



# Article **Productivity and Stability Evaluation of 12 Selected** *Avena magna* ssp. *domestica* Lines Based on Multi-Location **Experiments during Three Cropping Seasons in Morocco**

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Abstract: Avena magna (2n = 4x = 28) is a tetraploid oat with a very high protein content compared to the hexaploid common oat, A. sativa (2n = 6x = 42). The wild type of A. magna originates from Morocco; its domestication has been achieved only within the past 25 years. The present study aimed to evaluate the productivity potential of an A. magna ssp. domestica collection of 11 advanced lines and a control variety, 'Avery'. Twelve trials were conducted during three cropping seasons at four, three, and five locations and revealed significant differences among the accessions. Data on twelve agro-morphological characters and two disease traits were collected, and they confirmed the presence of variability in this oat germplasm set. Mean grain yield was 30.76 q/ha and varied from site to site, ranging from 6.89 q/ha at Bouchane\_19 to 85.5 q/ha at Alnif\_21. Across experimental sites, plant height ranged from 48.93 to 120.47 cm; thousand kernel weight from 32.83 to 49.73 g; and harvest index from 20.43 to 31.33%. Line AT6 was relatively tolerant of BYDV and crown rust infections, based on disease severity scoring at the heading stage. According to AMMI analysis, 78% of the grain yield variability was due to the environment factor and 4% was explained by the genetic factor. Among the highest-yielding lines, AT5 and ATC were relatively unstable. Line AT5 was more productive at the elevated site of El Kbab\_19, and ATC performed better at the oasis location of Alnif\_21 under irrigation. Line AT7 showed the most stable behavior; it was high yielding across the five environments and exceeded the general mean of the experiments. The A. magna ssp. domestica lines proved their suitability for cultivation under local farming conditions. Their nutritional quality, especially their high protein content, makes them good candidates for further testing in the Moroccan breeding program and for integration into local cropping systems.

**Keywords:** Avena magna ssp. domestica; oat; advanced lines; agro-morphological traits; yield; productivity; stability

# 1. Introduction

An ever-increasing world population and climate change are among the major contributors to famine. Crop yields must continue to increase to attain the Sustainable Development Goals and ensure safe, nutritious, and adequate food for everyone. Cereals and derivatives should play a key role in this challenge since they are the staple food of most countries of the world and the primary food for livestock. Cereal grains constitute more than half of the food energy and half of the protein consumed on Earth [1]. With the pressure on resources and the climate change scenario, future food supplies not only need to be



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**Copyright:** © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). increased but also enriched especially in nutrients and protein to address food and nutrient security. Nutrition deficiencies have a significant impact on a country's productivity and can reduce its gross domestic product (GDP) by as much as 7% globally and up to 9–10% in African and South Asian countries [2]. In this context, there is a need to develop new sustainable sources of protein and nutrients to avoid the 150 more people expected to be at risk of protein deficiencies by 2050 [3]. It is evident that protein plays an essential role within the human body, including building muscle and bone and brain development. Its components, amino acids, are the building blocks of this development and are critically important in the first 1000 days of life and throughout the lifecycle [4]. Animal-based foods are excellent sources of protein but contribute 14.5% of all greenhouse gas emissions [5]. In this view, development of new nutrient-rich crops such as high-protein oat, *Avena magna* ssp. *domestica*, becomes one of the pathways to diversify the sources of protein and help attack the dual challenge of increasing supply in a sustainable manner.

Oat ranks sixth in world cereal production after wheat, maize, rice, barley, and sorghum [6]. The most widespread cultivated species of oat is common oat (*Avena sativa*), with Abyssinian oat (*A. abyssinica*), diploid naked or hulless oats (*A. nuda*), and lopsided oat (*A. strigosa*) being of relatively minor importance [7]. Morocco is the center of origin and a major center of diversity of the *Avena* genus [8]; consequently, it represents an essential country for expanding genetic resource conservation efforts and an interesting location for expanding oat production.

Oat is a cereal that has long been prized for its nutritional attributes, particularly in terms of mixed-linkage soluble beta-glucan, protein, oil, and antioxidants. Oat grain is also free-gluten and has the highest protein content among cereals; as a consequence, it is tolerated by most celiac disease patients [9]. Several previous studies have shown oat's health-promoting effects in preventing obesity, type II diabetes, gastrointestinal diseases, coronary heart disease, and certain types of cancer [10]. For human consumption, an increasing supply of oat-based products has been exhibited in the market, including a diverse array of breads, oatcakes, biscuits, granola bars, and ever more novel foods such as yogurt-type products and oat-based drinks [11–13].

The newly domesticated Moroccan tetraploid species *A. magna* (2n = 4x = 28, CCDD genome) was developed via sexual transfer of the domestication syndrome from the hexaploid common oat *A. sativa* (2n = 6x = 42, AACCDD; [14]). Subsequently, Jackson [7] produced a set of *A. magna* ssp. *domestica* lines via mutagenesis within a population of F<sub>2:8</sub> recombinant inbred lines (RILs) from a cross between a stable domesticated backcross line, Ba13-13, and a wild *A. magna* parent [15]. Oliver et al. [15] also mapped three of the domestication syndrome genes, for shattering (*Ba*), geniculate awn (*Awn*), and lemma pubescence (*Lp*), and measured the linkage of *Awn* and *Ba* with a terminal knob on chromosome 2C at a distance of 2.1 cM.

While the lines developed by Jackson [7] are suitable for production under standard cultivation practices, they also possess much higher protein levels than common oats, exceeding 25% in the relatively new cultivar 'Avery'. *Avena magna* ssp. *domestica* also showed promise in improving dietary iron and zinc in comparison to other cereals, thus potentially reducing anemia [16,17]. These characteristics make *A. magna* a good grain resource for the development of high-quality protein products to address developing-world malnutrition, developed-world obesity, and high-quality livestock feed [11]. Since *A. magna* is already adapted to the semi-arid conditions of Morocco, it is a promising source of sustainable grain for a world increasingly affected by climate change. Nevertheless, there is still a need to continue breeding under Moroccan conditions for traits such as resistance to seed dehiscence, lodging, dormancy, productivity, and stability, as well as tolerance of diseases.

The main objective of this study was to assess the diversity and performance of *A. magna* ssp. *domestica* lines using 'Avery' as the control in seven diverse environments in Morocco. The evaluation included morphological and yield parameters, disease tolerance (crown rust, BYDV), and yield stability.

## 2. Materials and Methods

## 2.1. Plant Materials

Eleven *A. magna* ssp. *domestica* lines were used in this study along with 'Avery', which was registered in the Official Moroccan Catalog in 2019, as control (Table 1). These lines were selected from a set of 41 lines introduced in Morocco during the 2017–2018 and 2018–2019 cropping seasons for adaptation trials. *A. magna* was domesticated via hybridization with common hexaploid oat *A. sativa* followed by a single backcross cycle to produce line Ba13-13 [14]. Subsequently, Jackson [7] produced six foundational *A. magna* ssp. *domestica* lines from a domesticated Ba13-13 × wild *A. magna* # 169 population [15,18], segregating for the wild-type growth habit and resistance to field races of crown rust (*Puccinia coronata*) in Baton Rouge, LA, USA. According to Jellen et al. [19], a virtual pedigree using a genotype/phenotype model with the JMP Genomics software package version 10 (SAS Institute Cary, NC, USA) was used as instruction to produce the 41 lines and the internal control Avery by intercrossing the foundational lines.

**Table 1.** List of A. magna ssp. domestica lines used in this study.

IAV_ID	Correspond	LINE_ID	PEDIGREE
ATC (Avery)	A40	BAM_96-5-6	BAM_96-5-6
AT1	A18a	2013Y1193	BAM_34/55_1
AT2	A14	2013Y1397	BAM_6/235_44
AT3	A27	2013Y1291	BAM_55/231_22
AT4	A35	2013Y1302	BAM_55/231_33
AT5	A44	2013Y1307	BAM_55/231_38
AT6	A45	2013Y1200	BAM_34/55_36
AT7	A02	2013Y1297	BAM_55/231_28
AT9	A20	2013Y1275	BAM_55/231_6
AT13	A41	2013Y1508	BAM_34/235_21
AT14	A43	2013Y1310	BAM_55/231_41
AT15	A10	2013Y1373	BAM_6/235_20

Explanation: IAV\_ID: Institut Agronomique et Vétérinaire Hassan II Identifier. ATC: Avena magna spp. domestica variety 'Avery'.

#### 2.2. Experimental Locations

Field experiments were conducted in three consecutive growing seasons (2018–2019, 2019–2020, and 2020–2021), and at 4, 3, and 5 experimental sites in each of these respective winter growing seasons. The selected experimental sites belong to contrasting Emberger bioclimatic stages across the central part of Morocco including per-arid (Alnif in the Anti-Atlas/Sahara); arid (Bouchane in the Phosphate Plateau); semi-arid cold winter (El Kbab in the Middle Atlas); sub-humid (Ain Itto in the Saïs Plain); and sub-humid cold winter (Oukaimeden in the High Atlas; [20]).

Among the twelve trials conducted in this investigation, one was not successful; data from the other eleven trials were subjected to ANOVA analysis. As four tests did not reveal any productivity differences among the advanced lines, the productivity and stability evaluation comprised the seven remaining trials.

Site descriptions for the seven retained trials are reported in Table 2. During the 2018–2019 season, experimental trials were installed at El Kbab (mountain plateau) on 29 November and Bouchane (Phosphate Plateau) on 30 November. Experiments for the following season, 2019–2020, were conducted at only one location, Bouchane, with a sowing date of 23 November. The third season (2020–2021) consisted of four experimental stations: Ain Itto, Bouchane, Oukaimeden, and Alnif. Seeds were sown on 16 October in Oukaimeden, 18 October in Bouchane, 20 October in Ain Itto, and on 21 November in Alnif.



**Figure 1.** Experimental site photographs: (**A**) Bouchane, April 2020; (**B**) El Kbab, June 2019; (**C**) Oukaimeden, June 2021; (**D**) Alnif, April 2021; (**E**) *A. magna* panicle from Ain Itto site.

Location **Geographic Position** Soil Type Rain Hum S.H Harvest Date Zone Alt Temp Latitude Longitude Min Max 34°05'33" N 5°48′54″ W Ain Itto 21 Saïss Plain 855 Vertisols 8 36 609.8 61.8 3099 2 June 2021 Alnif 21 31°06'37" N 5°03'50" W 1320 9 43 432\* 17 May 2021 Oasis Fluvisols 2623529 Bouchane\_21 Phosphate Plateau 32°14'35" N 8°19'45" W 830 Cambisols 9 38 250.2 54.1 3304 25 May 2021  $31^\circ 14'07''$  N 7°48'42" W 2530 Oukaimeden 21 Atlas Mounain Fluvisols 11 40 319.3 47.03369 25 June 2021 Bouchane\_20 Phosphate Plateau 32°14'35" N 8°19'45" W 830 Cambisols 9 40 105.5 53.7 3376 22 June 2020 El kbab\_19 32°42′25″ N 5°31′57″ W Middle Atlas 1540 Fluvisols 2 35 573.0 50.9 3477 3 July 2019 Bouchane 19 Phosphate Plateau 32°14'35" N 8°19'45" W 830 Cambisols 9 33 313.1 53.4 3463 20 June 2019

**Table 2.** Location and description of the experiment agro-climatic sites. Climate data were provided by worldweatheronline.com. Only data covering the periods of the experiments (between October and July) are reported.

With additional 200 m<sup>3</sup> of irrigation during the cycle development of plants. \* By simplifying the number added on each location, the cropping season is specified, and each number is used for the rest of the article: 21 (season 2020–2021), 20 (season 2019–2020), and 19 (season 2018–2019). Alt: altitude (m); Temp: temperature (°C); Rain: rainfall (mm); Hum: humidity (%); S.H: sun hour (h).

In Alnif, Ain Itto, and Bouchane, mechanized moldboard plowing was used to prepare the soil for sowing, while for El Kbab and Oukaimeden, tillage was performed with a horse-drawn plow. Depending on the germination rate, the sowing dose was calculated to establish a density of 25 plants per linear meter. Trials were fertilized at the early tillering stage in the form of ammonium nitrate at the rate of 45 Kg/ha. Accessions were evaluated under rainfed conditions except for the Alnif site, where irrigation (1 m<sup>3</sup> of water per m<sup>2</sup>) was supplied due to aridity. Weed control was performed manually at the tillering and flowering stages; if necessary, the number of weeding times exceeded two, depending on the degree of weed infestation, to avoid competition between plants.

#### 2.3. Experimental Design

The field experiment design was a randomized complete block with three replications. The sowing plan varied from one site to another according to land availability for the trial. For the 2018–2019 season, the elementary plot included three six-meter rows at Bouchane and four three-meter rows at El Kbab with an inter-row spacing of 0.5 and 0.35 m, respectively. The space between elementary plots was 1.2 m for Bouchane and 1 m for El Kbab. Plots at Bouchane during the 2019–2020 season had four rows of 3.6 m length and were spaced 0.30 m apart. The 2020–2021 experimental plan was carried out in six rows of 12.5 m length and 0.3 m spacing. However, there was an exception at the Alnif and Oukaimeden sites, where eight rows of 8 m and four rows of 3 m were used, respectively, because of the land space limitations. The seeding rate per row was adjusted accordingly in those two sites.

#### 2.4. Notations and Measurements

Crown rust (RC) and barley yellow dwarf virus (BYDV) assessments were made under natural infection at the flowering stage. The percentage of leaf area showing pathogen symptoms was scored for each accession and site where diseases were noticeable. At maturity, 12 agro-morphological traits were scored on harvested individual plants. Plant height (PH, cm) was measured at maturity from the soil surface to the tip of the panicle. After hand-harvesting of the four plants per elementary plot, the panicles were threshed and dried at 35 °C for seeds and 70 °C for other parts of the plant (stem weight SW (g) and root weight RW (g)). Grain yield per plant YP (g) and dry matter per plant DMP (g) were measured using a weighing scale. Harvest index (HI, %) was derived as the ratio of grain yield to total biomass by the formula: HI = (YP/(YP + DMP)) × 100. At harvest, plant density was estimated by counting the number of plants on a one-meter row length. Subsequently, the yield in quintals per hectare (Yield q/ha) and dry matter in quintals per hectare (DM q/ha) were estimated according to plant density, yield per plant, and the plot area which varied between experimental sites. The root length RL (cm), number of fertile tillers NFT, and number of spikelets per panicle (NSP) were also assessed. Furthermore, the weight of a thousand unshelled kernels (TKW g) was estimated using three samples of 250 seeds.

#### 2.5. Statistical Analysis

Collected data were subjected to a variety of statistical analyses. Descriptive statistics, two- and three-way analyses of variance (ANOVA), and multivariate analyses such as principal component analysis (PCA) and additive main effects and multiplicative interaction (AMMI) were performed to assess the genetic diversity in terms of productivity, yield stability, and disease tolerance among lines and experimental sites. The R software version 3.5.1 was used for these tests. The ANOVA tests were conducted to assess the variability among lines within and between sites. For significant ANOVAs, determination of homogeneous groups of lines was performed using the Newman–Keuls post hoc test. Associations among pertinent traits, which were useful for line classifications, as well as significant correlations between those traits, were performed through multivariate principal component analysis (PCA) with Factominer package version 2.4 [21]. The AMMI analysis via R [22] combines both ANOVA and PCA to determine the main effects and genotype-by-environment interactions (GEI) in multi-location trials. The interaction principal component axes, IPCA1 and IPCA2, are calculated and displayed as biplots to project GEI patterns graphically. Initially, adaptability and phenotype stability across the locations were performed by the AMMI method described by Zobel et al. [23]. Subsequently, Purchase [24] developed the AMMI stability value (ASV) based on the AMMI model's principal components axis 1 and 2 scores for each genotype, respectively. Genotypes with small values of IPCA1, IPCA2, and ASV are more stable across environments. Of course, yield stability is a critical factor to protect small-holding subsistence farmers from starvation in adverse growing seasons.

## 3. Results

#### 3.1. Disease Assessments

Crown rust (RC; *Puccinia coronata* f. sp. *avenae*), barley yellow dwarf virus (BYDV), and powdery mildew (*Blumeria graminis* f. sp. *avenae*) are the three most common diseases found on oats in Morocco [19]. Powdery mildew was not noticeable in the experimental trials; consequently, only RC and BYDV infections were assessed at the flowering stage in Bouchane\_19, El Kbab\_19, Bouchane\_21, Ain Itto\_21, and Oukaimeden\_21. Table 3 shows that BYDV symptoms were more frequent than the two other diseases in five out of seven trials. The ANOVA test for BYDV revealed significant differences among oat lines at three sites: Bouchane\_21, Ain Itto\_21, and Oukaimeden\_21. The average leaf area covered by the virus was equal to 14.62 and 14.25% in Ain Itto\_21 and Bouchane\_21, respectively. El Kbab\_19 BYDV infection was the lowest at only 4.09% and with no significant differences among lines. Regarding RC, the ANOVA test was significant in Bouchane\_19 with an average infection value of 20.28%.

Table 3. Summary one-way ANOVA for BYDV and RC infestations.

Site	Season	Trait	F	Mean (%)	<i>p</i> _Value
Bouchane_19	2018-2019	BYDV	2.109 NS	6.11	0.061
		RC	6.811 ***	20.28	0.000
El Kbab_19	2018-2019	BYDV	0.731 NS	4.09	0.699
Bouchane_21	2020-2021	BYDV	7.928 ***	14.25	0.000
Ain Itto_21	2020-2021	BYDV	5.437 ***	14.62	0.000
Oukaimeden_21	2020-2021	BYDV	5.377 ***	9.38	0.000

NS = not significant; \*\*\* significant at *p* = 0.001. BYDV: barley yellow dwarf virus; RC: Crown rust.

The Student–Newman–Keuls test allowed ranking of the oat lines in locations where disease infections were significant (Table 4). There was an irregular ranking of the BYDV infection across sites apart from line AT6. This accession tended to show more tolerance than the others with a value of 9% at Bouchane\_21 (Rank 1), 10% at Ain Itto\_21 (Rank 2), and 5% at Oukaimeden\_21 (Rank 1). It was also ranked second for RC at Bouchane\_19 (13.33%).

			RC (%)								
Е	Bouchane_2	1		Ain Itto_21	l	Ou	ıkaimeden_	21	Bouchane_19		
AT6	9.00	а	AT3	8.33 a		AT6	5.00	а	ATC	10.00	а
AT4	10.00	ab	AT6	10.00	ab	AT13	7.50	b	AT6	13.33	ab
AT13	11.00	ab	AT14	11.67	abc	AT1	8.75	b	AT2	13.33	ab
AT5	12.00	ab	AT1	13.33	abcd	AT5	8.75	b	AT5	13.33	ab
ATC	12.00	ab	ATC	13.33	abcd	AT14	10.00	bc	AT1	16.67	ab
AT3	12.50	ab	AT2	14.17	abcd	AT15	10.00	bc	AT3	16.67	ab
AT15	13.50	ab	AT9	15.83	bcd	AT2	10.00	bc	AT4	16.67	ab
AT14	16.00	bc	AT15	16.25	cd	AT3	10.00	bc	AT14	23.33	ab
AT2	16.00	bc	AT7	17.08	cd	AT7	10.00	bc	AT15	23.33	ab
AT1	19.00	с	AT13	17.50	cd	AT9	10.00	bc	AT13	26.67	bc
AT9	19.00	с	AT4	18.33	d	ATC	10.00	bc	AT7	30.00	с
AT7	21.00	с	AT5	19.58	d	AT4	12.5	с	AT9	40.00	d

Table 4. Disease rankings of the 12 lines using the Student–Newman–Keuls test.

Values within a column followed by a common (a–d) are not significantly different (p < 0.05). BYDV: barley yellow dwarf virus; RC: crown rust.

### 3.2. Analyses of Agro-Morphological Traits

The average values (means) and coefficients of variation (CVs) of the different morphological (PH, RL) and agronomic (NFT, Yield, DM, HI, etc.) traits across sites are presented in Table 5. Plant height (PH) was less variable than the other traits, with CVs of 9.97% at Oukaimeden\_21 and 21.18% at Bouchane\_19. The variable TKW also possessed small CVs among samples but was quite variable from site to site (6.82% and 55.58%, respectively). As expected, traits related to grain yield or biomass showed large variation. For example, the CV for yield was over 55% across sites. The Alnif\_21 trial yield was the highest at 85.5 q/ha, while the Bouchane\_21 trial was the least productive at just 6.89 q/ha. Bouchane\_19 plants, in comparison to the other sites, were the shortest (48.93 cm) and had the deepest roots (16.16 cm).

**Table 5.** Descriptive statistics of the agro-morphological traits of domesticated *A. magna* for the three cropping seasons.

		Season 2	2018–2019		Season 2	019–2020		Season 2020–2021						
	El Kbab_19		Bouchane_19		Bouchane_20		Ain_I	Ain_Itto_21		Alnif_21		ane_21	Oukaimeden_21	
Traits	Mean	CV	Mean	CV	Mean	CV	Mean	CV	Mean	CV	Mean	CV	Mean	CV
PH	72.86	13.92	48.93	21.18	87.91	14.70	118.47	15.65	116.89	11.44	64.61	14.08	120.47	9.97
RL	15.41	19.84	16.16	22.28	15.66	21.83	14.19	20.05	12.58	19.69	14.42	22.6	11.87	14.10
NFT	4.35	69.81	3.10	34.25	4.80	44.98	4.42	43.24	11.09	32.09	3.59	51.99	5.60	36.07
DMP	15.36	56.65	9.87	74.84	9.35	88.19	12.54	41.16	35.51	40.92	4.08	58.74	13.59	48.41
YP	9.69	59.6	5.63	86.16	3.18	65.59	4.74	52.71	16.1	51.14	1.83	69.37	5.92	51.28
HI	25.74	79.56	20.43	86.38	27.23	27.33	27.12	22.53	30.68	23.67	31.33	24.14	30.37	17.32

		Season 2	018-2019		Season 2	.019–2020	Season 2020–2021								
	El Kbab_19		Bouchane_19		Bouchane_20		Ain_Itto_21		Alnif_21		Bouchane_21		Oukaimeden_21		
Yield	51.96	77.79	23.19	85.76	11.85	62.79	20.17	55.77	85.5	55.78	6.89	87.64	18.99	60.83	
DM	78.33	67.19	42.76	82.94	34.41	80.98	53.5	46.01	188.15	45.77	15.34	81.72	43.85	59.30	
NSP	53.89	58.81	29.74	76.45	16.17	38.40	25.3	52.15	43.43	34.23	14.24	53.21	24.83	32.50	
TKW	45.73	11.84	37.66	55.58	40.61	7.58	43.94	6.82	42.76	6.98	34.29	45.11	40.04	7.95	
SW	13.74	56.7	8.55	77.51	NA	NA	10.86	41.64	26.63	41.7	2.83	60.01	11.61	46.57	
RW	1.62	72.66	1.33	74.59	NA	NA	1.68	48.65	8.88	51.83	1.25	63.9	1.98	66.73	

Table 5. Cont.

Explanations: CV: coefficient of variation; PH = plant height (cm); RL = root length (cm); NFT = number of fertile tillers; DMP = dry matter per plant (g); YP = grain yield per plant (g); HI = harvest index (%); Yield = grain yield per hectare (q); DM = dry matter per hectare (q); NSP = number of spikelets per panicle; TKW = thousand-seed weight (g); SW = stem weight (g); RW = root weight (g); NA: not available.

The two-way ANOVA detected significant differences among lines for all the investigated traits except for DMP, TKW, and SW at Bouchane\_19.

Table 6 summarizes the line rankings for seed yield at the experimental sites based on the Student–Newman–Keuls test. Table 6 shows that there was no dominant line across all locations. For example, the ATC control performed well in El Kbab\_19 (73.8 q/ha) and Alnif\_21 (114.9 q/ha), while it ranked last at Bouchane\_20 (6.67 q/ha) and Oukaimeden\_21 (11.64 q/ha). Line AT5 had the highest yield at Bouchane\_19 (39.45 q/ha) and El Kbab\_19 (103.17 q/ha); it yielded relatively well at Bouchane\_21 (9.13 q/ha) and Oukaimeden\_21 (27.11 q/ha) but was less productive at the other locations.

Merely considering line performance through all sites combined does not allow for their correct ranking because they showed contrasting productivity potential. The three-way ANOVA was conducted to take into account line  $\times$  environment interaction. The ANOVA\_3 test revealed significant differences among genotypes for most of the traits except TKW. Furthermore, it showed a high location effect on genotype morphology and productivity.

The ranking of the experimental sites for productivity parameters showed that average Yield varied from 6.89 to 85.5 q/h; DM from 15.34 to 188.15 q/ha; and HI ranged from 20.43 to 31.33%. Alnif\_21 and El Kbab\_19 produced both high grain and biomass yields in comparison to the other sites. During the 2019\_2020 and 2020\_2021 seasons, the arid Bouchane site produced less than the other locations.

The Student–Newman–Keuls test results of the three-way ANOVA are reported in Table 7. Combining all the sites' data showed clearly that AT5 was the most productive line. It was ranked first for grain yield (43.41 q/ha), HI (34.76%), and TKW (49.73 g). For the DM, it was ranked second after AT1 with a value of 69.24 q/ha. On the other hand, the least productive lines were AT15 (23.90 q/ha) and AT9 (23.11). Regarding the morphological traits, the accession PH ranged between 84.07 cm (AT2) and 94.92 cm (AT15). Lines ATC (85.06 cm), AT6 (84.64 cm), and AT2 (84.07 cm) were the shortest. Root length (RL), NFT, and NSP varied between 13.52 (AT5) and 15.61 cm (AT15); between 4.03 (AT15) and 5.93 (AT1); and between 24.85 (AT2) and 36.06 (AT13), respectively.

	S	eason 2	2018–2019	)		Season 2019–2020						Season 2020–2021								
Βοι	uchane_19	)	I	El Kbab_1	9	Bouchane_20		A	Ain_Itto_21		Alnif_21		Bouchane_21			Oukaimeden_21				
AT5	39.45	а	AT5	103.17	а	AT14	22.13	а	AT3	31.64	а	ATC	114.9	а	AT4	12.26	а	AT9	34.83	а
AT9	28.86	ab	ATC	73.8	b	AT3	15.41	b	AT15	27	b	AT1	103.7	ab	AT7	11.84	а	AT5	27.11	ab
AT2	27.21	ab	AT1	68.52	bc	AT15	15	bc	AT13	22.29	bc	AT7	97.1	abc	AT1	9.28	ab	AT7	24.67	bc
AT3	25.09	ab	AT3	62.7	bc	AT13	14.14	bc	AT6	22.1	bc	AT14	93.5	abc	AT5	9.13	ab	AT14	19	bc
AT13	24.85	ab	AT6	59.01	bc	AT1	13.4	bc	AT1	21.69	bc	AT4	90.7	abc	AT2	8.88	ab	AT4	18.96	bc
AT7	24.17	ab	AT2	58.09	bc	AT4	11.23	bc	AT14	21.14	bc	AT15	90.3	abc	AT3	6.9	abc	AT13	18.48	bc
AT1	23.99	ab	AT7	44.8	bcd	AT9	10.82	bc	AT9	20.49	bc	AT6	88.2	abc	AT6	5.19	bc	AT15	17.24	bc
ATC	23.19	ab	AT13	38.34	bcd	AT5	9.99	bc	ATC	16.82	cd	AT13	87.7	abc	AT9	4.75	bc	AT2	15.47	bc
AT4	19.3	ab	AT4	36.12	bcd	AT7	9.99	bc	AT7	16.54	cd	AT5	86	abc	AT14	4.59	bc	AT6	14.24	с
AT14	15.24	b	AT14	30.76	cd	AT6	9.19	bc	AT5	16.46	cd	AT3	61.6	bc	AT13	4.2	bc	AT3	13.59	с
AT6	15.15	b	AT15	13.47	d	AT2	7.4	bc	AT4	15.93	cd	AT2	58.7	bc	ATC	2.83	с	AT1	12.6	с
AT15	9.08	b	AT9	10.35	d	ATC	6.67	с	AT2	9.99	d	AT9	53.7	с	AT15	2.81	с	ATC	11.64	с

Table 6. Ranking of the 12 lines for grain yield per hectare at each site where it was significant across the three cropping seasons.

Values within a column followed by a common (a–d) are not significantly different (p < 0.05).

		14	ble 7. Ranking	g 01 12 mie	s ioi pinicipa		phological tra		C (Avery) as c	.0111101.					
			Agronom	nic Traits				Morphological Traits							
Yi	eld	Ι	DM	]	HI		TKW		PH		RL	NTF		NSP	
AT5	43.41 <sup>a</sup>	AT1	80.05 <sup>a</sup>	AT5	34.76 <sup>a</sup>	AT5	49.73 <sup>a</sup>	AT15	94.92 <sup>a</sup>	AT15	15.61 <sup>a</sup>	AT1	5.93 <sup>a</sup>	AT7	36.06 <sup>a</sup>
AT1	35.93 <sup>ab</sup>	AT5	69.24 <sup>ab</sup>	AT4	31.78 <sup>b</sup>	AT4	42.94 <sup>ab</sup>	AT13	94.57 <sup>a</sup>	AT13	15.27 <sup>ab</sup>	AT14	5.69 <sup>ab</sup>	AT13	34.34 <sup>ab</sup>
ATC	35.66 <sup>ab</sup>	ATC	67.33 <sup>abc</sup>	AT3	31.33 <sup>b</sup>	AT9	41.93 abc	AT7	92.71 <sup>ab</sup>	AT14	15.23 <sup>ab</sup>	AT9	5.64 <sup>ab</sup>	AT14	33.13 <sup>ab</sup>
AT3	31.74 <sup>bc</sup>	AT13	66.75 <sup>abc</sup>	ATC	31.20 <sup>b</sup>	AT1	41.62 abc	AT5	89.93 <sup>bc</sup>	AT7	14.96 <sup>abc</sup>	AT4	5.6 <sup>ab</sup>	AT5	31.56 <sup>abc</sup>
AT7	31.64 <sup>bc</sup>	AT6	65.85 <sup>abc</sup>	AT6	30.35 <sup>b</sup>	AT7	41.27 <sup>abc</sup>	AT4	89.76 <sup>bc</sup>	AT4	14.83 <sup>abcd</sup>	AT6	5.51 <sup>ab</sup>	AT15	30.48 abc
AT6	30.15 <sup>bc</sup>	AT3	63.36 <sup>abc</sup>	AT2	29.67 <sup>b</sup>	AT6	40.99 abc	AT9	88.94 <sup>bcd</sup>	AT1	14.31 bcd	AT5	5.17 <sup>abc</sup>	ATC	30.47 <sup>abc</sup>
AT13	29.78 <sup>bc</sup>	AT4	62.83 abc	AT1	29.47 <sup>b</sup>	AT2	40.29 <sup>bc</sup>	AT1	88.58 <sup>bcd</sup>	AT6	14.13 bcd	ATC	4.98 <sup>bc</sup>	AT3	30.39 abc
AT14	28.75 <sup>bc</sup>	AT14	61.77 <sup>bc</sup>	AT7	22.57 <sup>c</sup>	AT14	40.19 <sup>bc</sup>	AT3	88.56 <sup>bcd</sup>	AT3	14.11 <sup>bcd</sup>	AT2	4.94 <sup>bc</sup>	AT1	28.77 <sup>abc</sup>
AT4	28.07 <sup>bc</sup>	AT2	61.28 <sup>bc</sup>	AT9	22.17 <sup>c</sup>	AT15	39.60 <sup>bc</sup>	AT14	88.07 <sup>cd</sup>	AT9	13.85 <sup>cd</sup>	AT13	4.86 <sup>bc</sup>	AT4	28.50 <sup>abc</sup>
AT2	27.32 <sup>bc</sup>	AT7	58.33 <sup>bc</sup>	AT14	20.33 <sup>c</sup>	AT13	38.72 <sup>bc</sup>	ATC	85.06 <sup>de</sup>	AT2	13.81 <sup>cd</sup>	AT3	4.58 <sup>cd</sup>	AT6	28.04 <sup>bc</sup>
AT15	23.90 <sup>c</sup>	AT15	52.64 <sup>bc</sup>	AT15	20.28 <sup>c</sup>	ATC	37.97 <sup>bc</sup>	AT6	84.64 <sup>de</sup>	ATC	13.65 <sup>d</sup>	AT7	4.45 <sup>cd</sup>	AT9	25.23 <sup>c</sup>
AT9	23.11 <sup>c</sup>	AT9	49.99 <sup>c</sup>	AT13	19.88 <sup>c</sup>	AT3	32.83 <sup>c</sup>	AT2	84.07 <sup>e</sup>	AT5	13.52 <sup>d</sup>	AT15	4.03 <sup>d</sup>	AT2	24.85 <sup>c</sup>

 Table 7. Ranking of 12 lines for principal agro-morphological traits with ATC (Avery) as control.

Values within a column followed by a common (a–e) are not significantly different (p < 0.05). Yield = grain yield per hectare (q); DM = dry matter per hectare (q); HI = harvest index (%); TKW = thousand-seed weight (g); PH = plant height (cm); RL = root length (cm); NFT = number of fertile tillers; NSP = number of spikelets per panicle.

### 3.3. Principal Components Analysis

The principal component analysis (PCA) was conducted to identify the main traits that contribute to differentiation among lines. PCA considers all the variables at the same time to cluster the oat lines through their similarities. The PCA outputs showed that 84.57% of the variability was explained by the first four principal components' axes. This high percentage reflects strong discrimination among the assessed lines. The main contributors to the first principal component (PC1) were PH, RL, HI, and RC (35.73%). Thus, PC1 can be considered an indicator of the plant morphology behind the RC disease. Both PC2 and PC3 accounted for 37.71% of the total variation; they were mainly linked to the grain and biomass yield components: NTF, NSP, SW, DMP, YP, DM, and Yield. The fourth axis was essentially explained by the TKW and BYDV degree of susceptibility.

According to the Pearson correlations matrix (Table 8), DMP exhibited both highly significant and positive correlations with YP and SW ( $R^2 = 0.81$ ;  $R^2 = 0.82$ ). Yield per plant (YP) was also positively correlated with NSP and RW ( $R^2 = 0.63$  and  $R^2 = 0.65$ ). Grain yield per hectare (Yield) and DM were positively correlated at 75%. A negative correlation was found between the HI and PH ( $R^2 = -0.59$ ), RL ( $R^2 = -0.74$ ), and RC ( $R^2 = -0.78$ ). On the other hand, the HI showed a positive relationship with grain yield ( $R^2 = 0.63$ ). The susceptibility to BYDV and RC diseases appeared together in oat plants up to 62%.

The biplot PC1  $\times$  PC2 revealed four accessions' clusters (Figure 2). Two accessions, AT5 and AT1, formed cluster I, which included high biomass and grain production potential. Cluster II gathered AT13 and AT14, which had good individual plant performance (grain yield and dry matter per plant). Cluster III included ATC and AT6, short size, and high harvest-index lines with better tolerance to BYDV and RC infection than AT7 and AT9. Cluster IV included AT4 with its high TKW.

Table 8. Pearson correlation with traits from principal component analysis results.

	PH	RL	NFT	NSP	RW	SW	DMP	YP	Yield	DM	HI	TKW	RC	BYDV
PH	1													
RL	0.72	1												
NFT	-0.48	-0.31	1											
NSP	0.60	0.54	-0.38	1										
RW	0.22	0.41	0.03	0.63	1									
SW	0.27	0.32	0.62	0.10	0.15	1								
DMP	0.36	0.55	0.51	0.39	0.49	0.82	1							
YP	0.43	0.34	0.36	0.63	0.65	0.67	0.81	1						
Yield	-0.15	-0.47	0.13	0.32	-0.07	0.00	-0.06	0.30	1					
DM	-0.26	-0.26	0.42	0.12	-0.27	0.29	0.25	0.19	0.75	1				
HI	-0.59	-0.74	0.25	-0.36	-0.50	-0.11	-0.41	-0.24	0.63	0.53	1			
TKW	0.06	-0.21	0.36	-0.04	0.10	0.28	0.10	0.35	0.40	0.14	0.23	1		
RC	0.54	0.38	-0.05	0.14	0.36	0.24	0.31	0.31	-0.56	-0.63	-0.78	-0.01	1	
BYDV	0.52	0.24	-0.10	0.23	0.13	0.17	0.10	0.30	-0.09	-0.29	-0.45	0.44	0.62	1

Bolded values are significant Pearson correlation. PH = plant height (cm); RL = root length (cm); NFT = number of fertile tillers; NSP = number of spikelets per panicle; RW = root weight (g); SW = stem weight (g); DMP = dry matter per plant (g); YP = grain yield per plant (g); Yield = grain yield per hectare (q); DM = dry matter per hectare (q); HI = harvest index (%); TKW = thousand-seed weight (g); RC: crown rust (%); BYDV: barley yellow dwarf virus (%).



**Figure 2.** Biplot principal component 1 (PC1), principal component 2 (PC2) of the 12 lines, and traits derived from the average linkage cluster analysis. Explanation: traits: PH = plant height (cm); RL = root length (cm); NFT = number of fertile tillers; DMP = dry matter per plant (g); YP = grain yield per plant (g); HI = harvest index (%); Yield = grain yield per hectare (q); DM = dry matter per hectare (q); NSP = number of spikelets per panicle; TKW = thousand-seed weight (g); SW = stem weight (g); RW = root weight (g).

# 3.4. AMMI Analysis

An AMMI analysis was performed to scrutinize yield stability of the experimental lines across environments. The analysis of variance (ANOVA) associated with the AMMI model revealed highly significant site, line, and their interaction (S × L) effects (*p*-value  $\leq$  0.001). The environment explained the largest grain yield variability (78%), followed by the interaction (18%; Table 9). Only 4% of the total sum of squares was assigned to the genetic factor of the *A. magna* ssp. *domestica* lines—the large contrast between the sites was intended to assess the specific adaptation of the experimental lines through the GxE interactions. Differences among lines were more expressed within the experimental sites. The two first axes, IPCA1 and IPCA2, explained 59.7% and 31.7%, respectively, of the genotype×environment interaction (GEI) sum of squares.

**Table 9.** Additive main effects and multiplicative interaction analysis (AMMI) analysis of variance for grain yield of 12 lines for three cropping seasons.

Source	Df	Sum Sq	Mean Sq	F Value	Pr (>F)	% Variation
Site	6	596,996	99,499	12.32 ***	$6.92  imes 10^{-5}$	78
Line	11	27,740	2522	6.04 ***	$1.40  imes 10^{-9}$	4
S  imes L	66	136,793	2073	4.96 ***	$2.20 imes10^{-16}$	18
IPCA1	16	19,821.10	1238.82	2.97 ***	0.0001	59.7
IPCA2	14	10,539.33	752.81	1.80 *	0.0344	31.7
Residuals	897	374,620	418			

\* significant at p = 0.05; \*\*\* significant at p = 0.001.

Figure 3 displays a scatter plot formed by genotypes and experimental locations according to their coordinates on the two first axes of GEI. The values of these coordinates

indicate the accessions' contribution to GEI. In this case, the lower the coordinate is, the lower its contribution to GEI and therefore the more stable the genotype is. Thus, lines AT7, AT6, AT13, and AT4 being closer to the biplot's center have more stable grain production across the experimental sites. In contrast, grain yields of the AT5, AT9, AT15, and ATC lines are unstable from site to site, as their position is far away from the biplot center. The other accessions are ranked intermediate with respect to their grain yield stability (AT1, AT2, AT3, and AT14). Furthermore, the length of vectors assigned to the experimental locations shows their ability to discriminate among the oat lines. El Kbab\_19 and Alnif\_21 sites showed more yield variation among lines. When a genotype projection is close to a site position on the biplot, that means the line has a specific adaptation to it; for example, AT5 was better suited to El Kbab\_19 (103.17 q/ha), and ATC interacted positively with the Alnif\_21 environment (114.9 q/ha), as did AT9 (34.83 q/ha) with Oukaimeden\_21.

AMMI analysis provided comparisons between productivity and stability (Figure 4). We observed two main categories of the studied lines. The first group consisted of high-yielding lines that exceeded the experimental site average yield (30.76 q/ha). Among these lines, two were the most productive, AT5 and ATC, though they were quite unstable (ASV = 9.62 and 6.37, respectively). Line AT1 had intermediate stability and a yield equal to 36.17 q/ha, while AT7, which was the most stable (ASV = 1.69), yielded 32.73 q/ha. The other lines produced below the mean yield, with AT6 and AT13 showing good yield stability and a slightly lower yield than average (30.44 q/ha and 29.24 q/ha, respectively).



**Figure 3.** Biplot between the two first components (IPCA1 and IPCA2) of the genotype × environment interaction (GEI) for the grain yield of the 12 *Avena magna* domestica ssp. lines. Explanations: Bolds represent the locations Al\_21: Alnif\_21; Ai\_21: Ain Itto\_21; Bo\_19: Bouchane\_19; Bo\_20: Bouchane\_20; Bo\_21: Bouchane\_21; El\_19: El Kbab\_19; Ou\_21: Oukaimeden\_21.



**Figure 4.** Average grain yield (Yield) and evolution of the AMMI stability values (ASV) of the 12 oat lines. The box ATC represents the control variety used in this investigation.

## 4. Discussion

The goal of this present work was to determine the agro-morphological variability of 11 A. magna ssp. domestica advanced lines and a control cultivar named Avery (ATC). Avena sativa (2n = 6x = 42) is the principal species of oat cultivated in Morocco, usually for fodder [25]. At the beginning of the local oat research program of the National Institute of Agricultural Research, varieties derived from the native hexaploid A. byzantina (red oat), which has a low water requirement and the ability to adjust its growth cycle to Moroccan environmental variability, were also released [26]. The array of wild Avena species native to Morocco-the center of origin of the genus-unfortunately lacks the required traits for broad cultivation such as resistance to shattering, semi-dwarfism, lodging resistance, erect growth habit, resistance to seed dormancy, etc. The neo-domesticated A. magna material first described by Ladizinsky [14] and later modified by Jackson [7] should have the potential to diversify the cultivated germplasm of oats. This new oat diversity contributes to the conservation of genetic resources of the genus and plays a positive role in maintaining crop diversity [6,17]. In addition, the significantly higher protein content of 'Avery' previously reported by Jackson [7] could encourage farmers and manufacturers to harness this asset to improve the crop's profitability for both human and animal feed. Over the course of the past 40 years, interest in oats for human consumption has gradually increased, concomitant with mounting clinical evidence regarding its nutritional benefits for cardiovascular health [27].

The disease assessment study had focused only on RC and BYDV, since there were no noticeable symptoms of powdery mildew at the heading stage when scoring was carried out. Several authors agree that RC (Puccinia coronata) is the major disease threatening global oat production [28]. This pathogen can drastically affect oat production by causing 10–40% yield loss [29]. Crown rust (RC) was only recorded at Bouchane in the 2018–2019 cropping season because at the other locations there were no noticeable symptoms in the experimental plots. The cause may be due to relatively dry and cool conditions at the experimental sites during 2020–2021. Nazareno et al. [28] reported that crown rust epidemics usually occur in warm areas as temperatures fluctuate between 20 and 25 °C and humidity surpasses 50-60%. At the El Kbab high-altitude site and in Alnif's dry environment, weather conditions would be expected to suppress crown rust development. The incidence of BYDV was more common than RC across the experimental locations. BYDV is probably the most economically important small-grain virus transmitted by insects, with 25 aphid species being involved as potential BYDV vectors [30]. High light intensity and low temperatures (15-18 °C) also promote increased intensity of BYDV symptoms [31]. All of these considerations and A. magna's well-known susceptibility to

BYDV [14] may explain the high incidence of the virus observed in our experiments. The trials' results did not show consistent tolerance to diseases of tested lines at all sites, except for line AT6, which appeared to be more tolerant to BYDV and RC infections. Combining data from all sites, PCA revealed that the control variety Avery and AT6 were relatively less susceptible to the diseases, which was not the case for AT7 and AT9. Jellen et al. [19] had already noted A02 (line AT7 in this study) among the lines showing RC symptoms in the Lahri experiment in 2018.

Data analyses revealed significant agro-morphological diversity between the domesticated *A. magna* lines. Plant height (PH) varied between 48.93 and 120.47 cm across the sites. Through the different sites, PH fluctuated between 84.07 cm for AT2 and 94.92 cm for AT15. Previous studies reported similar plant height values. Dumlupinar et al. [32], who studied *A. sativa* pure-line varieties, reported variation for plant height between 46 and 112 cm. Among our investigated traits, PH gave the lowest CV, between 9.97 and 21.18% across the five sites. This finding is in line with Solange et al. [33] and Dumlupinar et al. [32], who reported CVs of 11.16 and 8.7%, respectively, for this trait. A possible explanation for these observations is that plant height is affected by a relatively small number of major genes, which in this case might be largely fixed through selection. PCA analysis showed that PH was positively correlated with RL (0.72) and NSP (0.60); on the other hand, PH was significantly negatively correlated with HI. Other authors reported a significant negative correlation between PH and grain yield and explained the relationship as being due to lodging [34,35]. Plant size has to be examined closely in varietal selection to avoid lodging, in our case with lines AT13 and AT15.

Root length across locations ranged from 11.87 to 16.16 cm at Oukaimeden\_21 and Bouchane\_19, respectively. The longest roots were observed in Bouchane in three successive seasons. This behavior is likely due to the sandy soil at Bouchane, which facilitates and encourages deep root penetration as capillary water drains downward through the soil profile. Finer roots were also more easily retained as the plants were uprooted in the light-textured soil to take RL measurements. The higher clay content at the other experimental sites allowed for better soil water retention. This supports the previous observation that A. *magna* ssp. *domestica* has the ability to deeply penetrate the soil under water-stress conditions [19].

The three-way ANOVA detected significant differences among lines according to their tillering ability: 4.03 NFT/plant for AT15 and 5.93 for AT1 on average (Table 7). The genetic control of tillering capacity has been discussed previously in oat genotypes [36,37]. The mean NFT was mostly equivalent among our test locations except for Alnif\_21, where it reached an average of 11.09. Good crop management practices such as irrigation and fertilization have a positive influence on the tillering ability of plants; this may explain the significantly higher NFT value at this irrigated site.

The NSP varied among lines, ranging from 24.85 to 36.06 for AT2 and AT7, respectively. Solange et al. [33] observed an NSP mean of 26.63 for *A. sativa*, which is close to our findings. However, Jan et al. [6] counted 66 spikelets per panicle on average in their experiment. The number of spikelets is influenced by soil fertility, humidity, and photoperiod.

Thousand-kernel weight (TKW) is an important productivity and grain-quality trait for oats. According to our three-way ANOVA, TKW was more significantly influenced by growing location than genotype. Considering separately the experimental sites, two-way ANOVA showed a significant effect of the accessions at all testing sites except Bouchane\_19. Our line TKW values, similar to previous results in *A. sativa*, varied between 32.83 and 49.73 g for AT3 and AT5, respectively. Our results correspond well with *A. sativa* TKW values [6,32,33].

Seed partitioning on the total biomass is evaluated through the HI. Statistical analyses showed that HI was influenced by both the line and the environment; it varied between 20.43 and 31.33% across the five testing locations. Regarding the effect of the lines, the HI varied between 19.88% for AT13 and 34.76% for AT5. Jan et al. [6] and Li et al. [38] reported

on variation for HI among *A. sativa* genotypes and between environments and years; their HI values were comparable to ours.

It has historically been a major challenge for plant breeders to consistently identify superior-yielding genotypes across environments when GEI is highly significant. Several researchers testing crops in multi-location conditions have reported larger environmental than genotypic effects on grain yield [39–42]. In our case, the environmental effect represented 78% of the total grain yield variation, while the genotype explained only 4%. Grain yield varied extensively among our sites: from 6.89 q/ha at Bouchane\_19 to 85.50 q/ha at Alnif\_21. Previously, within a larger set of A. magna lines, Jellen et al. [19] identified the environment as the most important factor influencing yield, with genotype being the second most significant factor. Our AMMI analysis allowed classification of the A. magna lines based on their ASVs. Combining ASV and yield into a single index should represent a better way to evaluate a genotype's potential across locations. The yield stability index has been used by several authors to rank their germplasm [40,43,44]. Stable lines are usually less productive than low-stability ones. Stable genotypes have large adaptation and intermediate yield potential, while low-stability lines yield the maximum in the environment in which they are best adapted while ranking among the lowest in other locations. In this study, we presented a hybrid graph to display the A. magna line performance and separated them into two groups according to their ASV and grain yield. The first group included A. magna lines whose grain yield across locations exceeded the average yield of 30.76 q/ha. Two of the genotypes produced relatively higher grain yields, but they were unstable: AT5 (mean yield of 43.31 q/ha) Avery (35.66 q/ha). Line AT5 performed the best at El Kbab\_19 while Avery produced the most at Alnif\_21, with respective yields of 103.17 q/ha and 114.9 q/ha. Gadisa et al. [40], while investigating germplasm consisting of 15 bread wheat lines, noticed that the two highest-yielding genotypes were among the most unstable. Each of these two wheat lines had interacted positively at a given site. These results are in agreement with our findings. Among the tested A. magna lines, AT1 was moderately stable, while AT7 had the highest stability in the collection. Using the yield stability index, AT7 ranked first as being the superior genotype among the tested germplasm in terms of stability and grain yield. This accession, however, appeared to be less tolerant to diseases. Among the A. magna lines that produced below the mean grain yield, AT6 exhibited good yield stability and will be further scrutinized for its apparent tolerance to the main common diseases and its yield, which approached 30.44 q/ha.

The average grain yield of this present study across five sites and three years of experimentation was 30,76 q/ha. It may be recalled when Tam [45] tested 101 oat varieties of *A. sativa* from Germany, Sweden, Russia, Canada, the USA, and other countries, where the average yields ranged between 32.88 and 58.24 q/ha. In our trials, Bouchane's relatively low average yield of 6.89 q/ha is explained by the semi-arid climate conditions; moreover, Morocco is an arid to semi-arid country, unlike Estonia where Tam carried out his experiment. At the most favorable Moroccan site, Ain Itto\_21, rainfall barely reached 609.8 mm during the cropping season. However, it should be noted that with certain lines at certain locations, grain yield greatly exceeded the above-mentioned yield range: for example, AT5 at El Kbab\_19 and Avery at Alnif\_21. Tests of various *A. sativa* varieties selected for northern Morocco reached 45 q/ha under experimental conditions and 24 q/ha in farmers' production fields [46]; these previous results confirm that grain yield tends to decrease under working farm conditions, and some *A. magna* lines might express their best yield potential under good cultivation and environmental conditions.

## 5. Conclusions

This present study focused on the agronomic performance of advanced *A. magna* ssp. *domestica* lines under working farm conditions at five contrasting locations in Morocco. The results measured diversity among the investigated lines for agro-morphological traits. Grain yield was most highly influenced by the contrasted environments, followed by GEI, with genotype explaining very little of the variation for yield. The mountainous site of El

Kbab seems to be more suitable for growing *A. magna* under obligate rainfed conditions. The average grain yield obtained is in the range usually found for common oat production around the world, which justifies the adaptability of these *A. magna* ssp. *domestica* lines to their native zone. Line AT5 had the highest grain yield and is therefore expected to attain higher grain yields in different locations in Morocco experiencing ample rainfall. Line AT7 was interesting for its relatively high yield stability value, as measured by AMMI. We hope to be able to select one of these advanced lines for registration in Morocco along with the existing control variety, Avery. Further investigation of these lines' nutritional differences and molecular genotyping of these lines are the next steps for facilitating further improvement of domesticated *A. magna*.

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