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Research Article

Determining the Growth of Naked Oat Genotypes by Using Nonlinear Regression Models and Zadoks Growth Scale

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Abstract

Naked oat (*Avena nuda* L.) is a relatively recent cereal promoted by the food industry for its superior grain properties. Aim of this study were to evaluate the growth characteristics of four naked oat genotypes with nonlinear regression models. Field trials were conducted according to the split block design with three replications. Experimental data consisted of weekly dry weight observations covering the entire growth span of four genotypes (211 samplings in total) during two growing seasons. Curve fitting with sigmodial models successfully explained the dry weight accumulations, orientation of which were arranged as sampling weeks (SOR) and Zadoks growth stages (GSOR) in two separate analyses. Logistic, Logistic Power and Ratkowsky models were found as the best fitting models with the coefficient of determinations ranging from 0.992 to 0.942. According to results, G42 were found to develop the highest dry weights but were latest to grow when G8 were selected as the earliest genotype. SOR and GSOR analysis results indicated a higher dry matter growth as well as accelerated development in the second year, possibly due to higher precipitation. Moreover, last week of tillering stage were identified to be critical for naked oat development when the rate of growth reached to its peak around the booting stage. Implementing Zadoks growth stage as the time measure in curve fitting had several drawbacks but revealed unique interpretations about the crop development and environmental variation.

Key words: Naked oat; nonlinear regression; dry weight; point of inflection; Zadoks growth scale

Kavuzsuz Yulaf Genotiplerinde Büyümenin Doğrusal Olmayan Regresyon Modelleri ve Zadoks Büyüme Skalası ile Belirlenmesi

Öz

Kavuzsuz yulaf (*Avena nuda* L.) gıda endüstrisinde üstün tane özelliği nedeniyle öne çıkan yeni bir tahıl türüdür. Bu çalışma, kavuzsuz yulafın büyüme ve gelişmesinin doğrusal olmayan regresyon yöntemleri ile değerlendirilmesi amacıyla bölünmüş parseller deneme desenine uygun olarak üç tekerrür ile yürütülmüştür. Bu kapsamda iki yetiştirme sezonu boyunca kurulan tarla denemelerinde dört kavuzsuz yulaf genotipinin tüm büyüme ve gelişme dönemleri boyunca haftalık olarak (toplamda 211 örnekleme) kuru madde birikimleri kaydedilmiştir. Elde edilen büyüme verilerinde sigmoidal regresyon modelleri ile eğri uydurma yöntemi uygulanmış; veriler örnekleme haftaları (HO) ve Zadoks büyüme dönemlerinin (BDO) zaman ölçüsü olarak kullanıldığı iki ayrı oryantasyon ile analize tabi tutulmuştur. Logistic, Logistic Power ve Ratkowsky modelleri 0,992 ile 0,942 arasında değişen belirleme katsayıları ile kavuzsuz yulafta kuru madde birikimini en iyi açıklayan modeller olmuşlardır. Analiz sonuçlarına göre G42 en yüksek kuru madde birikimine ulaşan fakat en yavaş gelişen genotip olarak belirlenmiş, G8 ise en erkenci genotip olmuştur. HO ve BDO analizleri sonucunda ikinci yılda daha yüksek kuru madde birikimi ve daha hızlı bitki gelişimi gözlenmiş; bu durumun daha yüksek yağıştan kaynaklanmış olabileceği sonucuna ulaşılmıştır. Buna ek olarak, analiz sonuçları kavuzsuz yulafta kardeşlenme döneminin son haftasının büyüme ve gelişme açısından kritik bir hafta olduğunu, kuru madde birikiminin ise gebecik döneminde zirveye ulaştığını göstermiştir. Zadoks büyüme dönemlerinin zaman ölçüsü olarak kullanıldığı eğri uydurma analizleri zayıf yönleri olmasına rağmen bitki gelişimi ve çevresel faktörlerin değerlendirilmesi açısından özgün sonuçlar ortaya çıkarmıştır.

Anahtar kelimeler: Kavuzsuz yulaf, doğrusal olmayan regresyon modelleri, kuru madde, dönüm noktası, Zadoks büyüme skalası.

Introduction

Wide recognition of cold climate cereals as staple food led to their utilization in the food industry in many different forms. A recent accomplishment was the improvement of the hulless oat (*Avena nuda* L.) genotypes to be grown feasibly across the world. Hulless oats have loose hulls covering their grain which are easily separated during threshing, making them readily available for consumption. Historically, naked oat cultivation was relatively uncommon compared to the hulled genotypes except for China until its grain properties revealed to be superior (Sykut-Domańska et al., 2013; Hu et al., 2014; Webster, 2016). In the perspective of plant breeding, comparison is rather simple: Since hulls account for a remarkable proportion of oat grain weight, a breeder can choose to improve groat yield of hulled germplasms (Dumlupinar et. al. 2011) or the agronomic properties of the hulless germplasm (Batalova et. al. 2010). Since the nutrition value seems to be the major reason behind the demand for oat grain in food industry, popularity of hulless oats is expected to increase as well as the research aimed to its cultivation (Biel et. al. 2014).

In agronomy, understanding the plant growth and development is a constant challenge. Dry weight accumulations are considered as a reliable measure of plant growth since it represents the whole growth process and are useful in terms of evaluating the genotypic variation (Karadavut et. al., 2008). Using ANOVA in this type of data would not be ideal due to heteroscedasticity where sigmoidal growth models are implemented successfully (Peek et al., 2002; Sari et al., 2019). Curve fitting on dry weight accumulation produces useful parameters some of which can be biologically meaningful. Additionally, it can be used to generate accurate projections, revealing relationships between agronomic traits, or assisting decision making based on the plant physiology such as timing of fertilizers and harvest (Kang, 2013; Hocaoglu and Coşkun, 2018; Hao et al., 2021). Apart from its usefulness in terms of parameterizing the plant growth, curve fitting on plant dry weights provides little or no information about the progress of plant development. Plant development of cereals are assessed by designated “Growth stages” which are identified with easily observable physiological properties of plant morphology. Early stages of growth, for instance, are tracked by the number of leaves (GS 10-19) or tillers (GS 20-29) which is very useful in terms of deciding the optimal timing for cultural applications. Additionally, since identifying the growth according to morphological developments are comparable across environments or years, using Zadoks growth scale as a time measure on non-linear regression models would not only yield results related to the plant development but also expected to minimize the environmental variation. Despite this potential, using growth stages in the growth analysis is unprecedented (to the best of our knowledge), thus the potential of this approach remains undiscovered.

In this study, sigmoidal growth models were used in the curve fitting process to explain the growth of naked oat genotypes where their stage of development were assessed separately by the respective growth stages of each sampling time. We aim to 1) determine their characteristic growth habits to understand their responses and 2) discuss the potentials and restrictions of the curve fitting process with and without incorporating the Zadoks growth stages.

Materials and Methods

Experimental data was collected during the 2019-2020 and 2020-2021 growing seasons in the Unit of Agricultural Production and Research, a division of Çanakkale Onsekiz Mart University which is located at the Çanakkale region of Turkey. Climate of the region is classified as the Mediterranean type (Yılmaz and Çiçek, 2018). Temperature and precipitation regimes of both growing seasons were presented in Tables 1 and 2. Climate data were acquired from Turkish State Meteorological Service (Turkish State Meteorological Service, 2022). Soil analysis showed that the soil of the trial site was clay loam, having low organic matter (1.48%) and salinity (0.666 mS cm-1) with medium lime content (12.2%) and slightly alkaline pH (7.99).

Naked oat genotypes no 8, 40, 41 and 42 were selected in a previous trial as promising candidates by their high grain yield and thousand kernel weights. Field trials were conducted with the density of 550 plants m-2 on November 6th and November 13th in the first and the second year, respectively. Plots were arranged as 6 m2 including six plant rows. Experimental design was the split block design with three replications where genotypes were arranged as the main plots with sampling times were the subplots. Phosphorus fertilizers applied during sowing in the form of diammonium phosphate by 6 kg da-1 ratio when 8 kg da-1 nitrogen were added as top fertilizer in the beginning of the stem elongation stage. Prior to the start of plant samplings, 300 plants were marked in each plot to guide all the future plant samplings when germinations were completed (GS10 stage; Zadoks, 1974). Plant samplings started after the plant markings and repeated weekly (each Friday in both trial years) until all plants in a plot reached maturity (exceeding GS90). Sampling period took 25 to 28 weeks depending on the genotype and year when the total number of plant samplings reached to 211. In every sampling, the number of tillers and the plant heights of 10 plants were measured for each plot. Based on these measurements, three plants were selected as the most suitable specimens representing the status of each plot (3 plant samples in 211 samplings, n = 633 plants were assessed in total). In addition to the determination of growth stages according to Zadoks (1971), above ground parts of selected plants were collected and cleaned for dry weight measurements after 48 hours of drying in the drying oven at 105°C. Weekly dry weight averages of each genotype were used as the growth data for the curve fitting.

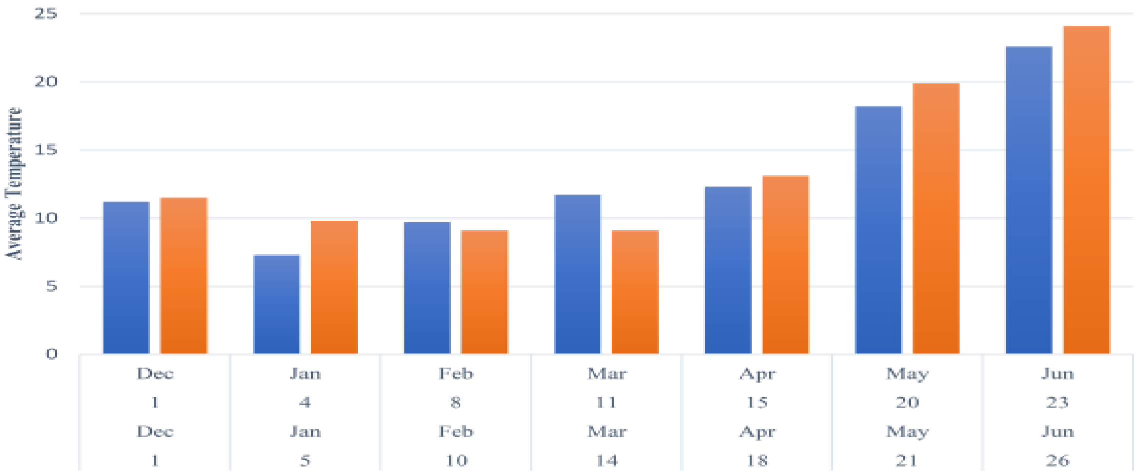

Figure 1. Monthly temperature averages (°C) during the growing seasons of first (blue) and second years (orange) with corresponding sampling weeks.

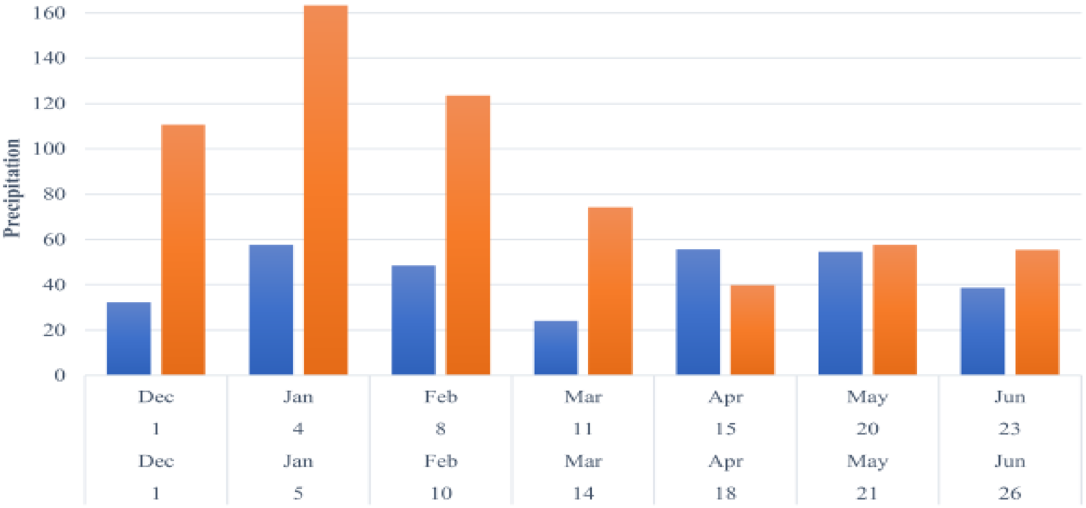

Figure 2. Monthly total precipitations (mm) during the growing seasons of first (blue) and second years (orange) with corresponding sampling weeks.

Growth curves were fitted, and the curve parameters were obtained on Curve Expert Professional v. 2.7.3 software which uses Marquart-Levenberg method (Hyams, 2010).

Sigmoidal growth models were the best fitting models to explain dry weight increases of naked oat genotypes. Gompertz, Logistic, Logistic Power, MMF, Ratkowsky, Richards and Weibull models were fitted in each dataset.

Model equations were as follows:

Gompertz, $y = ae^{-e^{b-cx}}$ (1)

MMF, $y = \frac{ab+cx^d}{b+x^d}$ (2)

Logistic Power, $y = a \Big/ \left(1 + \left(x/b\right)^c\right)$ (3)

Weibull, $y = a - be^{-cx^d}$ (4)

Ratkowsky, $y = a/(1 + e^{b-cx})$ (5)

Logistic, $y = a/(1 + be^{-cx})$ (6)

where a, b and c are curve parameters, y is dry weight (g), x is sampling time (weeks) and e is the mathematical constant. Results of Wald-Wolfowitz tests were lesser than %5 for all presented analysis, which is an indication of randomly distributed residuals (Juhász et al., 2020; Hyams, 2020). Model efficiencies were compared by their high coefficient of determinations (R2), low standard errors and low corrected Akaike's information criterion (AICC). Since there were too many analyses with similar outputs, three best fitting sigmoidal models for each analysis were presented in the results. Additionally, points of inflections were calculated from Gompertz and Logistic curve parameters for each analysis using the method presented in Mischan et al. (2011) and Wen et al. (2019) and their locations and values were confirmed on the Curve Expert Professional v. 2.7.3 software. Dry weight data of naked oat genotypes from the growing seasons of 2019-2020 and 2020-2021 were evaluated by curve fitting with sigmoidal growth curves. Number of weeks and corresponding zadoks scales of each sampling were used as time measures in two separate analysis where former were mentioned as the sampling oriented (SOR) and the latter as the growth stage oriented (GSOR) analysis.

Results and Discussions

Curve fitting with non-linear regression models succesfully explained the dry matter accumulation of naked oat genotypes with high coefficient of determinations (R^2) and low standard errors (Table1). Logistic Power were among the best fitting growth models for both SOR and GSOR data when the goodness of fit of other models varied with the data orientation. R^2 values of SOR varied between 0.992 and 0.999, eclipsing the GSOR data, R^2 values of which ranged from 0.942 to 0.991. In terms of all godness of fit parameters including R2, standard error and AICC, Logistic and Ratkowsky models fitted SOR graphs better in comparison to Gompertz, MMF and Weibull which were more suitable to the data in the GSOR analysis (Table 1).

Curve parameters a, b and c of Logistic model were presented in Table 2. Model parameter a is often associated with asymptotic value of the curve (de Bem et al., 2018) which relates to the maximum growth (Carini et al., 2020). The parameter a values of SOR and GSOR were comparable and related to DWmax, therefore the higher dry weight accumulation for each genotype in second year can be confirmed on their respective parameter a values. In terms of genotype comparisons based on this parameter, G42 had the highest dry matter accumulations (31.05 and 57.70 g in first and second years, respectively) in all models and data orientations (Table 2).

Despite parameter a, biological meaning of the parameter b is a topic of discussion. According to Sari et al. (2019) and Carini et al. (2020), parameter b can be related to the initial production, however the findings of other several research did not support this conclusion (de Bem et al., 2018; Mello et al., 2022). In our results, comparison of parameter b values from SOR and GSOR analysis revealed that it may be regulating the overall shape of the curve more than a particular partition, which makes it difficult to evaluate on its own.

Lastly, parameter c is reported to indicate precocity (Diel et al., 2020) or the production rate (Sari et al., 2019) which confirms our findings. Our results of parameter c did not indicate a considerable variability among genotypes, but variation among trial years and data orientation were noteworthy. Higher parameter c values of SOR Logistic analysis, in general, were due to a sharper increase of dry weight of naked oats compared to advancement of growth stages represented by GSOR analysis. Higher parameter c of second year SOR Logistic curves indicated faster dry weight accumulation over time when lower parameter c of GSOR Logistic curves of second year were due to lesser number of samplings for each major growth stage, thus revealing an even faster growth stage advancement (Table 2). Effect of year variation is also evident in GSOR graphs except for G40 in Figures 3-5.

Table 1. Goodness of the fit of sigmoidal models

Gn	Year	Orientation	Model	Std Err[a]	R^2	AICC[b]	Gn	Year	Orientation	Model	Std Err	R^2	AICC
G8	1	SOR[c]	Logistic	0.401	0.999	-49.821	G40	1	SOR	Log Power	0.473	0.996	-39.165
			Ratkowsky	0.401	0.999	-49.821				Gompertz	0.480	0.996	-38.324
			Log Power[d]	0.477	0.998	-40.155				Ratkowsky	0.508	0.996	-35.224
		GSOR[e]	Gompertz	1.013	0.992	2.046			GSOR	Gompertz	1.133	0.980	8.067
			MMF	1.107	0.991	8.399				MMF	1.153	0.980	10.418
			Log Power	1.141	0.990	8.685				Log Power	1.158	0.979	9.238
	2	SOR	Ratkowsky	1.022	0.994	2.485		2	SOR	Log Power	1.052	0.996	3.884
			Logistic	1.022	0.994	2.485				Logistic	1.083	0.996	5.344
			Log Power	1.163	0.992	9.209				Ratkowsky	1.083	0.996	5.344
		GSOR	MMF	1.787	0.982	32.930			GSOR	Gompertz	3.536	0.953	64.501
			Weibull	1.803	0.981	33.399				Log Power	3.636	0.950	65.899
			Log Power	1.846	0.980	33.216				Logistic	3.921	0.942	69.664
G41	1	SOR	Log Power	0.341	0.998	-56.724	G42	1	SOR	Log Power	0.774	0.995	-12.526
			Gompertz	0.341	0.998	-56.840				Gompertz	0.766	0.995	-13.060
			Ratkowsky	0.382	0.997	-50.640				Ratkowsky	0.819	0.994	-9.485
		GSOR	Gompertz	1.143	0.976	8.543			GSOR	Weibull	1.834	0.971	35.456
			MMF	1.170	0.976	11.184				Log Power	1.848	0.970	34.471
			Log Power	1.175	0.975	10.042				Gompertz	1.846	0.970	34.410
	2	SOR	Logistic	0.658	0.997	-19.565		2	SOR	Logistic	1.216	0.996	11.511
			Ratkowsky	0.658	0.997	-19.565				Ratkowsky	1.216	0.996	11.511
			Log Power	0.680	0.997	-17.944				Log Power	1.374	0.995	17.845
		GSOR	Log Power	2.326	0.960	43.565			GSOR	Log Power	3.112	0.973	60.370
			Gompertz	2.440	0.956	45.964				Gompertz	3.248	0.971	62.600
			Ratkowsky	2.752	0.944	51.959				Logistic	3.503	0.967	66.521

*Gn: Genotype, A: Std Err, Standard Error, b: AICC, Corrected Akaike's information criterion, c: SOR, Sampling oriented data, d: GSOR, Growth stage-oriented data, e: Log Power, Logistic power

Table 2. Curve parameters of sigmoidal models

SOR	Logistic Model Parameters							
Genotypes	Year	a	b	c	DW_{max}[a]	PI[b] (Week)	TNS[c]	TNS%[d]
G8	1	27.53	46746.44	0.54	27.02	19.87	28.00	70.95
	2	37.86	227721.92	0.59	40.62	21.02	26.00	80.85
G40	1	21.41	27170.44	0.50	20.83	20.44	27.00	75.72
	2	50.38	34036.35	0.51	45.56	20.44	25.00	81.77
G41	1	20.55	13388.76	0.46	19.66	20.51	27.00	75.98
	2	39.73	30839.44	0.49	33.62	21.18	25.00	84.72
G42	1	40.26	2847.35	0.34	31.05	23.25	27.00	86.10
	2	71.36	218323.80	0.54	57.70	22.87	26.00	87.95
				Mean	34.509		Mean	80.505
				Std Dev[e]	12.112		Std Dev	5.4867

GSOR	Logistic Model Parameters				
Genotypes	Year	a	b	c	PI (GS[f])
G8	1	25.59	860.49	0.17	39
	2	35.56	87.11	0.08	55
G40	1	18.25	1163.22	0.18	39
	2	38.10	875.93	0.18	38
G41	1	17.14	1337.96	0.19	38
	2	27.51	362.49	0.15	40
G42	1	29.36	88.81	0.09	51
	2	76.58	95.32	0.06	76
				Mean	47
				Std Dev	13

A: Dwmax, Maximum dry weight, b: PI, Point of inflection, c: TNS, Total number of samplings, d: %TNS, PI as the percentage on TNS, e: Std Dev, Standard Deviation, f: GS, Growth Stage, *nc: not calculated.

Point of inflections on SOR and GSOR graphs

Logistic, Gompertz and Richards have points of inflection (PI), which remarks the point where the rate of growth is maximum (Goshu and Koya, 2013). Point of inflections are calculated from the model parameters and their evaluation reveals critical points of plant growth (Wen et al., 2019). In this study, PI's and several other statistics were calculated using Logistic model (Table 1). Calculating the PI of the SOR curves indicate a theoretical week of the highest growth rate when the PI of GSOR curves indicate the approximate growth stage that coincides with it. Our results showed that G8 were the earliest genotype to initiate rapid growth (Figure 3) which were also indicated by the PI of its SOR growth analysis (Table 2). On the other hand, G42 were the latest to initiate rapid growth by weeks (SOR) and by the stage of development (GSOR). GSOR analysis were also more useful to reveal the effect of year variation on the development of naked oat genotypes. All genotypes responded to the higher precipitation of the winter months of second year (Figure 2) by increasing dry weight accumulations during tillering stage (GS 20-29, Table 2). The year variation is not visible in SOR graphs for any genotype but apparently influenced the durations of the growth stages. In every GSOR graph, growth stages after the stem elongation took less and less samplings in the second year when compared to the first year. In other words, higher winter precipitation in the second year may have accelerated the generative growth of the naked oat genotypes, especially from the booting stage (GS40). Additionally, increased winter precipitation of the second year seems to have a positive effect on DWmax, which were increased between %50-118 for all genotypes (Table 2).

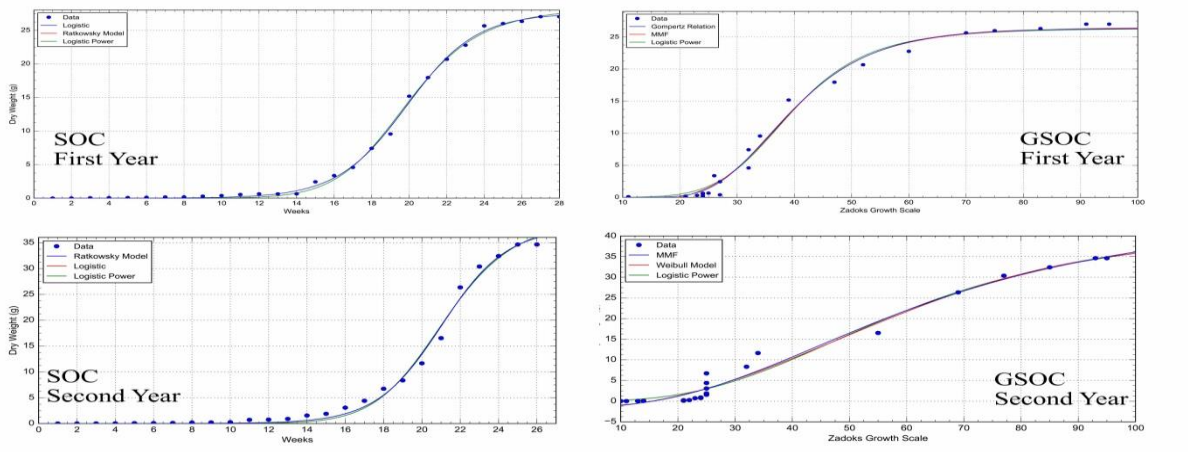

Figure 3. Dry weight increases of G8 in sample (SOC) and growth stage orientations (GSOC)

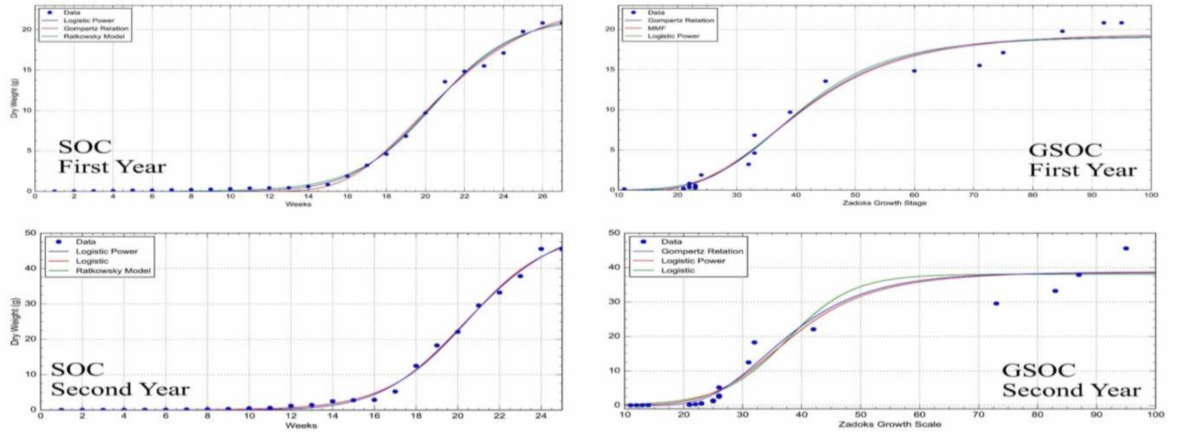

Figure 4. Dry weight increases of G40 in sample (SOC) and growth stage orientations (GSOC)

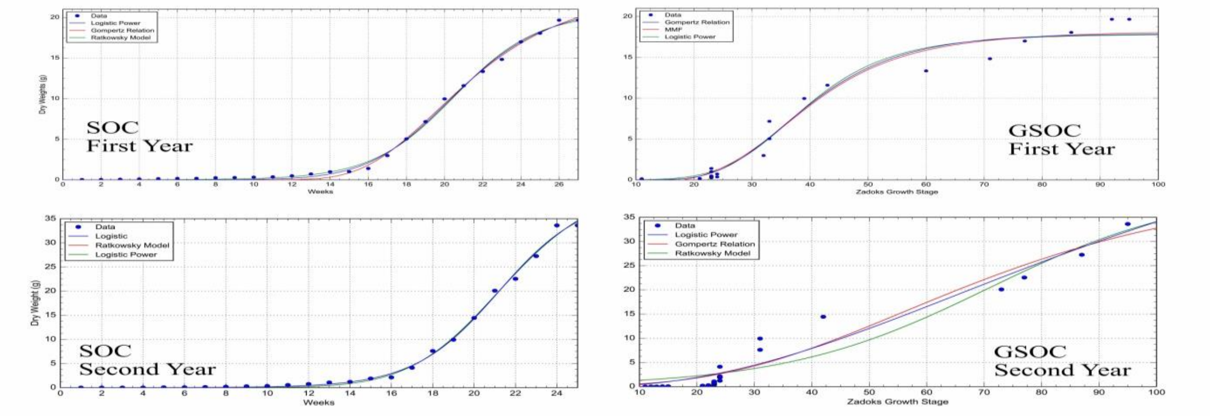

Figure 5. Dry weight increases of G41 in sample (SOC) and growth stage orientations (GSOC)

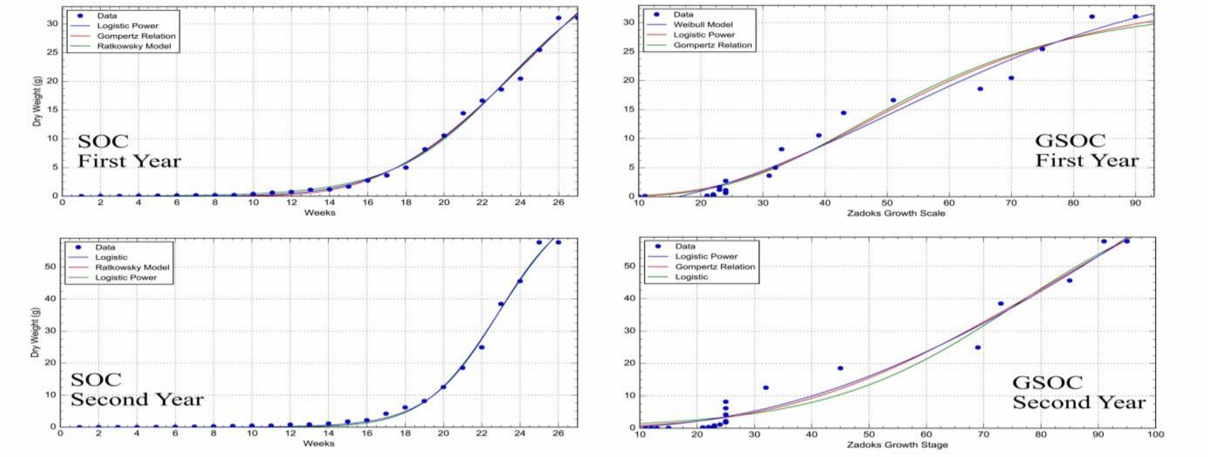

Figure 6. Dry weight increases of G42 in sample (SOC) and growth stage orientations (GSOC)

Points of Inflections of Logistic models of SOR curves varied between 19.87 and 23.87 weeks, which can be more meaningful if it is expressed as the percentage of the total number of samplings (TNS%) since it took different number of samplings (TNS) for naked oat genotypes to reach maturity(GS>90). TNS% average of all naked oat genotypes was 80.51% when the year variation is more apparent for all cultivars except for G42. G8 (70.95% in first and 80.85% in second year) were the earliest developing cultivar when G42 were the latest (86.10% in first and 87.95% in second year).
Points of Inflections of Logistic models of SOR curves varied between 19.87 and 23.87 weeks, which can be more meaningful if it is expressed as the percentage of the total number of samplings (TNS%) since it took different number of samplings (TNS) for naked oat genotypes to reach maturity (GS>90). TNS% average of all naked oat genotypes was 80.51% when the year variation is more apparent for all cultivars except for G42. G8 (70.95% in first and 80.85% in second year) were the earliest developing cultivar when G42 were the latest (86.10% in first and 87.95% in second year).

PIs were also calculated on the GSOR growth analysis. Results of the Logistic model indicated that naked oat genotypes reached to their PI during the middle or late of booting stage (GS40) on average, which varied between stem elongation (GS30) and flowering (GS50) depending on the genotype and year. Year variation on the PI of GSOR data were more apparent than SOR when the results of the Logistic model of both data orientation were reliable for comparison. Different environmental conditions of the experiment years had an observable effect on the pace of the growth stages, which also reflected on these results.

It should be noted here that unlike the SOR data, PI's of GSOR analysis should be taken as broad approximations rather than precise data points. For example, PI of G40 (first year) is calculated as 39 GS which does not mean that G40 having 9 nods visible on its main stem since it is the actual diagnosis for GS39. Growth analysis can't account for growth stage subgroups (the units digits) since their definitions vary, therefore the PI value of GS39 simply indicates the late stem elongation stage. To this direction, we interpret the results as G42 were the latest developing naked oat genotype due to having the PI of 51 in the first year. In other words, dry weight increase rate of G42 were the highest in the later stages of growth: it was around flowering stage in the first year (GS50). Second year projection of G42 coincided with the milk development stage (GS70) which was inaccurate since the model parameters did not converge the data, hence its model parameters (a, b and c) and the PI were inaccurate. Variation among the PIs of other genotypes were minimum (38-40) with the only exception of G8 on second year (Table 2).

Comparing the goodness of fits of SOR and GSOR analyses

Monitoring the growth in a weekly basis corresponds well to the idea of sigmoidal growth curves, which are used to represent the biological process of growth on even measures of time. Zadoks scale, on the other hand, serves a different purpose. It is a useful tool to numerically express the plants stage of development based on its morphology. Since the time (and the number of samples) between consecutive growth stages cannot be expected to be equal, GSOR of the dry weight increase did not correspond with the models as well as SOR did. A good example of this relationship can be observed when comparing SOR and GSOR graphs of Figure 3. Both figures were drawn from the same weekly dry weight data but the uneven distribution of samplings in GSOR graphs were apparent: oat remains in tillering stage (GS 20-29) for eight and nine consecutive weeks (for the first and second years, respectively) with minimum dry weight increase, causing an accumulation in the second partition of the y axis. This is perfectly normal since oat is grown as a winter crop in the Marmara region of Turkey, thus tillering stage coincides with the winter months. Despite these disarrays observed in the GSOR graphs, dry weight increase was still adequately explained with the coefficient of determinations ranging from 0.94206 to 0.99177 (Table 1). GSOR graphs indicated that rapid dry weight increases of the naked oat genotypes tended to begin in the last week of tillering stage. Stem elongation stage is known to be critical for winter cereals to achieve high yields (Ye et. al., 2011). According to our findings, this critical period might be extended to one week earlier when oat stem erects. Therefore, we suggest that the timing of the top fertilization of naked oats would be more accurate if aimed to meet the plant consumption at late tillering stage.

Conclusions

In general, using sigmoidal growth models on the dry weight accumulations of four naked oat genotypes provided several conclusions:

1. We recommend using Logistic, Ratkowsky and Logistic Power models to evaluate the dry weight increases of naked oat. Additionally, we also used an alternative analysis where dry weight accumulation was expressed with the Zadoks growth stages (the GSOR data) which were explained better by Gompertz, Log Power, MMF and Weibull models. We found that this unconventional approach provided a slightly less reliable fit on sigmoidal models in general and in several cases, a lack of convergence to the growth data which led to certain inconsistencies. Since using this orientation yielded a different perspective that contributes to our understanding of the genotypic variation, we conclude that incorporating growth scales into nonlinear regression analysis would be useful but statistical aspect of handling this data orientation may be improved.

2. We determined that naked oat genotypes reached their maximum rate of dry weight increase during the late booting stage which were compatible with earlier foundings (Malhi et al., 2006).

3. Effects of increasing precipitation in the second year (Table 2) could be the major influence behind the increasing dry weights of all genotypes in the second year as well as their faster developments during the generative growth stages.

4. Due to the results of curve fitting, G42 were found prominent for its potential to develop highest dry weight accumulations where G8 were selected as the earliest genotype.

Based on the results of this study, we recommend using growth stages on curve fitting with sigmoidal regression models which enabled the evaluation of the plant development. We predict that use of non-linear regression models on plant agronomy will increase and diversify, improving our knowledge about the complexity of plant growth and development.

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