acireale (seasons I to IV); E5–E8: Giarre (seasons I to IV); E9–E12: Mascali (seasons I to IV).

## 4. Conclusions

Once a new genotype is proposed for cultivation, its GEI with a specific area should be assessed. For this reason, the present multi-environmental trial was carried out to evaluate the productive performances of five recently introduced potato genotypes over four years and three locations in a Mediterranean climate. The GEI of all productive traits was significant, with the environment (and in particular the year) explaining the highest amount of variation, except for TSG and CT < 40 mm and >60 mm. AMMI and GGE biplot analyses recognized Arizona and Generosa as the superior genotypes in the studied region by virtue of their above-average mean performances and stability throughout the environments. In particular, Arizona and Generosa were the winning genotypes in most environments for MY, NMTP, and AMTW, whereas Levante was recognized as the leading genotype for TSG. The environments belonging to Acireale were the closest to the ideal environment, likely due to its higher soil fertility, while Season II (E2, E6, and E10) showed unfavorable climatic conditions, as demonstrated by the low NMTP and high UT. In conclusion, both AMMI and GGE proved to be effective tools for local potato breeding, the selection of protected geographical identifications, and the commercial introduction of high-yielding and stable potato cultivars across the Mediterranean climate.

**Supplementary Materials:** The following supporting information can be downloaded at https://www.mdpi.com/article/10.3390/agronomy13010101/s1: Table S1: F values of main effects and their interactions resulting from three-way analysis of variance (ANOVA) of potato yield and yield-related traits; Table S2: IPC1 and IPC2 scores derived from AMMI analysis of the five potato genotypes and 12 environments under study; Table S3: PC1 and PC2 scores derived from GGE analysis of the five potato genotypes and 12 environments under study.

**Author Contributions:** Conceptualization, G.M. and A.I.; methodology, A.S. and A.I.; software, data curation and formal analysis, A.S.; investigation, A.S., G.M. and A.I.; writing—original draft preparation, A.S. and A.I.; writing—review and editing, A.S., G.M. and A.I.; supervision, G.M. and A.I. All authors have read and agreed to the published version of the manuscript.

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

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