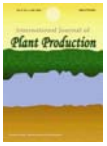

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Optimization of traits to increasing barley grain yield using an artificial neural network

M. Gholipoor[a,*], A. Rohani[b], S. Torani[a]

[a]*Department of Crop Sciences, Shahrood University of Technology, P.O. Box 36155-316, Shahrood, Iran.*
[b]*Department of Farm Machinery Engineering, Shahrood University of Technology, P.O. Box 36155-316, Shahrood, Iran.*
*Corresponding author. E-mail: manouchehr.gholipoor@gmail.com

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Abstract

The grain yield (Y) of crops is determined by several Y components that reflect positive or negative effects. Conventionally, ordinary Y components are screened for the highest direct effect on Y. Increasing one component tends to be somewhat counterbalanced by a concomitant reduction in other component (s) due to competition for assimilates. Therefore, it has been suggested that components be manipulated in conjunction with other traits to break the competition-resulting barrier. The objective of this study is to optimize the effective components in conjunction with certain participant traits for increased barley Y using an artificial neural network (ANN) and a genetic algorithm (GA) as an alternative procedure. Two field experiments were carried out separately at the Agriculture Research Station located in Gonbade Kavous (37°16' N, 55°12' E and 37 asl), Iran. Ten genotypes were grown in each experiment, and the Y and certain traits/components were measured. Among the components/traits, those with a significant direct effect and/or correlation with Y were selected as effective for the ANN and GA analysis. The results indicate that the remobilization of stored pre-anthesis assimilates to grain (R_1), crop height (R_2), 1,000-grains weight (R_3), grain number per ear (R_4), vegetative growth duration (R_5), grain-filling duration (R_6), grain-filling rate (R_7), and tiller number (R_8) were effective. The R^2 for the training and test phases was 0.99 and 0.94, respectively, which reveals the capability of the ANN to predicting Y. The optimum values obtained by GA were 14.2%, 104.34 cm, 36.9 g, 41.9, 100 d, 48 d, 1.22 mg seed^{-1} day^{-1}, and 3.38 plant^{-1} for R_1 through R_8, respectively. The optimization increased the potential Y to 5791 kg ha^{-1}, which was higher than that observed for the genotypes (3527 to 5163 kg ha^{-1}).

Keywords: Barley; Grain yield; Yield components; Genetic algorithm; Artificial neural network.

Introduction

Grain yield (Y), as a function of various yield components, is a complex characteristic that affects the economic value of crops. Y can be determined by several components that reflect positive or negative effects. Conventionally, ordinary Y components, such as 1,000-grains weight, grain number per ear, spikelet number per spike, spike number per plant, number of primary branches per plant, number of siliquae per plant, and harvest index, are screened for higher genotypic coefficient variability, broad sense heritability, genetic advance, highly significant positive correlation, and maximum direct contribution to improve the Y of crops (e.g., Akanda and Mundt, 1996; Akbar et al., 2007; Ahmed et al., 2003; Ball et al., 1993; Costa and Krostand, 1994; Dogney et al., 1998; Maria et al., 1984; Mehetre et al., 1997; Stafford and Seiler, 1986). The selected component is used for the subsequent steps of plant breeding programs.

On the one hand, increasing the value of a component in crops tends to be somewhat counterbalanced by concomitant reductions in other component (s); this is due to the competition for photo-assimilates, which is known to be a barrier to increasing crop Y (Slafer et al., 1996). On the other hand, the excluded components, i.e., those with significant positive correlations but statistically negligible direct effects, usually tend to have considerable indirect effect (s) via other component (s) on Y, which are usually neglected.

Slafer et al. (1996) suggested that the components should be manipulated in conjunction with other traits, including the duration of the grain-filling phase and the remobilization of stored pre-anthesis assimilates to the grain to break the competition barrier. They believed that increasing the grain-filling phase could increase the assimilate availability and, consequently, increase the Y via decreased competition between some components. However, it should be noted that a longer duration of grain-filling increases the risk of facing warm temperatures at the end of the growing period, thus neutralizing the benefits of a longer reproductive phase if the optimum value is not employed. This optimum value may not be the same for different regions that have not yet seen any published quantitative reports.

The above-mentioned state might also be true for other significant participant traits. For instance, taller plants generally have a higher capacity to support the grains by the remobilization of stored pre-anthesis assimilates. Additionally, in some cases, the taller genotypes tend to produce more tillers than dwarfs (Bush and Evans, 1988). However, tallness tends to increase the risk of lodging, leading to decreased Y. Moreover, late-

formed tillers, which usually prevail in taller genotypes, do not contribute to Y. This situation, which was mentioned for a few traits, necessitates the determination of the optimum value of all significant participant components and traits together. We found no published report regarding such optimization. An attempt is therefore made in this paper to optimize the value of those traits/components that have significant direct (multiple regression coefficient) and/or indirect effects (correlation) on Y to increase the potential Y of barley by adapting an artificial neural network (ANN) and a genetic algorithm (GA).

An ANN mimics somewhat the learning process of a human brain. An ANN basically provides a non-deterministic mapping between sets of random input-output vectors. In fact, any linear or nonlinear relationship of multiple inputs and multiple outputs can be learned and approximated simultaneously by an ANN. The absence of any preliminary assumed relationship beforehand between input-output quantities in-built dynamism and robustness toward data errors is one of the advantages of these networks over statistical methods (Rohani et al., 2011). In addition, inherently noisy data do not seem to create a problem, as ANNs are tolerant to noise variations. ANNs are used in a wide variety of applications, including crop development modeling (Fortin et al., 2010; Huang et al., 2010; Zhang et al., 2009) and crop yield prediction (Green et al., 2007; Kaul et al., 2005; Park et al., 2005).

GA has been applied successfully to a wide variety of optimization problems (Goldberg, 1989). The merits of GA include simplicity, ease of operation, and flexibility. GA is now widely recognized as an effective search paradigm in many areas. Although GAs have been widely used in engineering applications, such as solving either single or multi-objective optimization problems (e.g., Rauch and Harremoes, 1999), we could not find any published report for optimization in regard to crops. In this study, ten genotypes of barley were grown to measure Y, yield components and certain other traits. The participant traits/yield components were used as inputs for an ANN and then GA. The results may be useful for breeding programs.

Materials and Methods

Experimentation

Two field experiments were carried out separately at the Agriculture Research Station located in Gonbade Kavous (37^{o}16' N, 55^{o}12' E and 37 asl), Iran, on December 15, 2008 and January 10, 2009. In each

experiment, 10 barley (*Hordeum vulgare* L.) genotypes (Table 1) were planted using a randomized complete block design in three replications. Each plot comprised six rows, which were 5 m long and had a 0.2 m inter-row spacing. The soil was loam silty with 1.46% organic carbon. All soil samples were taken prior to sowing, and the necessary nutrients were added to the soil before planting according to soil test data. Nitrogen was applied in 3 equal splits: at sowing, tillering and anthesis.

Table 1. The pedigree of barley genotypes used in the experiment.

Pedigree	Entry
Check - (Sahra)	1
Gloria'S'/Copal'S'//As46/Aths/3/Rhn-03	2
Productive//As46/Aths	3
ARABIANBARLEY/3/	4
C63//Kavri//Badia	5
Alanda/Hamra//Alanda-01	6
Arar/Lignee527//Arar/PI386540	7
CIRUELO	8
CHAMICO/PETUNIA1//CIRU	9
KAROON/KAVIR//Rhodes'S'//Tb/Chzo/3/Gloria'S'	10

Data on Y were collected from 3.4 m^{-2} in each plot. Ten plants were randomly used to measure Y components and certain traits (R; regressors). The regressors were the remobilization of stored pre-anthesis assimilates to grain (R_1), crop height (R_2), 1,000-grains weight (R_3), grain number per ear (R_4), vegetative growth duration (R_5; days from planting to heading), grain-filling duration (R_6), grain-filling rate (R_7), tiller number (R_8), harvest index (R_9), spike length (R_{10}), and main stem diameter (R_{11}). The following equations were used to calculate R_1 (Arduini et al., 2006; Cox et al., 1986; Papakosta and Gagianas, 1991):

$$ARDM=DMSHT\ (Ant) - DMSHT\ (Mat) \quad (1)$$

$$RP=ARDM / DMSHT\ (Ant)\times 100 \quad (2)$$

Where ARDM is the amount of remobilized dry matter (g/plant) to grain, DMSHT (Ant) is the aboveground dry matter of plant parts at the anthesis stage (g/plant), DMSHT (Mat) is the aboveground dry matter of plant parts at the physiological maturity stage (g/plant), except grain weight and RP is the remobilization percentage. R_7 was simply calculated as the division of Y by R_6. The range of Y and the regressors was calculated based on average values over two experiments.

Artificial Neural Network and Genetic Algorithm analysis

The participant regressors were used in the ANN analysis. First, multiple regression coefficients and a correlation of all regressors with Y were calculated using SAS software. Then, regressors with significant direct effects and/or correlation coefficients were considered to be participant to Y. The dataset was shuffled and split into a training set (80% of total patterns) and a test set (20% of total patterns). These subsets were used to estimate the ANN model parameters and to check the generalization ability of the model, respectively. The following equation was used to normalize the dataset (Rohani et al., 2011):

$$X_n = \frac{X - X_{\min}}{X_{\max} - X_{\min}} \times (r_{\max} - r_{\min}) + r_{\min} \quad (3)$$

Where X is the original data, X_n the normalized input or output values, X_{max} and X_{min} are the maximum and minimum values of the concerned variable, respectively, and r_{max} and r_{min} correspond to the desired values of the transformed variable range. A range of 0.1-0.9 is appropriate for the transformation of the variable onto the sensitive range of the sigmoid transfer function.

A Multilayer Perceptron (MLP) was used, which has maximum practical importance among various ANN models. Figure 1 shows an MLP with one hidden layer. Every node computes a weighted sum of its inputs and passes the sum through a soft nonlinearity. The soft nonlinearity, or the activity function of neurons, should be non-decreasing and differentiable. In this regard, the most popular function is the unipolar sigmoid:

$$f(\theta) = \frac{1}{1 + e^{-\theta}} \quad (4)$$

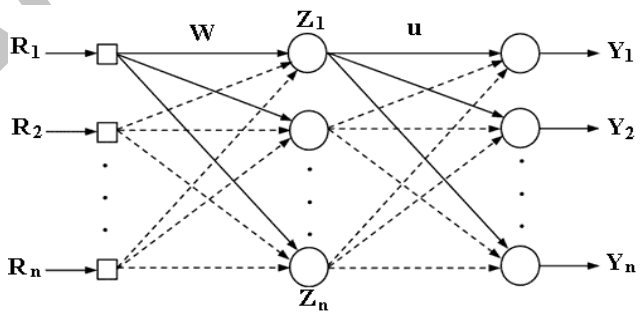

Figure 1. Configuration of the MLP with one hidden layer (Vakil-Baghmisheh, 2002).

The network is in charge of vector mapping, i.e., by inserting the input vector X^q and then answering through vector Z^q in its output (for q=1,…,Q). Among the many variants of the MLP training method, a new one called the Back-Propagation with Declining Learning-Rate Factor (BDLRF) was employed. In this algorithm, the total sum-squared error (TSSE) is considered to be the cost function and can be calculated as:

$$TSSE = \sum_q E_q \tag{5}$$

$$E_q = \sum_k (d_k^q - z_k^q)^2 \quad \text{for } q=1, \ldots, Q \tag{6}$$

Where d_k^q and z_k^q are the k^{th} components of the desired and actual output vectors of the q^{th} input, respectively. Network learning happens in both forward and backward passes. In a forward pass, an input vector is inserted into the network, and the network outputs are computed by proceeding forward through the network, layer by layer:

$$\begin{cases} net_j = \sum_i x_i w_{ij} \\ y_j = \dfrac{1}{1+e^{-net_j}} \end{cases}, j = 1,\ldots,l_2 \tag{7}$$

$$\begin{cases} net_k = \sum_j y_j u_{jk} \\ z_j = \dfrac{1}{1+e^{-net_k}} \end{cases}, k = 1,\ldots,l_3 \tag{8}$$

Where w_{ij} is the connection weight between nodes i and j, and u_{jk} is the connection weight between nodes j and k; w_{ij} and u_{jk} are set to small random values [-0.25, 0.25]; and l_2 and l_3 are the number of neurons in the hidden and output layers. In a backward pass, the error gradients versus weight values, i.e., $\frac{\partial E}{\partial w_{ij}}$ (for i=1,...,l_1, j=1,…,l_2) and $\frac{\partial E}{\partial u_{jk}}$ (for j=1,..l_2, k=1,…l_3), are computed layer by layer, starting from the output layer and proceeding backward. The connection weights between nodes of different layers are updated using the following equations:

$$u_{jk}(n+1) = u_{jk}(n) - \eta \times \frac{\partial E}{\partial u_{jk}} + \alpha(u_{jk}(n) - u_{jk}(n-1)) \tag{9}$$

$$w_{ij}(n+1) = w_{ij}(n) - \eta \times \frac{\partial E}{\partial w_{ij}} + \alpha(w_{ij}(n) - w_{ij}(n-1)) \quad (10)$$

Where η is the learning rate and α is the momentum factor. The momentum factor is used to speed up the convergence. In this algorithm, the training is initiated with a relatively constant large step size of η and α, i.e., 0.9. For every *T* epoch, i.e., 5, these values are decreased monotonically by means of arithmetic progression until they reach *x%* (equal to 5) of their initial values. The following equations are used to decrease η and α (Rohani et al., 2011):

$$m = \frac{Q - n_1}{T} \quad (11)$$

$$\eta_n = \eta_\circ + n\eta_\circ \frac{x-1}{m} \quad (12)$$

Where *m* is the total number of arithmetic progression terms, n_1 is the start point of BDLRF, η_n is the learning rate in the n^{th} term of the arithmetic progression, and $\eta_\circ$ is the initial learning rate. The criteria for optimizing the learning rate and momentum are based on the learning error and the iteration number, which is calculated throughout the trial-error method. The process continues before destabilizing the network or when the convergence is about to slow down (Vakil-Baghmisheh and Pavešic, 2003).

Four criteria were used to evaluate the performance of the model: mean absolute percentage error (MAPE), root mean-squared error (RMSE), TSSE and the coefficient of determination of the linear regression line between the predicted values from the MLP model and the actual output (R^2). These criteria are defined as follows:

$$MAPE = \frac{1}{nm} \sum_{j=1}^{n} \sum_{i=1}^{m} \left| \frac{d_{ji} - p_{ji}}{d_{ji}} \right| \times 100 \quad (13)$$

$$RMSE = \sqrt{\frac{\sum_{j=1}^{n} \sum_{i=1}^{m} (d_{ji} - p_{ji})^2}{nm}} \quad (14)$$

$$TSSE = \sum_{j=1}^{n} (d_j - p_j)^2 \quad (15)$$

$$R^2 = \frac{\left(\sum_{j=1}^{n}(d_j - \bar{d})(p_j - \bar{p})\right)^2}{\sum_{j=1}^{n}(d_j - \bar{d})^2 \quad . \quad \sum_{j=1}^{n}(p_j - \bar{p})^2} \tag{16}$$

Where d_{ji} is the i^{th} component of the desired (actual) output for the j^{th} pattern, p_{ji} is the i^{th} component of the predicted (fitted) output produced by the network for the j^{th} pattern, $\bar{p}$ and $\bar{d}$ are the average of the desired output and predicted output, respectively, and n and m are the number of patterns and variable outputs, respectively. The model with the smallest RMSE, TSSE, and MAPE and the largest R^2 was considered to be the best. A computer code was developed in MATLAB software to implement the analysis.

The optimization process is performed in cycles called generations. During each generation, a set of new chromosomes is created using the crossover and mutation operator. Because the population size is finite, only the best chromosomes are allowed to survive to the next cycle of reproduction. The cycle repeats until the population converges; that is, the diversity of the feature values among the population is very low, and further exploration seems pointless. In this study, we used a continuous GA because the values of the variables were continuous. Generally, this algorithm is initiated with the definition of the cost function, cost, variables and selection of GA parameters. Here, the MLP model was considered to be a cost function for the prediction of Y, the cost was the values of observed Y, and the participant regressors were variables (N_{var}). The GA was initiated by defining a chromosome as follows:

$$\text{Chromosome} = [R_1, R_2, \ldots, R_n] \tag{17}$$

Then, an initial population was defined by random values of N_{pop} chromosomes.

$$pop = rand\,(N_{pop}, N_{\text{var}}) \tag{18}$$

Each chromosome had a cost (grain yield), which was found by evaluating the cost function:

$$cost = -f_{MLP}(chromosome) = -f(p_1, p_2, ..., p_{N_{\text{var}}}) \tag{19}$$

Where f_{MLP} is the MLP neural network for the predicted grain yield as a cost function. The minus sign in this equation was for the

maximization goal; as cost is something to be minimized, the optimization becomes minimization. Of the N_{pop} chromosomes in a given generation, only the top N_{keep} were kept for mating, and the rest were discarded to make room for the new offspring (selection of mates). Two parents were chosen, and the offspring were combinations of these parents (mating). A single offspring variable value, p new, comes from a combination of the two corresponding offspring variable values. By randomly selecting a variable in the first pair of parents to be the crossover point, it can be seen that:

$$\alpha = ceil(N_{\text{var}} \times rand(1, M)) \quad (20)$$

$$parent_1 = [p_{m_1}, p_{m_2}, p_{m_3}, \quad \cdots \quad , p_{mN_{\text{var}}}] \quad (21)$$

$$parent_2 = [p_{d_1}, p_{d_2}, p_{d_3}, \quad \cdots \quad , p_{dN_{\text{var}}}] \quad (22)$$

Where the *m* and *d* subscripts distinguish the *mom* and the *dad* parent. Then, the selected variables were combined to form new variables that will appear in the children:

$$p_{new1} = p_{m_\alpha} - \beta(p_{m_\alpha} - p_{d_\alpha}) \quad (23)$$

$$p_{new_2} = p_{d_\alpha} + \beta(p_{m_\alpha} - p_{d_\alpha}) \quad (24)$$

Where β is also a random value between 0 and 1. The final step was to complete the crossover with the rest of the chromosome as before:

$$offspring_1 = [p_{m_1}, p_{m_2}, \quad \cdots \quad , p_{new_1}, \quad \cdots \quad , p_{dN_{\text{var}}}] \quad (25)$$

$$offspring_2 = [p_{d_1}, p_{d_2}, \quad \cdots \quad , p_{new_2}, \quad \cdots \quad , p_{mN_{\text{var}}}] \quad (26)$$

If care is not taken, the GA can converge too quickly into one region of the cost surface. If nothing is done to solve this tendency to converge quickly, the process could end up in a local rather than global minimum. To avoid this problem of overly fast convergence, the routine was forced to explore other areas of the cost surface by randomly introducing changes or mutations in some of the variables. The details can be seen in Haupt and Randy (2004). A computer code was also developed in MATLAB software to implement these ANN and GA models.

Results

The results indicate that R_1 to R_8 had a significant positive effect and/or statistically considerable correlation with Y. Therefore, the input layer in the ANN analysis had 9 neurons representing the regressors and bias term (b= -1), while the output layer corresponded to Y (Figure 2). The performance of the MLP tended to be improved by an increase in the number of hidden neurons. However, too many neurons in the hidden layer caused overfitting problems, which resulted in good network learning and data memorization, but an inability to generalize. However, the network could not learn, as only a small number of neurons in the hidden layer were used. For this data set, the MLP model with 15 neurons in the hidden layer appeared to be appropriate for the prediction and optimization of Y. This optimal number of hidden neurons was attained when the value of the learning rate (η), the momentum factor (α) and the epoch in the iteration process reached 0.9, 0.8 and 50000, respectively.

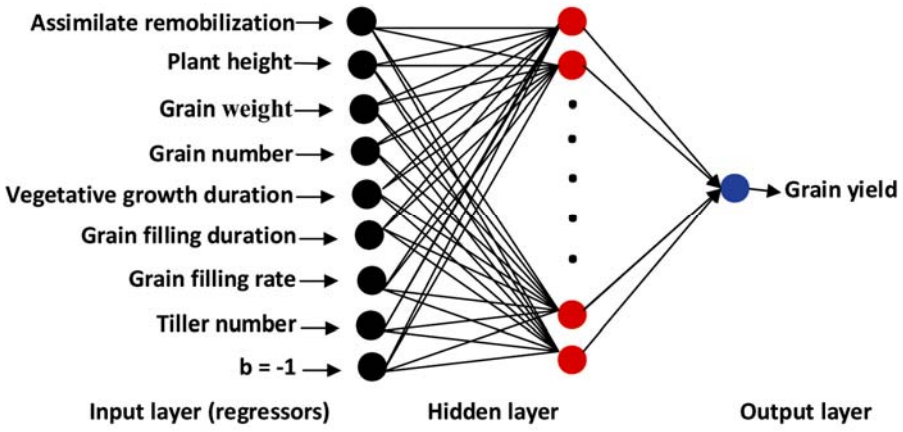

Figure 2. Multilayer neural network used for optimization of traits and grain yield components to increase barley grain yield.

The performance of the ANN is shown in Tables 2 and 3. The low values of MAPE, RMSE, and TSSE proved the capability of the BDLRF algorithm for generating accurate estimates within the preset range by using the MLP neural network. Considering the mean value, standard deviation, variance, and other statistical variables, it can be deduced that the values and the distribution of the observed and predicted data are analogous. Accordingly,

the MLP neural network has learned the training set well; hence, the training phase is completed. The skewness, kurtosis, sum, minimum, maximum and the average values are similar; hence, it could be said that both series are similar for the observed and predicted Y.

Table 2. Performances of MLP in prediction of grain yield.

Phase	Performance criterion		
	MAPE (%)	RMSE	TSSE
Training	0.15	0.23	0.79
Test	0.19	0.28	2.7

Table 3. Some statistical properties of observed and predicted values of barley grain yield in training and test phases.

Value type	Mean	Variance	Standard deviation	Kurtosis	Skewness	sum
Training phase						
Observed	4131.2	301292	548	2.3	-0.12	206563
Predicted	4131.3	301291	548	2.3	-0.12	206562
Test phase						
Observed	3686.5	112666	335.6	2.6	-0.8	36865
Predicted	3696.6	113660	355.6	2.6	-0.8	36866

The predicted and observed values were evenly distributed throughout the entire range (Figure 3). Although the results of the training phase were generally better than the test phase, the latter reveals the capability of the MLP neural network to predict the Y with new data. The high R^2 demonstrated that the trained network was reliable and accurate and, hence, could be employed for Y prediction.

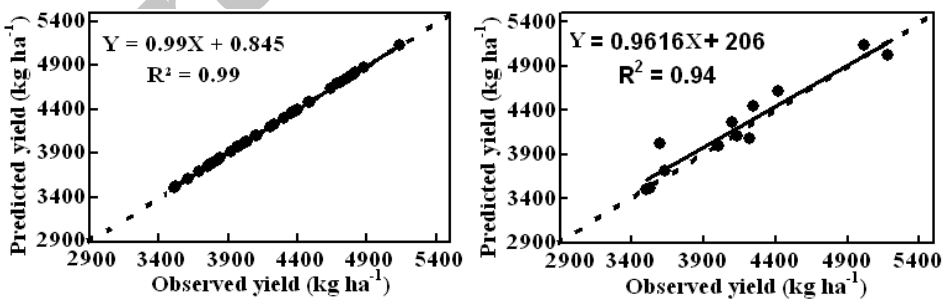

Figure 3. Predicted values of grain yield by MLP neural network versus observed values in training (left) and test (right) phases.

In an attempt to obtain the optimal combination of the 8 parameters for maximum grain yield, the ANN grain yield model was integrated with a GA model. To achieve this, the output of the developed ANN was utilized in calculating the values of the fitness function for the GA. The results indicated a population size of 100, a mutation rate of 0.5, and a generation number of 1000 for the selection method of tournament pairing. As Figure 4 illustrates, the convergence for the GA model reached a grain yield of 5791.2 kg ha^{-1}, which is the maximized grain yield. The optimum values of the regressors for this amount of grain yield are shown in Table 4.

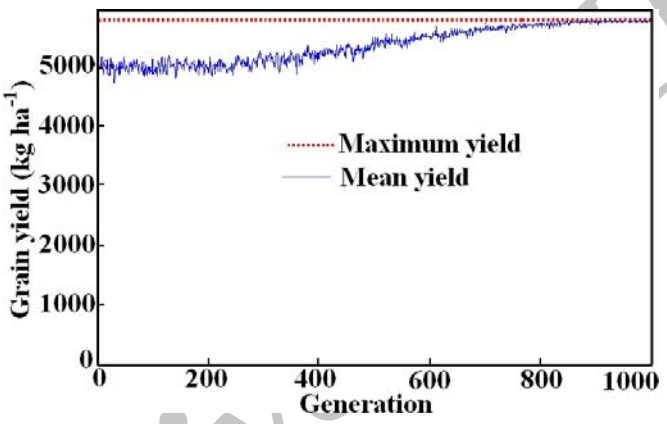

Figure 4. Convergence for the grain yield function.

Table 4. Optimal values of yield parameters for maximum grain yield as determined by GA optimization process.

Parameter	Optimum value
Assimilate remobilization	14.2%
Crop height	104.34 cm
1000 grains weight	36.9 g
Grain number per ear	41.9
Vegetative growth duration	100 d
Grain filling duration	48 d
Grain filling rate	1.22 mg $seed^{-1}$ day^{-1}
Tiller number	3.38 $plant^{-1}$

Discussion

The neural network designed in this study appeared to be the best when it was equipped with a single hidden layer. This result is in agreement with the

universal approximation theorem, which states that a neural network with a single hidden layer and a sufficiently large number of neurons can well approximate any arbitrary continuous function (Haykin, 1994).

There are compensatory processes between the components of Y due to their close interrelationship. Therefore, increasing one component would be counterbalanced by a reduction in other component (s). This study aimed to optimize the important traits and Y components together using an ANN and GA to minimize competition for photo-assimilates for increased Y. As Slafer et al. (1996) suggested, the remobilization of stored pre-anthesis assimilates to the growing grains appears to be an important trait in statistically increasing Y. A study by Bidinger et al. (1977) on one cultivar of barley and wheat revealed that approximately 12% of the Y of well-watered barley comes from these remobilized assimilates. These compounds could buffer Y against unfavorable situations, including a rise in temperature, which occurs frequently during the grain-filling stage of barley in many growing regions. In this situation, where the vapor pressure deficit tends to be high, the plants would suffer form water shortage even in well-watered conditions (Gholipoor and Sinclair, 2011). For these genotypes, the mean remobilization percentage was 13%, with a range of 4.32%. The results indicate that it is possible to maximize the percentage to as high as 14.2% when it is considered in conjunction with other components, including plant height and vegetative growth duration.

Taller plants potentially have a higher capacity to store assimilates in vegetative organs for the future re-translocation to grains. However, tallness increases the risk of lodging and, hence, affects flowering negatively and reduces the photosynthetic capabilities of the plant. Tallness interferes with the transport of nutrients and moisture from the soil and, thus, with food storage in the developing kernels. The decrease in barley Y resulting from lodging has been measured at 20% (Briggs, 1990) and 30% (Pinthus, 1973). For wheat, this reduction has been found to be as low as 40% (Eassen et al., 1993) and as high as 66% (Berry et al., 2003), depending on the crop development stage at the date of lodging and on the intensity of the phenomenon. In our investigation, the lodging varied between 0 to 7% for tested genotypes that appeared to have an average height of 100.6 cm with a range of 17 cm. The optimum height obtained was 104.34 cm.

Mean grain weight is an important component of grain quality in barley, as grain size is related to potential malt extract and screening losses (Lee et al., 1989). Path analysis results have revealed that the participation of the number of grains per ear to Y is more than the grain weight (Moreno et al.,

2003). Grain weight and the number of gains per ear appeared to be inversely related ($r=-0.33^{**}$). Re-analysis of the mean data of Cantero-Martı´nez et al. (2003) for barley also indicates such relationship ($r=-0.45^{**}$; n=54). This effect is due to the decreased availability of assimilates for grain growth (Slafer et al., 1996).

One approach that is important to increasing assimilate availability is dealing with growth characteristics, such as changes in the crop's ability to intercept more radiation (Bingham et al., 2007). It has been reported that increasing the length of the vegetative and reproductive phases could affect assimilate availability (Bingham et al., 2007; Slafer et al., 1996; Miralles et al., 2000). Halloran and Pennell (1982) have reported that the lengths of phenophases in a number of wheat genotypes are independent of each other. However, in most regions of Iran, prolonging the duration of phenophases too much may lead to the crop experiencing warm temperatures at the grain-filling stage and, hence, decreased Y. The optimum values for vegetative growth duration, grain-filling duration, 1000 grains weight and grain number per ear are 100 d, 48 d, 36.9 g, and 41.9, respectively. These optimum values came from genotypes that tended to have average values of 98 d (with a range of 8), 44 d (12), 36.8 g (13), and 35.1 (12), respectively.

The rate of grain filling could be an indicator of both the photosynthetic rate at the grain-filling stage and the remobilization of stored pre-anthesis assimilates to the grain. As has been found previously (Leon and Geisler, 1994), the genotypes differed in the grain-filling rate. The average over the sowing dates ranged from 0.99 to 1.36 mg $seed^{-1}$ day^{-1}. A significant negative correlation ($r= -0.75^{**}$) was found between the grain-filling rate and duration (reproductive length), which is in agreement with the report of Long et al. (1998) on barley and Wheeler et al. (1996) on wheat. The optimum, or maximum, grain-filling rate tended to be 1.22 mg $seed^{-1}$ day^{-1} when it was estimated in conjunction with other factors, including grain-filling duration.

The reports indicate that tillers account for 40.4% of the variability in the Y of barley (Kole, 2006). High levels of tillering are accompanied by high levels of intercepted radiation and have been associated with modern cultivars (Abeledo et al., 2004). Later-formed tillers tend to die, which could be wasteful for plants. In conjunction with other above-mentioned traits/ components, especially plant height, the optimum tiller number was 3.38. The average value of this trait over the two experiments ranged from 1.4 to 3.5. This optimization tended to enhance the potential Y to 5791.2 kg ha^{-1} which is higher than those observed for the genotypes (3527 to 5163 kg ha^{-1}).

Conclusion

This study demonstrated that an ANN and GA are useful tools for simulating and optimizing grain yield. The optimization of Y components in conjunction with participant traits could increase the Y of barley to levels higher than the observed values. Here, the output was limited to Y. As shown in Figure 1, the ANN is able to optimize regressors for more outputs, such as the Y for barley malt or for the oil content and quality of soybeans, which should be employed in future investigations. The optimum value of traits tends to change with changing locations. In windy regions, for example, the optimum plant height might be shorter than the value obtained in this study. This example highlights the necessity of having separate optimizations of traits for each region.

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