EXPERIEMENT V.

An Educational Mechanistic Model for Simulating Dry Matter Accumulation of Barley under Various Temperature Levels and Hypoxia Conditions

Objectives

1. To construct an educational mechanistic model; namely "the Barley Growth Under Hypoxia Model (BGUHM)" in order to quantify and simulate the behavior of barley grown under aerated and hypoxic condition with various ambient temperatures.
2. To validate the "BGUHM" on shoot and root dry matter accumulation of barley grown under aerated and hypoxic condition with various ambient temperatures.

Materials and Methods

Model construction

Results from the study of the photosynthetic rates, dry matter accumulation and partitioning of barley genotypes under aerated and hypoxic condition with various ambient temperatures (i.e. 20, 25, 30 and 40 $^{\circ}$C) in the Experiment III and IV, were used to describe and construct the model. The results under aerated and hypoxic at 20 $^{\circ}$C did not discuss in the Experiment III, however they were presented in Appendix 15. In addition, the results of the Experiment IV due to only under the 1st hypoxia at 25, 30 and 40 $^{\circ}$C were used for the model construction.

The BGUHM model was formulated using the "Stellar®" software (Version 5.11 for Windows®, High Performance Systems, Inc.). In order to ensure the performance of the model, the "BGUHM" was tested with the results of the Experiment III and IV relating to the shoot and root dry matter accumulation of each barley genotypes.

Model validation

The validation processes involved comparing the performance of the model in terms of its output against the observed data. The observed data was obtained from the specific experiment in the growth chamber. This experiment was described as following;

The experiment was conducted in the growth chambers (Fitotron™, SANYO Gallenkamp PLC, SGC970 Model) at LARTC, Lampang in 1999. Three barley genotypes i.e. SMG1, FNBLS#140 and BRBRF9629 were grown in the aerated nutrient solution and stagnant agar nutrient solution (as hypoxia). The plant culture in this experiment was done as in the Experiment III. The plant growth chambers were set for diurnal cyclic and photoperiodic control by computerized system. Daily light intensity (PAR) varied between 250-1346 μmole/m^2/s under natural light and day length was 12 hours. The daily maximum light intensity was set at 1,346 μmole /m^2 /s. The maximum ambient temperatures in 24 hours (i.e. 20, 25, 30 and 40 $^{\circ}$C in the mid day and controlled at 15 $^{\circ}$C during the night), were differed in each growth chambers. The ambient CO_2 concentration was set 330-400 ppm. Humidity in the growth chambers was set to 80%.

Data collection

Shoot and root dry matter accumulation of each barley genotype were recorded every other day at 3-4 leaf stage for 9 days of aerated and hypoxic condition. Each observation, seven plant samples of each treatment were separated into the shoots and roots of barley plants and were dried at 75 $^{\circ}$C for 24 hours by hot dry air oven and weighed.

Data input of the "BGUHM"

Data used as an input in the "BGUH" model were;

(i) maximum ambient temperatures i.e. 20, 25, 30 or 40°C, were selected only one level for each simulation;

(ii) maximum light intensity in the growth chamber; 1,346 μmole /m^2 /s was used the same level in the experiment.

(iii) the initial total dry matter of each barley genotype at the beginning of recording was input;

(iv) either aeration or hypoxic condition which was selected only one condition for each simulation.

Validation process

The model was validated using data of dry matter accumulation and partitioning of the shoot and root of barley genotypes grown under either aeration or hypoxia at ambient temperatures i.e. 20, 25, 30 and 40 $^{\circ}$ C. They were graphically plotted and studied behavioral patterns of the simulated result as compared with the observed data for assessment of model accuracy in simulating barley growth. Goodness of fit was evaluated visually by computing a standardized mean square error (*V*) (Graf *et al.*, 1991).

Model description

Flow diagram (Figure 20) described the relationship among the variable symbols in the "BGUH" model using Forrester's symbols (Forrester, 1968) as modified into the Stellar's symbols. According to the flow diagram, light interception was conversed to the gross photosynthetic rate of each barley genotype under aerated and hypoxic condition with ambient temperatures. Then the dry matter of the shoots and roots of each barley genotype from the photosynthate was reduced by the maintenance respiration. The plant growth rate and the ratio of dry matter partitioning of them were also determined to calculate the dry matter accumulation. In the

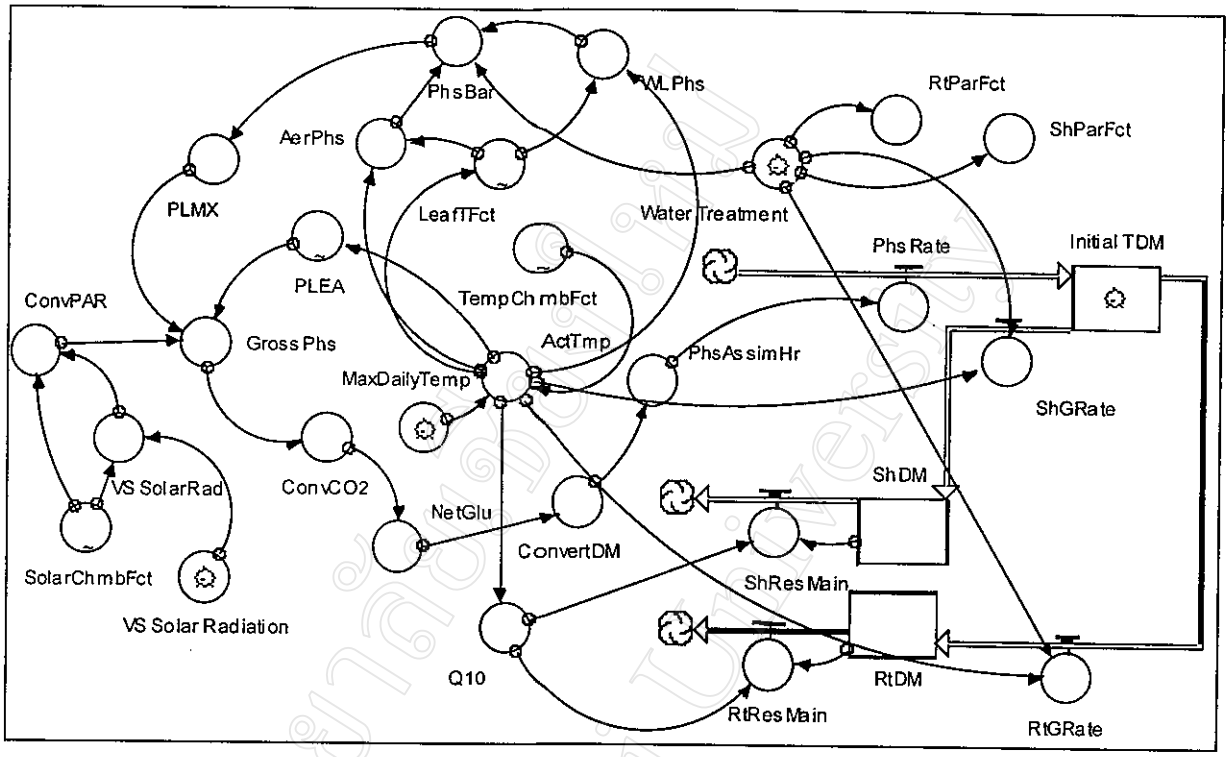


Figure 20 The pattern of flow diagram of the machanistic model constructed by the Stellar program version 5.11 The responses of the photosynthetic rate, the shoot and root dry matter accumulation and partitioning of each barley genotypes.

Note:

: the connecter; the job of the connector is to connect elements, such as converter to flow, stock to flow and stock to converter.

Variable1 : the converter; to serve a utilitarian role in the software. It holds values for constants, calculates algebraic relationships, and serves as the repository for graphical function.

Variable2 : the star inside the converter, means must input data as independent variable.

Stock1 : the accumulated stock type. If it has a star inside the stock, it means to be independent stock which must input the data as symbol .

flow1 : the flow rate; it is the job of flows is to fill and drain accumulation. The unfilled arrow head on the flow pipe indicates the direction of the flow.

"BGUHM" construction, the maximum visible solar radiation for each simulation was set at 1346 μmole /m^2 /s as the same PAR in the experiment data. And the maximum ambient temperatures i.e. 20, 25, 30 and 40 $^{\circ}$ C were also selected as an input data for each simulation in the "BGUHM". The key system variables in the "BGUHM" were described as following;

The amount of daily visible solar radiation (*VS SolarRad*) in the "BGUHM" was calculated using the daily fraction of visible solar radiation (*SolarChmbFct*) multiplied by the maximum visible solar radiation (*VS Solar Radiation*). Where the value of daily fraction of visible solar radiation was the actual light intensity divided by the maximum light intensity for each hour (Figure 21). In this simulation process, the daily visible solar radiation was converted the unit of μmole quanta/m^2/s into W/m^2 which illustrated in the equation at the *ConvPAR* variable as following;

Daily visible solar radiation = 4.2553 * *VS_SolarRad* * *SolarChmbFct*

In addition, this daily solar radiation was also used to calculate the gross photosynthetic rate (*GrossPhs*).

In the "BGUHM", the daily ambient temperature (*ActTmp*) was calculated using the daily fraction of temperature (*TempChmbFct*) multiplied by the maximum temperature (*MaxDailyTemp*). Where the daily fraction of temperature was calculated the same as the fraction of visible solar radiation and was shown in Figure 22. This daily ambient temperature was used to control the maximum photosynthetic rate of each barley genotype grown under aerated condition (*AerPhs*), and under hypoxia (*WLPhs*). It also control the values of the initial photosynthetic rate (*PLEA*), the fraction of leaf temperature effect for barley plant(*LeafTFct*), the shoot growth rate (*SHGRate*), the root growth rate (*RtGRate*) and the respiration reaction (Q_{10}). These relationships were described by Penning de Varies *et al.* (1989).

It was determined to calculate the photosynthetic rate of each barley genotypes for 9 days of aerated condition (*AerPhs*) and hypoxic condition (*WLPhs*) relating to various ambient temperatures. Their relations were shown in mathematical equations from the fitted curved. All the equations were the quadratic forms which

Table 10 The average ratio of shoot and root dry matter of barley genotypes under aerated and hypoxic condition at ambient temperatures which were used to be the fractions of dry matter partitioning to the shoots and roots of each barley genotypes in the "BGUH" model.

Treatments	Barley genotypes	The ratio of dry matter partitioning	
		to the shoots	to the roots
Aeated condition	SMG1	0.809	0.191
	FNBLS#140	0.778	0.222
	BRBRF9629	0.800	0.192
Hypoxic condition	SMG1	0.877	0.123
	FNBLS#140	0.816	0.154
	BRBRF9629	0.832	0.138

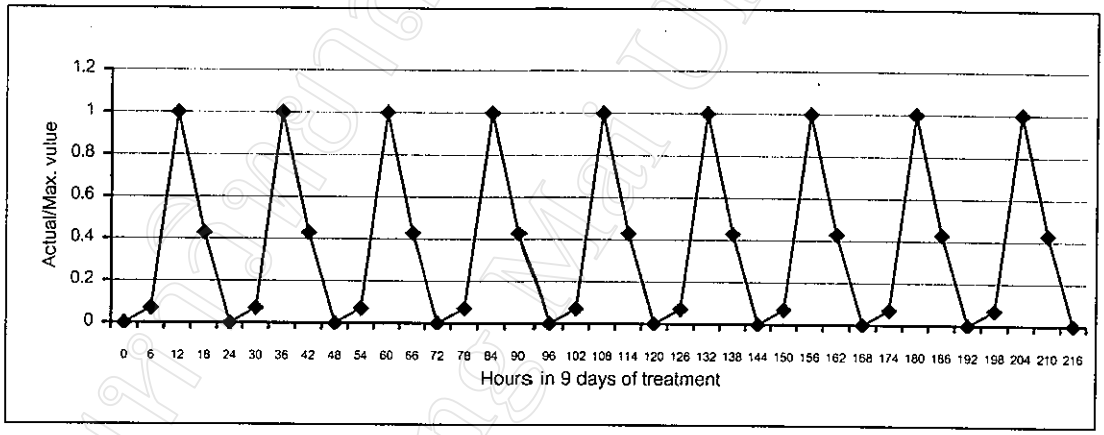
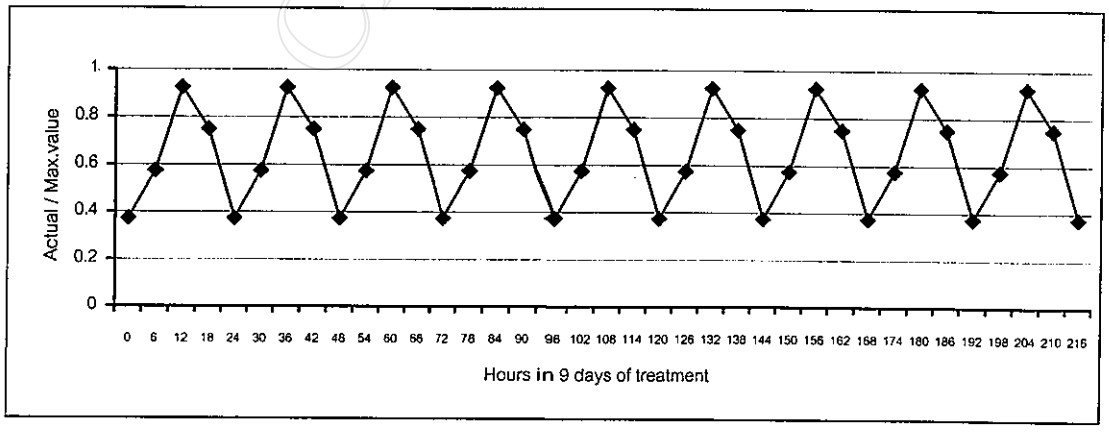


Figure 21 The fraction of daily visible solar radiation in the growth chamber which was used to construct the "BGUH" model.



Figue 22 The fraction of daily ambient temperature in the growth chamber which was used to construct the "BGUH" model.

tended to decreased at 40 $^{\circ}$ C (Figure 23) and were used calculation of *AerPhs* and *WLPhs* variables.

The *Watertreatment* variable was set as a control variable in order to select the effect of either the aerated or hypoxic condition. It also controlled some values depending on both of the aeration and hypoxic condition i.e. the actual photosynthetic rate (*PhsBar*), the shoot growth rate (*ShGRate*), the root growth rate (*RtGRate*) and the fractions of dry matter partitioning to the shoots (*ShParFct*) and the root (*RtParFct*).

Penning de Varies *et al.* (1989) described that the response of leaf photosythesis to absorbed light as a curve, relates the daily gross photosynthetic rate (*GrossPhs*) to the intensity of absorbed radiation (*ConvPAR*, J/m^2/s) exponentially. The exponential form was shown in the following equation;

The *GrossPhs* value = *PLMX**(1.0 – *EXP*(- PLEA * *ConvPAR / PLMX*)

This type of curve is characterized by two parameters; the slope at the origin or the values of the initial photosynthetic rate (*PLEA*), and the photosynthetic rate at saturated light intensity (*PLMX*). The initial efficiency of the use of absorbed light characterizes, in particular, the biophysical processes and has a fairly constant value. The maximum rate depends strongly on plant properties and environmental conditions and particularly reflects biochemical processes and physiological conditions (Penning de Varies *et al.*,1989). Therefore in the "BGUHM", the fraction of leaf temperature effect (*LeafTFct*) of barley crops was used as the daily effect of ambient temperatures to control the *GrossPhs* value. Moreover, the *PLMX* value was the photosynthetic rate of barley (*PhsBar*) associated with the selection either *AerPhs* or *WLPhs* variable.

The calculation of *GrossPhs* value (unit: kg CO_2 /ha /h) was converted to daily total dry matter (unit: g / plant /day) by changing the amount of CO_2 concentration into g of glucose and then into g of dry matter as described the steps of calculation by Loomis and William (1963). There were some system variables in the "BGUHM" associated with this calculation i.e., *ConvCO$_2$*, *NetGlu*, *ConvertDM*, *PhsAssimHr* and *PhsRate* (Figure 20).

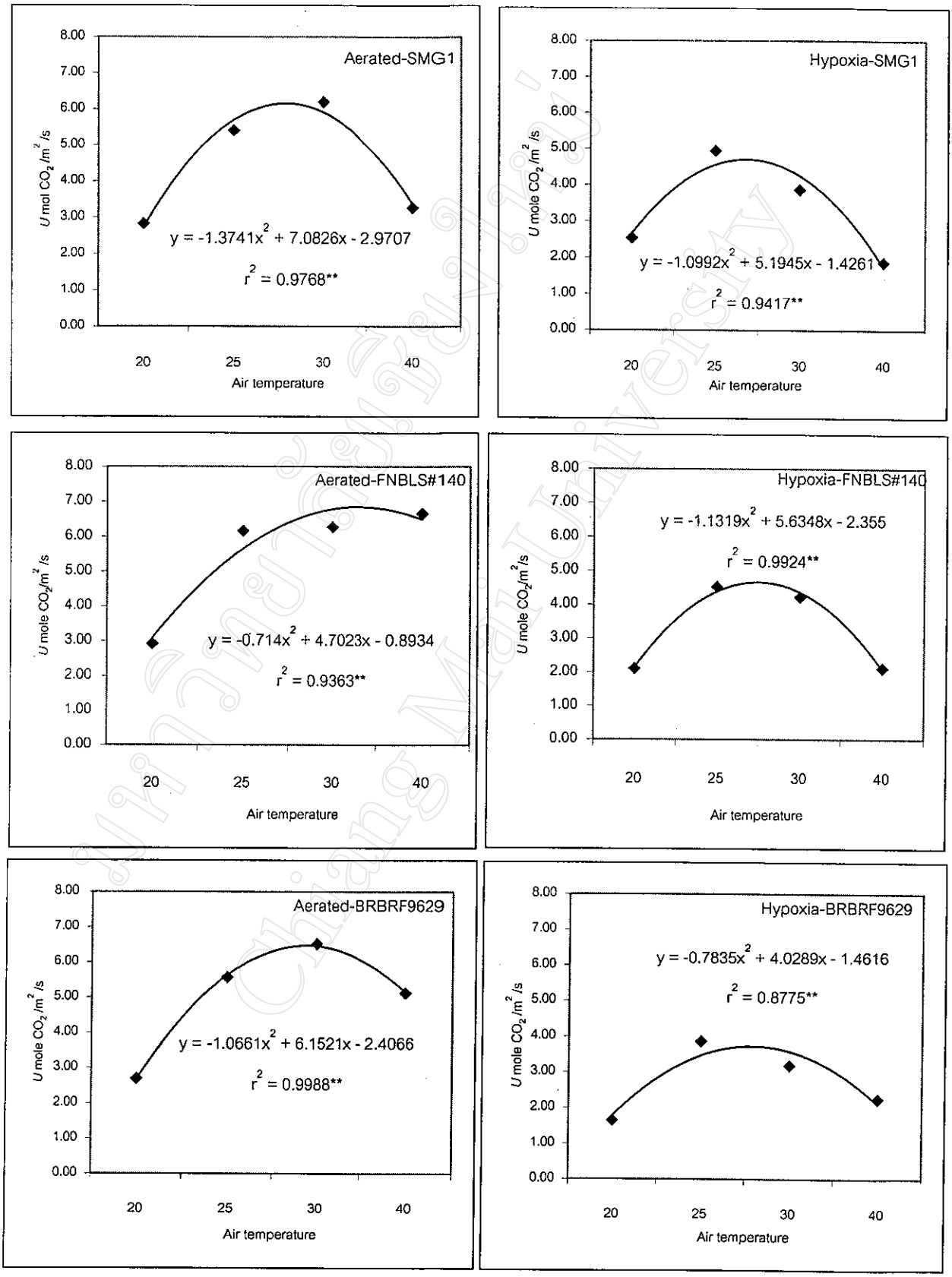


Figure 23 The relationship between the photosynthetic rate of barley genotypes and the maximum diurnal air temperatures in the growth chambers. (all data from the 3rd and 4th experiments).

Daily dry matter partitioning to the shoot (*ShDM*) and root (*RtDM*) were calculated using the value of initial total dry matter (*InitialTDM*) and net photosynthetic rate (*PhsRate*). Where the *ShDM* value was calculated by multiplying the fraction of shoot dry matter partitioning (*ShParFct*) with the *InitialTDM* value. Likewise, the calculation of *RtDM* value was performed the same way as the *ShDM* value.

According to, the ratios of the shoots and roots of each barley genotypes were slightly different among various ambient temperatures as shown in Figure 19 and Appendix 15. Thus, their means were used as the fraction of dry matter partitioning to the shoot (*ShParFct*) and the root (*RtParFct*) under aerated and hypoxic condition in the "BGUHM" (Table 10).

The relationship between the shoot growth rate (*ShGRate*) of FNBLS#140 and BRBRF9629 genotype, and various ambient temperatures were linear response (Figure24). On the other hand, the shoot dry matter of SMG1 under hypoxia slightly decreased during 20-30 $^{\circ}$C and tended to increase at 40 $^{\circ}$C. Thus it caused to relate to ambient temperature as a quadratic function. Whereas the relationship of SMG1 under aerated condition was in linear curve (Figure 24).

The root growth rates (*RtGRate*) of SMG1 and BRBRF9629 under aerated condition relating to ambient temperatures were in negative linear function. Whereas the relationship of FNBLS#140 under aerated condition was in quadratic function. For growing under hypoxic condition, the relationships between root growth rates of all barley genotypes and ambient temperatures were quadratic response (Figure 24).

The energy required for plant maintenance is reasonably quantified (Penning de Varies *et al.*,1989). In the "BGUHM", the shoot dry matter accumulation was reduced by the maintenance respiration as shown the following equation (Penning de Varies *et al.*,1989);

The shoot respiration maintenance (*ShResMain*) = $ShDM*0.75*Q_{10}$

This showed that the *ShResMain* value was the function of the shoot dry matter (*ShDM*) and the respiration reaction (Q_{10}). It was indicated that the Q_{10} value was set at 2.0 to be a reasonable average (Penning de Varies et al.,1989). Thus, the Q_{10} value

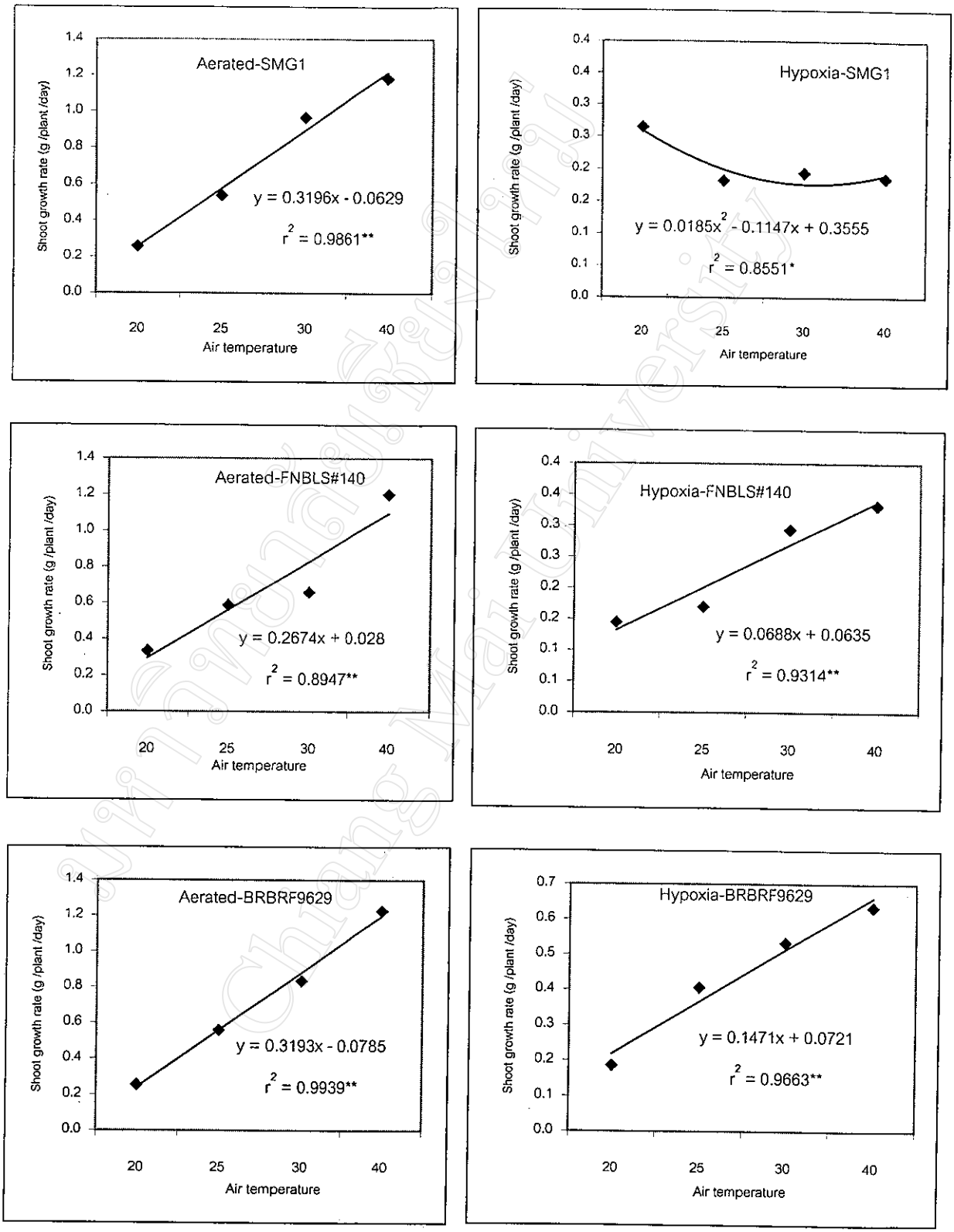


Figure 24 The relationship between the shoot and root growth rates of barley genotypes and daily maximum ambient temperatures in the growth chambers. (all data from the 3rd and 4th experiments).

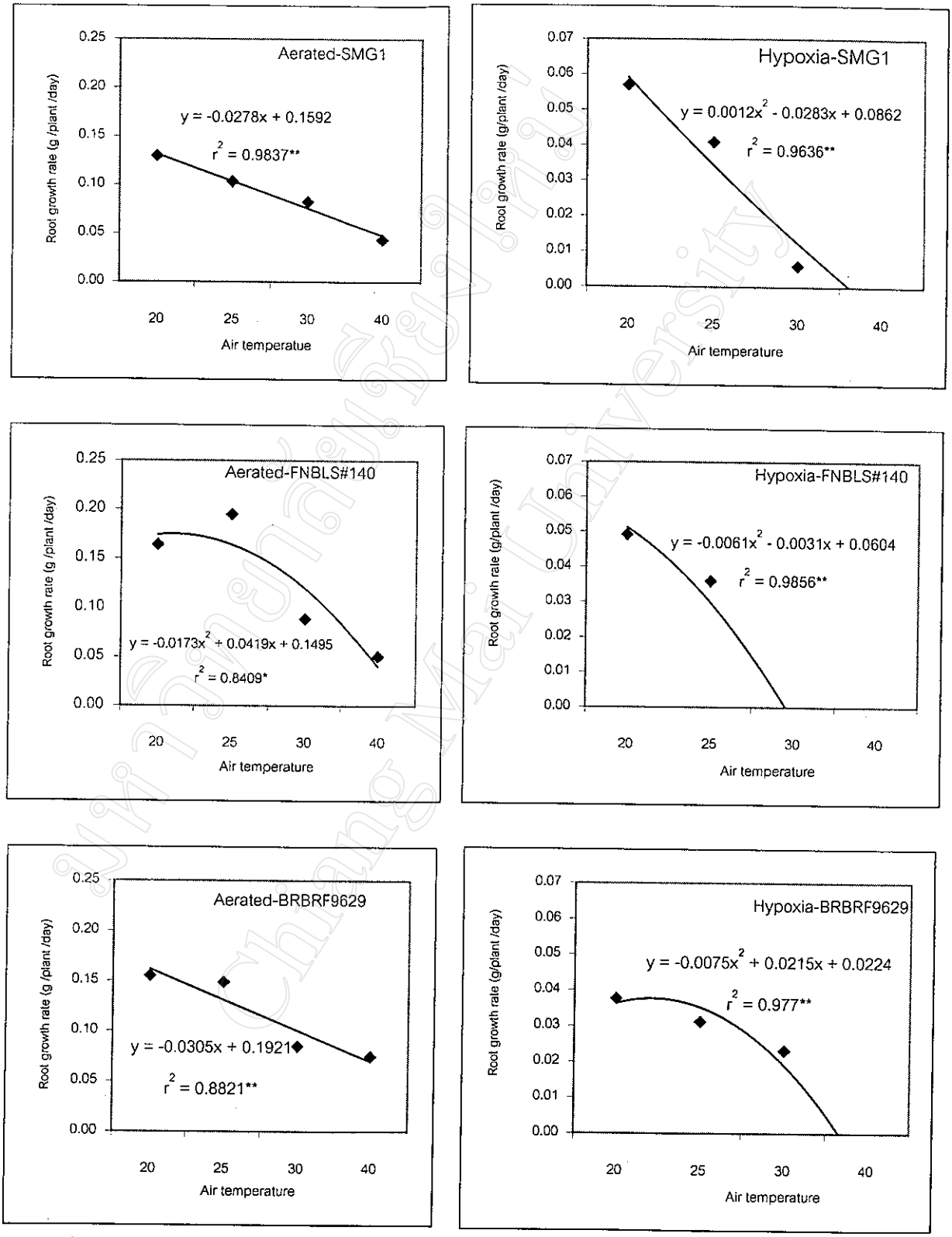


Figure 24 (continued)

The relationship between the shoot and root growth rates of barley genotypes and daily maximum ambient temperatures in the growth chambers. (all data from the 3rd and 4th experiments).

was controlled by writing with the program language as following; (IF ((*ActTmp*-10)/10)>2 then (2) else ((*ActTmp*-10)/10). This means the Q_{10} value was controlled at 2.0 while ambient temperature increased more than 10 °C. In addition, the root maintenance respiration (*RtResMain*) was also calculated the same way as the *ShResMain*.

Results and Discussion

Model testing

The model testing was performed comparing the simulated results and the observed data from the Experiment III and IV in terms of the shoot and root dry matter of each barley genotype. The results of model testing were presented in Figure 25-27.

The shoot dry matter of each barley genotypes under aeration increased at 20-40 °C as the same results of the observed data from Experiment III and IV. The shoot dry matter of FNBLS#140 and BRBRF9629 under hypoxia were also similar to the results in the Experiment III and IV. High temperature reduced shoot dry matter accumulation more than the effect of hypoxic condition as the observed data from the Experiment IV. The model slightly overestimated shoot dry matter of each barley genotypes under aerated condition at 20-25 °C as compared to the observed data. This was probably due to lack of the model structure relating to the function of regulating growth rate associated with temperature in the early growth stage (Murata,1975). The shoot dry matter of barley genotypes especially FNBLS#140 grown under hypoxia, were reduced at 30-40 °C more than at 20-25 °C. Thus the results were similar to those found in the Experiment III and IV. The simulated shoot dry matter of SMG1 under hypoxia across the ambient temperatures were the highest as compared to the other genotypes. These results were clear that the stimulated shoot dry matter was quite accurate with the observed data from the Experiment III and IV across ambient temperatures and oxygen concentration conditions.

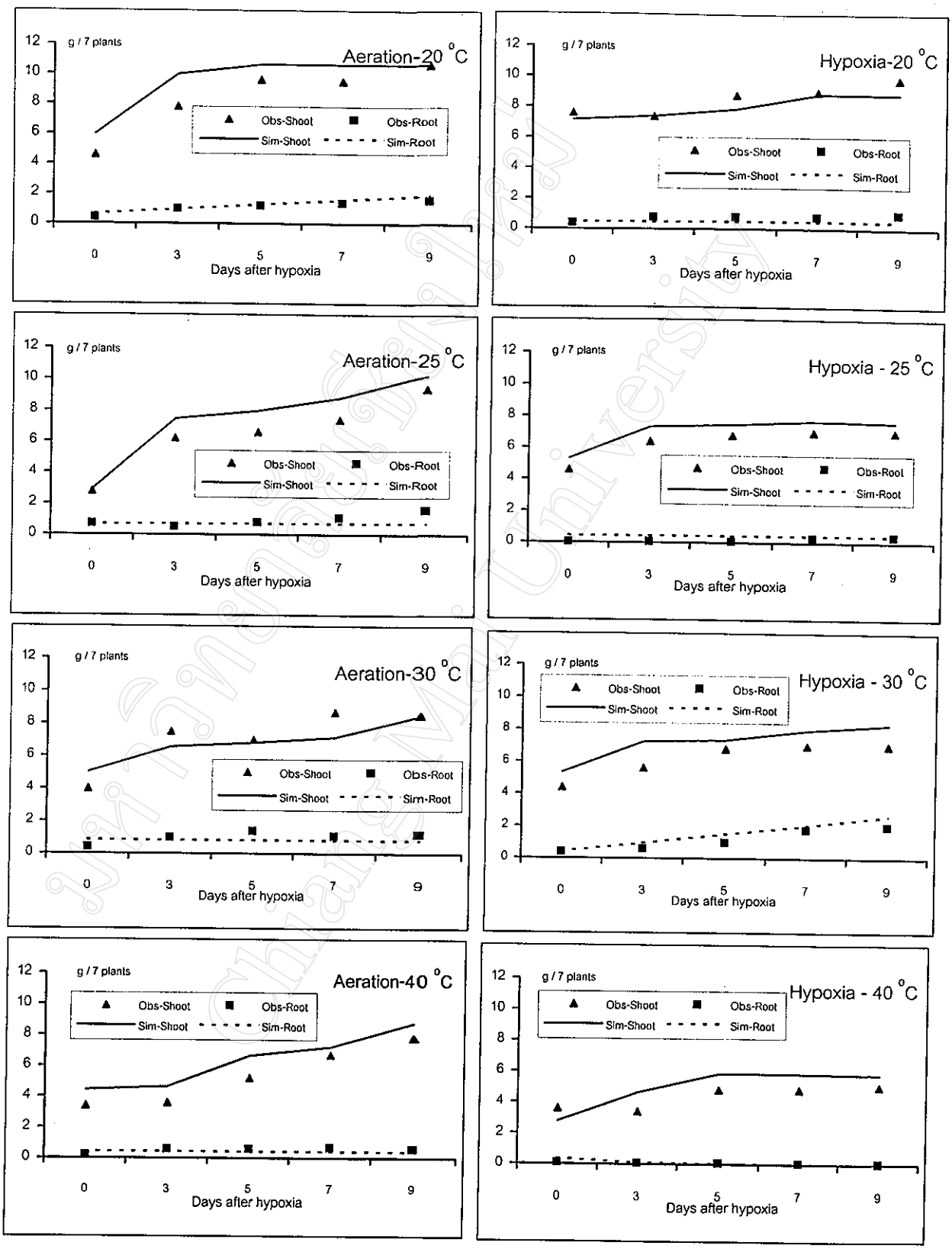


Figure 25 Comparison between simulated and observed shoot and root dry matter accumulation of SMG1 genotype under aerated and hypoxic condition at ambient temperatures for model testing.

Note : Obs = Observed data, Sim = Simulated data.

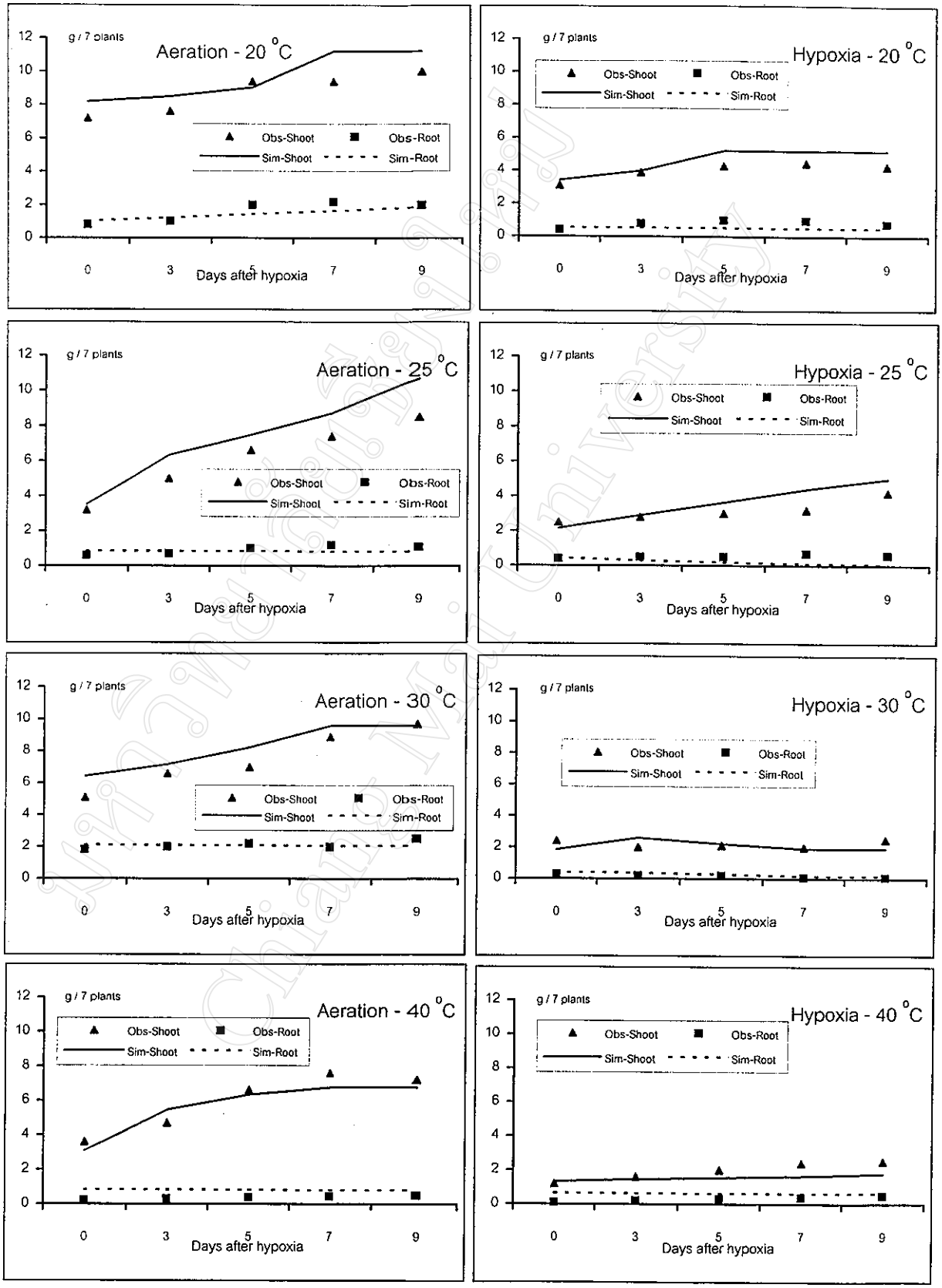


Figure 26 Comparison between simulated and observed shoot and root dry matter accumulation of FNBLS#140 genotype under aerated and hypoxic condition at ambient temperatures for model testing.

Note : Obs = Observed data, Sim = Simulated data.

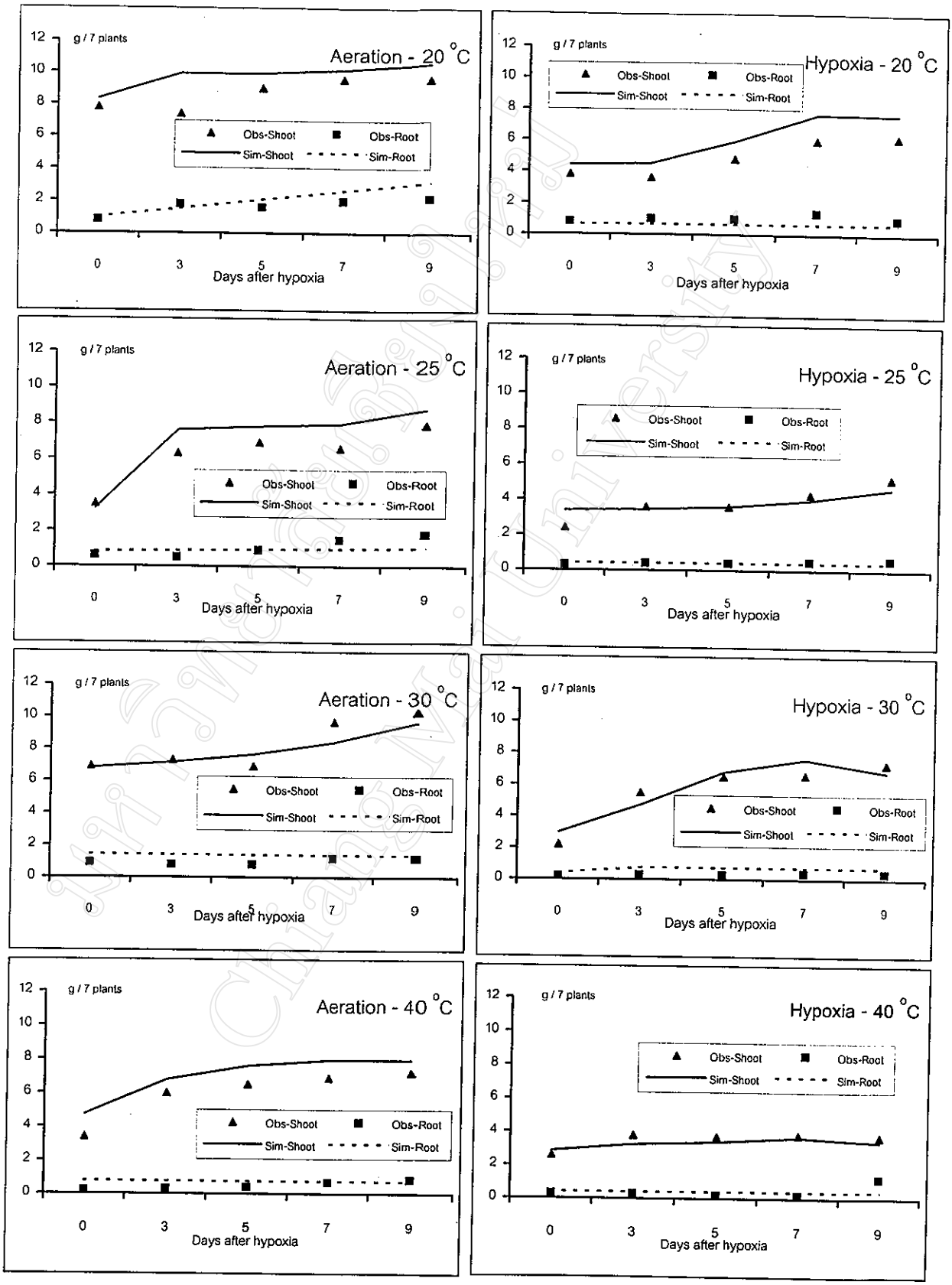


Figure 27 Comparison between simulated and observed shoot and root dry matter accumulation of BRBRF9629 genotype under aerated and hypoxic condition at ambient temperatures for model testing.

Note : Obs = Observed data, Sim = Simulated data.

The model slightly overestimated root dry matter across 20-25 °C and slightly underestimated across the aerated and hypoxic condition with 30-40 °C. The model estimated the root dry matter of SMG1 under hypoxia at 40 °C was slightly less than the result observed in the Experiments IV. In general, the model satisfactory simulated the shoot and root dry matter accumulation of barley genotypes across the aerated and hypoxic condition with ambient temperatures.

Model validation

The simulated shoot dry matter of SMG1 under aerated and hypoxic condition with various ambient temperatures were slightly higher than the observed data (Figure 28). It was also clear that the "BGUHM" accurately simulated shoot dry matter of SMG1 since the standardized mean square error was low (0.003-0.090) (Table 11). It was noted that the simulated root dry matter of SMG1 at 30-40 °C was slightly lower than the observed data (Figure 28) and low standardized mean square error (0.104-0.670) (Table 11). It might improve the maintenance respiration equation in *RtResMain* variable due to be high dry matter reduction. Thus it slightly affected the behavior of SMG1 growth. All carbohydrates required for crop maintenance are substracted from daily photosynthesis and the reminder are left for growth (Penning de Varies *et al.*,1989).

The simulated shoot dry matter of FNBLS#140 evidently overestimated as compared to the observed data (Figure 29). Especially, the standardized mean square error of FNBLS#140 under aerated condition at 25 °C was 0.147 and higher than the other treatments. It was possibly associated with the behavior of shoot growth rate following as the quadratic response. The "BGUHM" slightly overestimated the root dry matter of FNBLS#140 at 40 °C (Figure 29). These results were shown high standardized mean square error under aerated and hypoxic condition (1.556 and 2.305, respectively) (Table 11). It may probably due to the equation of the maintenance respiration of the roots. However, the "BGUHM" model could estimate the dry matter accumulation of FNBLS#140 similar to the observed data.

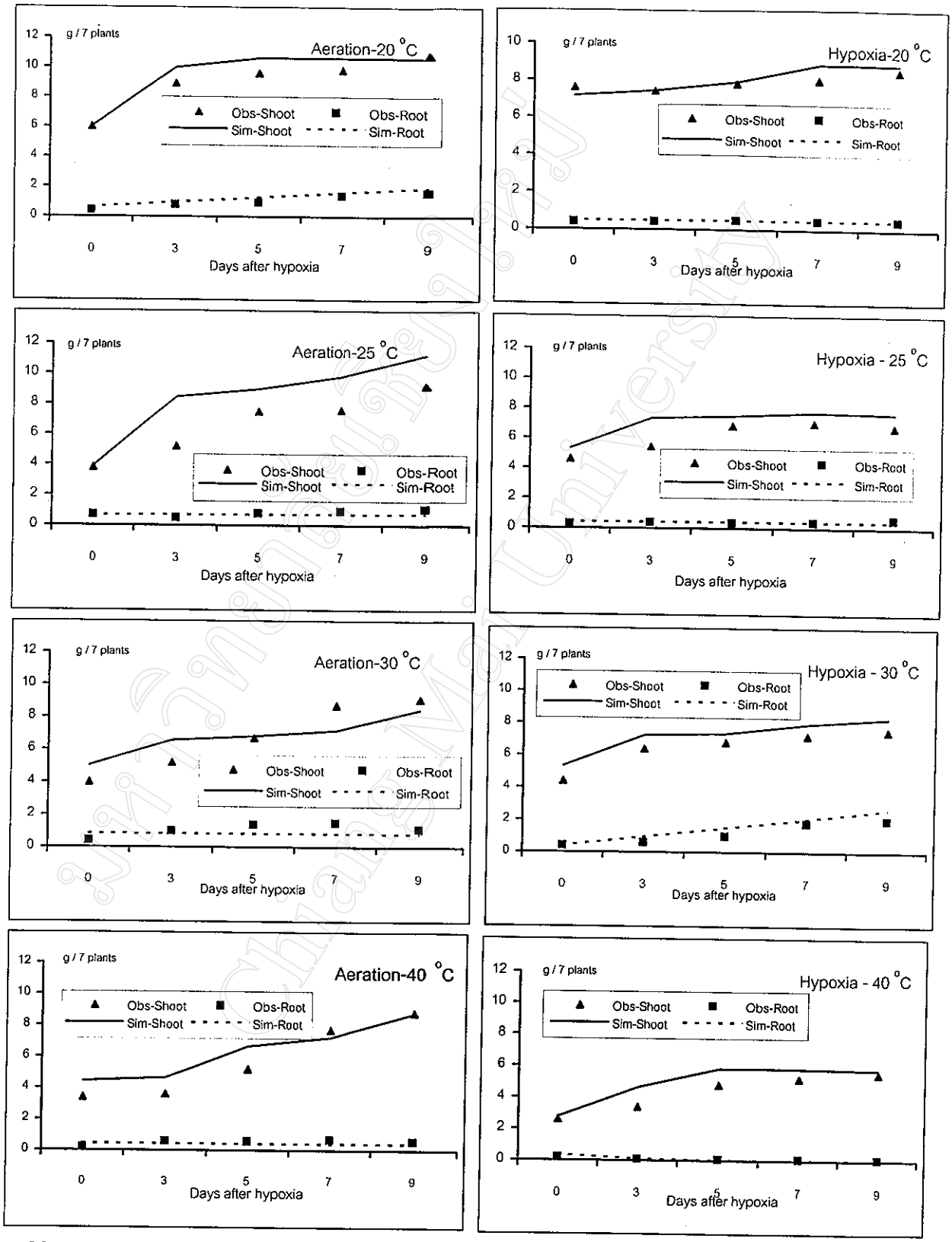


Figure 28 Comparison between simulated and observed shoot and root dry matter accumulation of SMG1 genotype under aerated and hypoxic condition at ambient temperatures for model validation.

Note : Obs = Observed data, Sim = Simulated data.

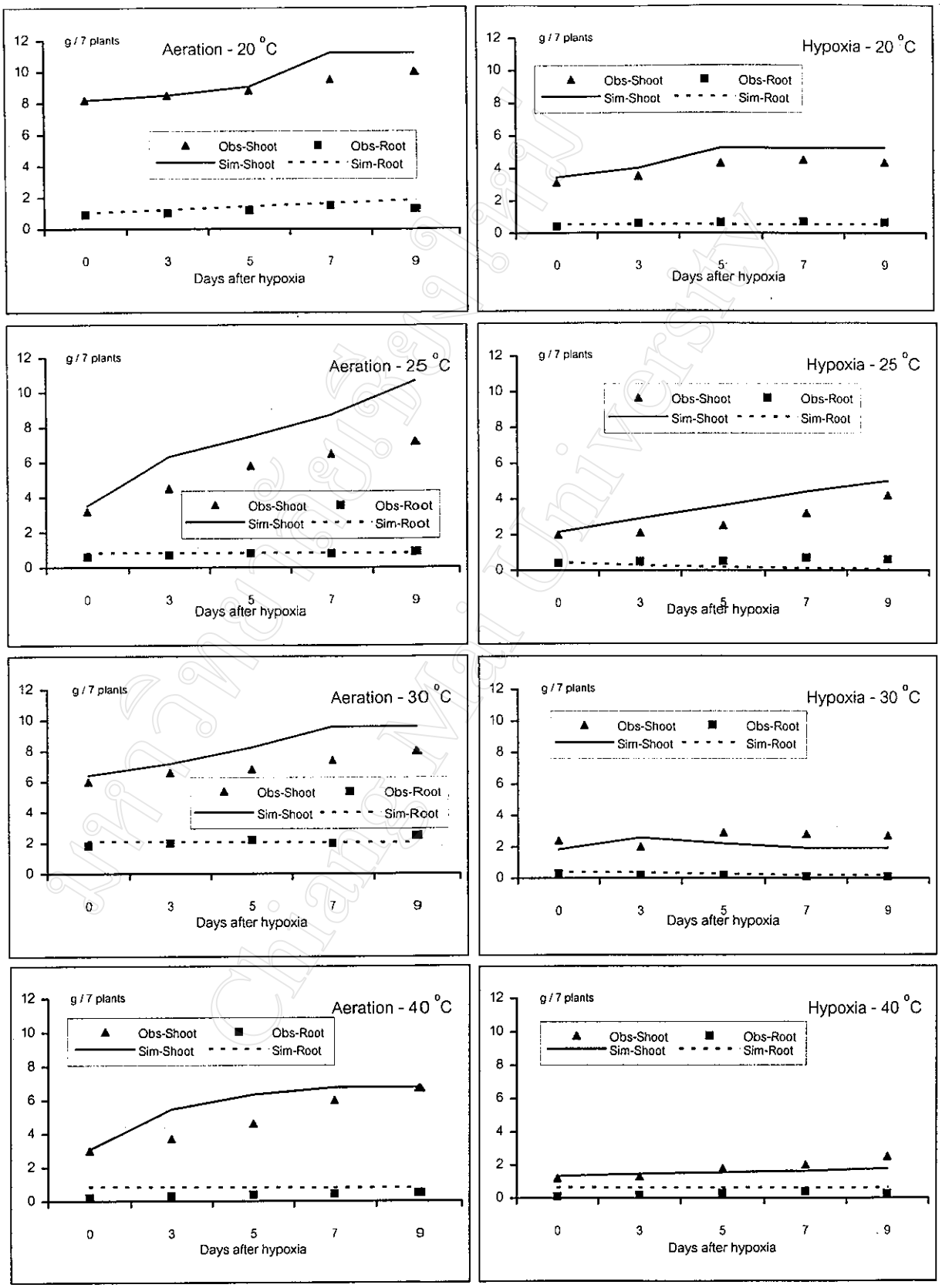


Figure 29 Comparison between simulated and observed shoot and root dry matter accumulation of FNBLS#140 genotype under aerated and hypoxic condition at ambient temperatures for model validation.

Note : Obs = Observed data, Sim = Simulated data.

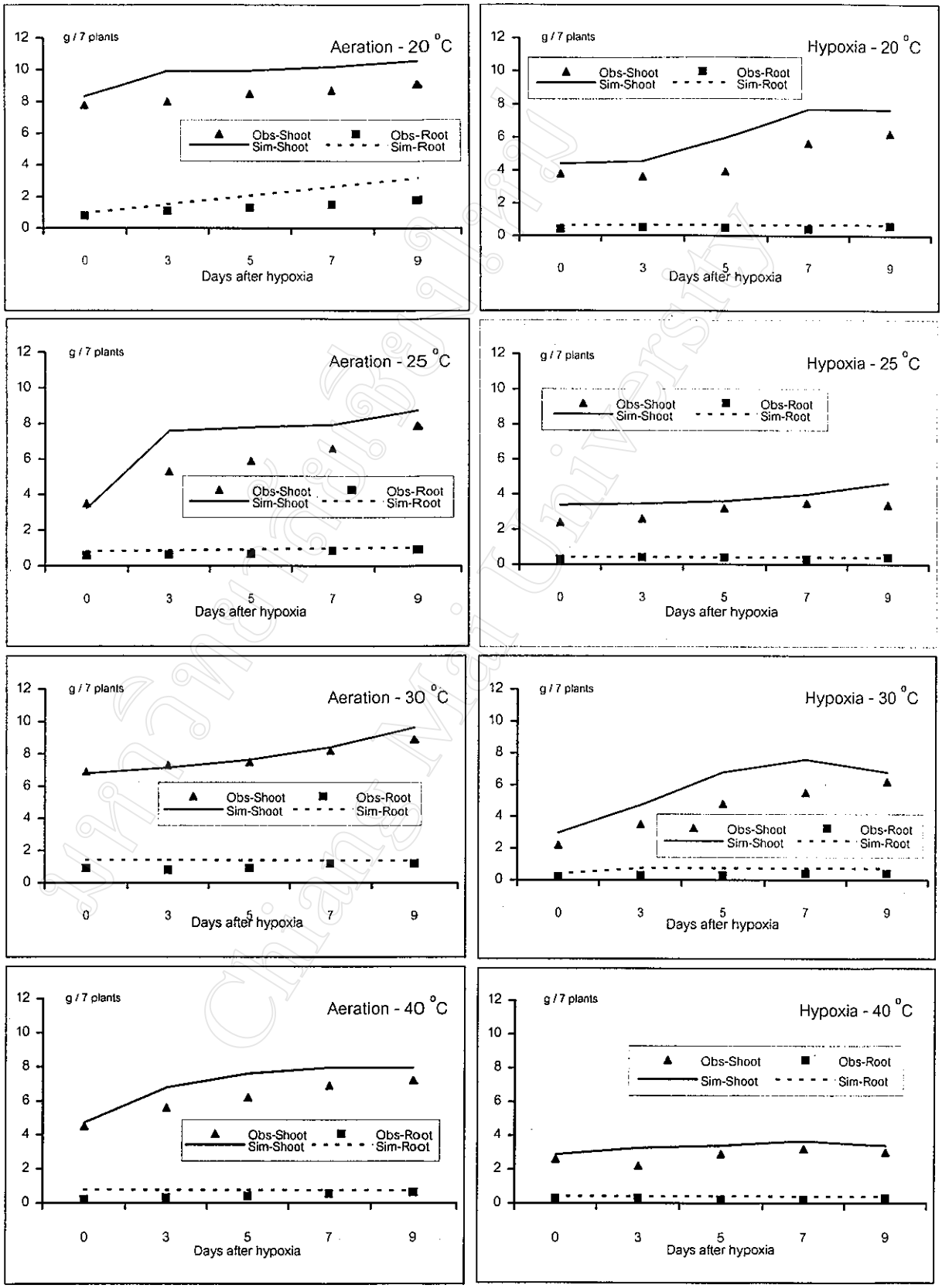


Figure 30 Comparison between simulated and observed shoot and root dry matter accumulation of BRBRF9629 genotype under aerated and hypoxic condition at ambient temperatures for model validation.

Note : Obs = Observed data, Sim = Simulated data.

Table 11 Standard mean square error (V) for the comparison of observed and simulated values of dry matter accumulation for barley genotypes under aerated and hypoxic condition with ambient temperatures.

Barley genotypes		Aerated condition				Hypoxic condition			
		20/15 °C	25/15 °C	30/15 °C	40/15 °C	20/15 °C	25/15 °C	30/15 °C	40/15 °C
SMG1	Shoot	0.007	0.090	0.023	0.024	0.003	0.031	0.014	0.031
	Root	0.054	0.065	0.169	0.135	0.008	0.064	0.104	0.670
FNBLS#140	Shoot	0.011	0.147	0.040	0.054	0.033	0.094	0.075	0.045
	Root	0.066	0.029	0.015	1.556	0.043	0.507	0.347	2.305
BRBRF9629	Shoot	0.029	0.063	0.002	0.027	0.103	0.078	0.099	0.046
	Root	0.445	0.072	0.187	0.725	0.157	0.041	1.264	0.338

The simulation of shoot dry matter of BRBRF9629 at 30 °C was fit to the observation as the standardized mean square error was nil (0.002) (Table 11). The simulated root dry matter of BRBRF9629 under aerated condition was also slightly overestimated (Figure 30) and high standardized mean square error (0.072-0.725) (Table 11). This error may be affected by using the same *RtResMain* value. The calculation of Q_{10} value of each barley genotype for simulation should have differences in the rates of maintenance respiration between lines of crop species (Penning de Varies *et al.*,1989). Whereas the simulated root dry matter of BRBRF9629 under hypoxia at 30 °C was high standardized mean square error (1.264). It was possibly that the root growth rate of BRBRF9629 was quadratic response.

In conclusion, the simulated root dry matter of all barley genotypes under aerated and hypoxic conditions at 40 °C should agree to the observed data. Even they tended to be high standardized mean square error as compared to the other ambient temperature, their comparisons between the simulated and observed data were very low difference. Likewise, the model was capable of simulating shoot dry matter accumulation across aerated and hypoxic condition with ambient temperatures

as well. In consequence, all the results of the validation of the "BGUHM" showed that the model was satisfactory simulated shoot and root dry matter accumulation across aerated and hypoxic condition with ambient temperatures.

SUMMARY AND CONCLUSIONS

Grain yield, yield components, vegetative and reproductive growth rate and the partitioning coefficient of barley genotypes significantly decreased under transient waterlogging at 3-4 leaf stage. Although all barley genotypes especially the susceptible genotypes had high photosynthetic efficiency before tillering stage under transient waterlogging at 3-4 leaf stage, but they did not differed under the sufficient watering after the 1st tillering stage. Leaf growth rate of barley genotypes significantly decreased under transient waterlogging. However, the tolerant genotypes had consistently in grain growth rates, high crop growth rates and a large amount of dry matter partitioning to the seeds under transient waterlogging.

Total dry matter at maturity had the highest positive correlation with grain yield. The difference in grain yield under transient waterlogging was due to the ability of spike production. Among nine barley genotypes, SMG1 was the best tolerant genotype which likely had high growth rate, high dry matter partitioning to seeds, a large amount of total dry matter at maturity. In addition, it had high spikes production and a high grain yield under transient waterlogging as compared to FNBLS#140 (moderately tolerant genotype) and BRBRF9629 (susceptible genotype).

In the 1999-2000 pot experiment, transient waterlogging affected seed growth, total soluble sugar and nitrogen accumulation and partitioning to the seeds, and also affected the leaf photosynthetic efficiency. The increasing of NR activity at early maturity stage related to the increase of leaf chlorophyll fluorescence for photosynthetic process and also increased total nitrogen content in the seeds.

Seed growth for SMG1 genotype under 3 days of flooding was remarkably consistentcy by increasing leaf chlorophyll fluorescence. However, SMG1 produced high NR activity at the early maturity. It consequently increased high seed protein content. FNBLS#140 genotype had high growth rates under transient waterlogging, but

low dry matter partitioning to seeds especially under 3 days of flooding. The total soluble sugar and starch in the seeds of FNBLS#140 and BRBRF9629 decreased under 3 days of flooding whereas total nitrogen in the seeds increased until maturity. BRBRF9629 genotype was the most sensitive to transient waterlogging.

All barley genotypes grown under transient waterlogging had low leaf growth rates, high stem growth rates, consistently root growth rates and slightly high grain growth rate, including high crop growth rate except for BRBRF9629. SMG1 had highest dry matter partitioning to the seed under 3 days of flooding. In consequence, all barley genotypes were met the standard of 1,000 seed weight. However, they had high seed protein content which could not be used for malting quality. SMG1 grown under 3 days of flooding had a good seed size and well seed germination, but it only had high seed protein. In addition, FNBLS#140 under 1 day of flooding did not met the standard of seed germination for malting.

In the laboratory experiment (in 1999), when barley plants were grown under hypoxia, the ADH activities of barley genotypes especially BRBRF9629 immediately increased. Then the aerenchyma was formed in the roots for the transportation of oxygen from the shoot and caused to decrease in ADH activity. Internal ethylene production and aerenchyma formation in the roots occurred at the fifth days of hypoxia. During 7-9 days of hypoxia, the more internal ethylene production and the higher aerenchyma formation in the roots was found. SMG1 and FNBLS#140 genotypes produced the highest internal ethylene in the nodal roots, but were less aerenchyma formation. BRBRF9629 adapted by producing a large amount of aerenchyma formation when hypoxia was extended.

The combining effect of hypoxic conditions with high temperatures was studied in the growth chamber in 1999. It was found that the nodal roots /plant increased only under the 1st hypoxia with high temperatures. All barley genotypes except for SMG1 grown under the 2nd hypoxia condition, suppressed the new nodal root production especially at 40/15 $^{\circ}$C. Total root length /plant was affected by high temperature more than the hypoxic effect. In addition, total root length /plant decreased under the 2nd

hypoxia more than under the 1st hypoxia. BRBRF9629 genotype was the most sensitive under the 2nd hypoxic condition with high temperature.

ADH activities of barley genotypes increased especially under the 2nd hypoxia with 40/15 ° C. BRBRF9629 had lower ADH activity than the other genotypes. NR activities decreased under hypoxic condition with high temperatures. Only SMG1, tolerant genotype could produce high ADH activity and maintain NR activity under the 2nd hypoxia with 40/15 ° C. This may be the acclimatic adaptation of tolerant genotype under hypoxia with high temperature. NR activity had a positive relationship to the photosynthetic efficiency under this severe stress condition.

The photosynthetic rates of all barley genotypes except for SMG1 decreased under hypoxia with 30-40/15 ° C. SMG1 could maintain photosynthetic efficiency due to high leaf chlorophyll fluorescence. The leaf chlorophyll fluorescence only increased under the 1st hypoxia with 25/15 ° C, and decreased under either the 2nd hypoxia or high temperature condition. Transpiration rate was negative correlation with the stomatal resistance especially under the 2nd hypoxia with high temperatures.

Total soluble sugar in the shoots of all barley genotypes especially FNBLS#140 increased under the 1st hypoxia with 25-30/15 ° C. However, it decreased under the 2nd hypoxia with 40/15 ° C. The hypoxic condition decrease the total nitrogen content in the shoots more than in the roots. Total nitrogen accumulation in the shoots decreased under the 2nd hypoxia and was lower than under the 1st hypoxia. Only SMG1, tolerant genotype could produce total soluble sugar and nitrogen in the shoots under the 2nd hypoxia with 40/15 ° C.

Total dry matter accumulation in the shoots was more sensitive to hypoxia. High temperature affected dry matter accumulation in the shoots more than the effect from hypoxia. Shoot dry matter accumulation increased under the 2nd hypoxia . SMG1 genotype had high ability to maintain the total dry matter accumulation under the 2nd hypoxia with high temperatures.

Among different waterlogged tolerant genotypes, SMG1 showed the most acclimatic adaptation under hypoxic conditions with high temperature by controlling the potential demand of total soluble sugar and nitrogen between the shoots and roots for survival. This was also used to maintain the photosynthetic efficiency for growth recovery. SMG1 had high ADH and NR activity, had consistently in total nitrogen accumulation and accelerated leaf chlorophyll fluorescence under the severe stress. FNBLS#140 genotype had the same hypoxic adaptation as SMG1 except at 40/15 $^{\circ}$C. It had high ADH activity but low NR activity under the severe stress. In addition, total soluble sugar and nitrogen in the shoot, and the photosynthetic efficiency markedly decreased under the 2nd hypoxia with 40/15 $^{\circ}$C. BRBRF9629, susceptible genotype, had the lowest adaptability especially under the 2nd hypoxia with 30-40/15 $^{\circ}$C.

The physiological adaptation to hypoxia of barley genotypes associated with anaerobic root respiration. Thus the waterlogged tolerant genotypes should have a high ADH and NR activities for root survival. Increasing nodal roots/plant and the more advanced formation of aerenchyma are the root morphological adaptation under hypoxia especially with high temperature. The development of aerenchyma in the roots is an important adaptation to waterlogging. Roots of tolerant genotypes develope more extensive aerenchyma than the sensitive genotypes in response to hypoxia. Variations in the degree of aerenchyma formation between genotypes with differential tolerant to waterlogging could be related to difference in root ethylene production or response of root to ethylene, or both.

High total dry matter acclimation at maturity, high spikes /m^2 and high dry matter partitioning to the seeds could be used as agronomic traits for identifying the waterlogged tolerant genotypes. The selected tolerant genotypes should have the 1,000 seed weight and the percent of seed germination and seed protein content in the standard range for malting quality. The barley production in paddy field should be solved for a long terms of waterlogging. Under rainfed lowland field, high seeding bed should be made for drainage and improved the soil aeration.

In this study, SMG1 was the best waterlogged tolerant genotype, but unfortunately, it had high seed protein content which does not met the standard for malting. Awareness of the total nitrogen accumulation and how to control the seed protein content especially growing under transient waterlogging with high temperature could aid in bringing about large increases in barley production for malting quality.

Growth and development of barley genotypes under transient waterlogging was directly affected by the influence of respiration especially for root survival. Likewise, respiration is linked in one way or another to all facets of plant metabolism especially nitrogen assimilation, partitioning and degradation which depends on ambient temperature level. So the maintenance of respiration is more interesting to be considered as the trait to be improved. Moreover, the efficiency of root respiration especially with high temperature should be considered as the criteria for waterlogged tolerant and seed malt quality.

For the educational mechanistic modeling, the model was capable of simulating shoot and root dry matter accumulation across aerated and hypoxic condition with ambient temperatures as well. Although, the simulation of root dry matter under aerated and hypoxia at 30-40 $^{\circ}$C could not have the same value as the observed data. Even the mechanistic model can evaluate the shoot and root dry matter under hypoxia at various air temperatures as the observed data. In this study were specified only 9 days at the seedling stage. Thus it is not still recognized how high temperature stress affects the lately vegetative and reproductive growth. Identifying the weakness and understanding the maintenance respiration of each plant part would improved the validation of the model.

In summary, SMG1 was relatively more tolerant to hypoxia, FNBLS#140 was moderate, and BRBRF9629 was most sensitive. The characteristics that contribute to the better growth under hypoxic conditions, were associated with the more advanced formation of aerenchyma, consistently in growth rate, high partitioning of photosynthate to the seeds, high number of spikes/m^2, high photosynthetic efficiency, high nitrate reducatase (NR) activity, high alcohol dehydrogenase (ADH) activity, and highly

acclimatic adaptation to the combining effect of hypoxia with high temperature. Breeding for waterlogging tolerant could be facilitated by selecting genotypes with these characteristics.