

# International Journal of Multidisciplinary Comprehensive Research

---

## Mechanisms and role of genetic regulation in improving crop yields

Fikadu Kumsa<sup>1</sup>, Tolera Kuma<sup>2\*</sup>

<sup>1, 2</sup> Department of Biology, Ambo Universities, College of Natural and Computational Science, Ethiopia

\* Corresponding Author: **Tolera Kuma**

---

### Article Info

**ISSN (online):** 2583-5289

**Volume:** 01

**Issue:** 03

**May-June** 2022

**Received:** 22-07-2022;

**Accepted:** 05-08-2022

**Page No:** 34-38

### Abstract

As the population nowadays is booming increasing the amount of crop manufacturing would end in such lots of inconveniences. This can be obvious thanks to the actual fact the additional population will increase want, the greater yield might be accustomed satisfy food demand. To beat this kind of phenomenon, it miles too much encouraged to apply better yielded higher crops. However, most of the countries did no longer supply attention to growing and using genetically-regulated crops. This practice and therefore the use of genetically modified organisms are often hampered by limited resources and knowledge base. On the other hand, current temperature change, which threatens the globe, appears to pose a practical and potential danger to crop production, because it causes crop failures and associated yield declines. Current review papers are created from topic-related literature to produce summarized knowledge of the mechanisms of crop improvement and use.

**Keywords:** Crops, demand, gene regulation, population, yield

---

### Introduction

The world population is now growing much faster and faster than ever before in history. The results of growth could be a reduction in existing agricultural land and environmental degradation, which could lead to a general food deficit (Egal, 2019)<sup>[9]</sup>. These common issues are addressed through a variety of mechanisms, including the use of plant varieties with high yield per unit area. The impact of genetic improvement on recent crop varieties production requires the identification of genetic diversity of morphological, structural, and physiological characteristics that affect yield. This is often associated with the manipulation of complex signs associated with plant growth and development (Lauria *et al.*, 2015; Kumsa, 2020)<sup>[25, 111]</sup>. Some characteristics of plant development, such as plant structure, leaf characteristics, and vascular structure, are the most important characteristics that determine crop yield (see Figure 1). The leaves are the site of photosynthesis and can be genetically engineered to improve photosynthetic yields. The plant's vasculature is another function that regulates the overall performance of the plant, providing not only mechanical strength, but also a conduit for the transport of water, minerals, and photosynthesis (Mathan *et al.*, 2016)<sup>[26]</sup>.

Regulation of gene expression is also recommended for yield production (Lauria *et al.*, 2015)<sup>[25]</sup>. This gene regulates cell number and organ size, which can increase yield. For example, Gou *et al.* (2011)<sup>[14]</sup>, isolated and defined, and determined the gene (CNR1) from the maize cell count. Absolutely, CNR1 has been shown to reduce overall plant size when ectopically overexpressed, but the plant and organ size increased when its expression was co-suppressed or silenced. Genomic engineering may be a relatively new experience for improving crop yields, nutritional value, herbicide tolerance, biological and abiotic stress tolerance (Wang *et al.*, 2015)<sup>[39]</sup>. During this review, the mechanistic role of gene regulation in crops for better yields was evaluated.

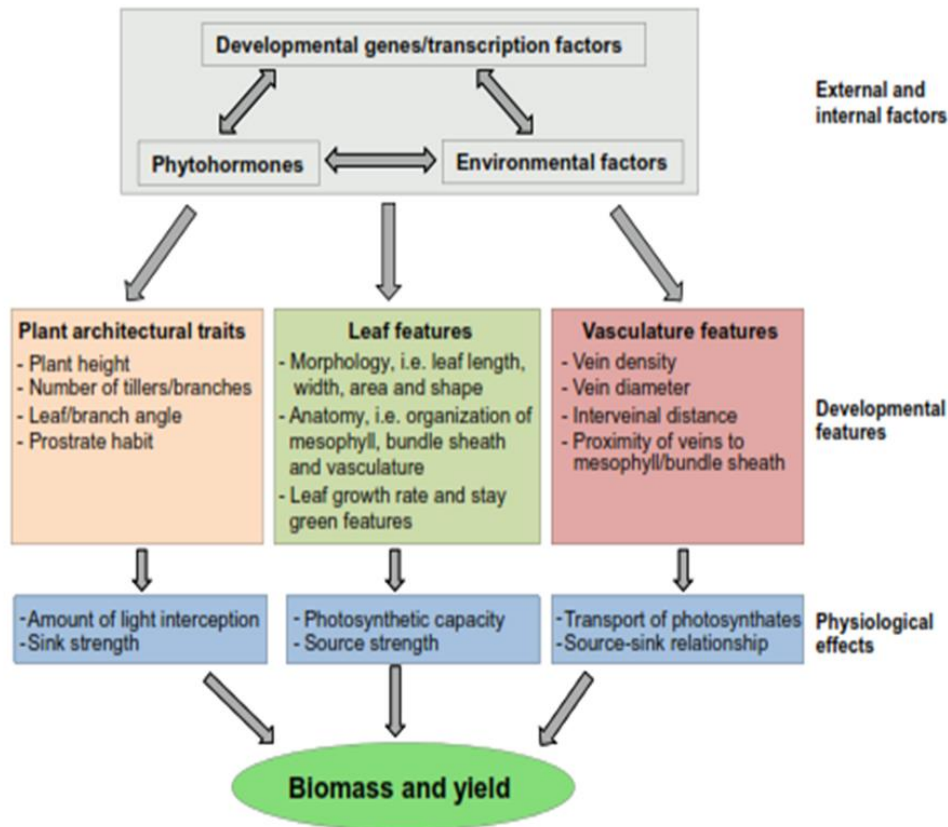
### Analysis of the Related Literature Reviews

#### Regulation and Expression of Plant Genes

The genetic growth regulators of plants are present within the nucleus. The nucleus contains most of the functional genes of a plant in the genome, which is organized consistent with the final model of eukaryotes (Kozlowski & Pallardy, 1997)<sup>[23]</sup>. For several years, the regulation of organic phenomenon in plants has been studied at the phenotypic level. The biological

revolution led to biochemical and molecular genetic techniques has displayed possibilities for understanding the links between genetics and physiology like genotype and phenotype (Kozłowski & Pallardy, 1997) <sup>[23]</sup> to external factors. However, a few years ago, the underlying basis of those reactions at the molecular level was preferentially selected. Important traits like plant structural traits (plant

height, branching, and canopy traits with significant agronomic traits) may be identified using molecular techniques. For several years, breeders are modifying these architectural plant features to optimize yield and yield (Horton, 2000) <sup>[17]</sup>. Many genetic factors regulate these architectural traits of plants (Figure 1).



**Fig 1:** Plant developmental features relevant to crop biomass: and yield (Source: Mathan *et al.*, 2016) <sup>[26]</sup>.

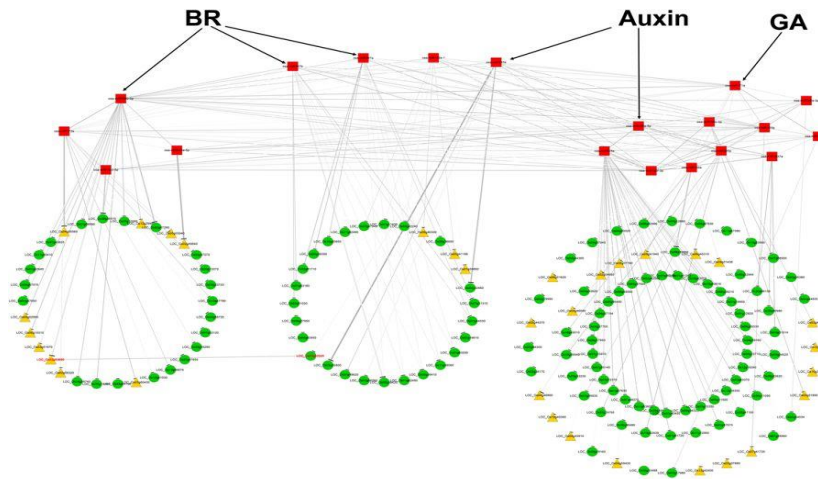
### Regulation of Plant Leaf

Leaf characteristics such as shape, size, and thickness are one of the important morphological characteristics that directly affect crop yield (Bar and Ori, 2014) <sup>[3]</sup>. Many recent reviews discuss the mechanisms of the most genetic mechanisms that support leaf events and morphogenesis in both the same coil and bidirectional plants and may increase crop yields. For example, the YABBY PLETHORA (PLT) and JAGGED (JAG) genes actively regulate leaf and leaf plate enlargement within Arabidopsis (Sarojam *et al.*, 2010). The YAB3 gene is involved in stimulating rice leaf growth (Horigome *et al.*, 2009). In addition, the WUSCHELRELATED HOMEODOMAIN (WOX) gene is a gene used to influence leaf size and promote photosynthesis. The rice NARROWLEAF genes (NAL1, NAL2, and NAL3) belonging to the WOX family are associated with increased leaf width through regulation of the cell cycle in early leaf primitive development (Jiang *et al.*, 2015; Eliezer Burko *et al.*, 2011) <sup>[21, 33]</sup>. Many of the above transcription factors affect leaf shape and size by regulating the cell cycle or cell proliferation, making these cellular processes attractive targets manipulated to regulate leaf properties. The "cell cycle arrest front" is the

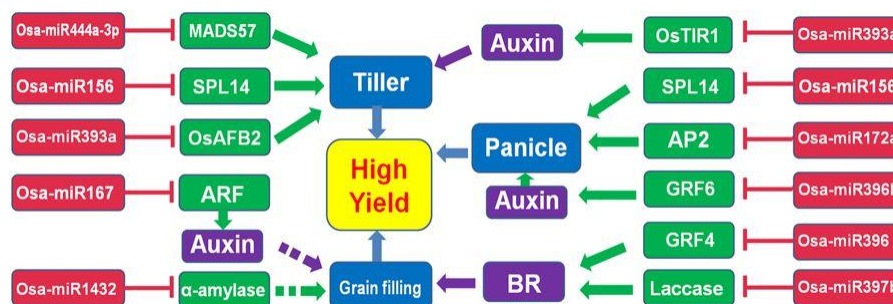
boundary within the leaflet primitive where the transition from proliferation to expansion occurs and is important for leaf size regulation (Mathan *et al.*, 2016) <sup>[26]</sup>. However, further research is needed on its importance in crops and its potential use as a developmental marker of photosynthesis in crops.

### 2.3. Unraveling miRNA Regulation

MicroRNAs (miRNAs) can be small, unencoded RNAs of nearly 21 nucleotides that regulate gene expression at post-transcriptional levels (Bartel, 2004; Hu *et al.*, 2016) <sup>[4, 18]</sup>. miRNAs and retargeting genes are widely used to improve the agricultural traits of crops by the expressive master of microRNA genes (Tang and Chu, 2017) <sup>[36]</sup>. The relationship of miRNAs between miRNA targets allows users to obtain expressive genes involved in similar biological processes and functions of plants (Hu *et al.*, 2018; Yu *et al.*, 2015) <sup>[19]</sup>. In their study, Hu *et al.* (2018) <sup>[19]</sup>, scrutinize gene regulatory networks and identify key regulatory microRNAs in plant development, they have developed an entirely new algorithm called Differential Edge Transformation (DT) (see Figures 1, 2, and 3).



**Fig 2:** Co-expression of miRNAs identified by differential edge-like transformation target genes for high yields during tillering of rice. Reported yields of miRNAs and their confirmed targets BR (brassinosteroids), auxins and GAs, gibberellins (Source Hu *et al.*, 2018)



**Fig 3:** The potential regulatory network model of miRNAs for yields at three stages: tillering, panicle branching, and grain filling in rice. Solid and dashed arrows are the verified and predicted regulatory relationships, respectively (Hu *et al.*, 2018) [19].

Ongoing studies show that miRNAs are involved in the regulation of many genes involved in plant structure. For example, OsmiR397 regulates overall yield by controlling grain number and branching per ear through downregulation of its target gene, OsLAC (Zhang *et al.*, 2013). miRNAs also regulate other SPL genes that regulate panicle morphology, grain size, and plant structure (Si *et al.*, 2016; Wang *et al.*, 2015; Guo *et al.*, 2015). The molecular properties of the gene

indicate that multiple genes contribute to crop yield (Dagang *et al.*, 2018) [7]. For example, the OsNAC2 gene appears to play an important role in the development of rice yields. Typically, Chen *et al.* (2015) [39] revealed that plants overexpressing OsNAC2 under the control of the CaMV35S promoter showed an increase in rice yield. Extensive study of the role of genes in fortifying crops for better yields (see Table 1).

**Table 1:** Knowledge, mechanisms mechanism, and role of gene regulation on crop improvement improvements

Findings/knowledge	Author(s)/year
Regulation of gene expression in higher plants	Kuhlemeier <i>et al.</i> /1987
Genetic strategies for improving crop yields	Bailey-Serres <i>et al.</i> /2019
Transcriptome analysis and crop improvement (A review)	Dunwell <i>et al.</i> /2001
Crop improvement in the 21st century	Mifflin/(2000
Wild barley: a source of genes for crop improvement in the 21st century?	Ellis <i>et al.</i> /2000
Molecular plant breeding as the basis for crop improvement in the 21st century. Plant physiology	Moose & Mumm /2008
Refocus on crop improvement for the changing climatic conditions of the 21st century.	Mba <i>et al.</i> /2012
Application of biotechnology to improve crop: prospects and limits	Sharma <i>et al.</i> /2002
Farmers' participatory varietal selection: A sustainable crop improvement approach for the 21st century	Singh <i>et al.</i> /2014
Mutation breeding for crop improvement	Kharkwal <i>et al.</i> /2004
Strategies for improving crops against salt and drought stress: overview	Athar & Ashraf/2009
Shifts in African crop climates by 2050, and the implications for crop improvement and genetic resources conservation	Burke <i>et al.</i> /2009
Tissue culture-derived variation in crop improvement. Euphytica	Jain /2001
Improved yields for future agricultural systems. Improving harvest for sustainable agriculture	Francis & Callaway/ 1993
30 underutilized crops: trends, challenges, and opportunities in the 21st century. Managing plant genetic diversity	Padulosi <i>et al.</i> /2002
Population genetics of genome-based methods for crop improvement	Hamblin <i>et al.</i> /2011

The molecular properties of the genes are too necessary to analyze the genes of the plant structure used to achieve better yields (Moose & Mumm, 2008).

### 3. Conclusion

Crop yield is highly dependent on plant growth and growth. Some developmental traits of the plant, such as general plant structure, leaf traits, and vascular structure, are the most important traits that determine the total yield of the crop. Therefore, enhancing such developmental characteristics has great potential for increasing yields. Regulation of plant genes for plant developmental traits and advances in genomics are revealing the ability to decipher the genes and gene regulatory networks that underlie the developmental traits that are important to agriculture. Combined with an effective approach in the field of phenomenology, this effectively controls the signs of plant growth and increases yields. We hope that these approaches will greatly improve our understanding of the genetic basis of domestication of plants and identify additional factors that are targeted for crop improvement. Finally, it should be noted that almost all of these developmental and photosynthetic traits are regulated by many genes and gene regulatory networks. Therefore, modeling, simulation, and systems biology approach also help plant biologists integrate and link genetic networks with developmental and physiological characteristics. This will give you a better understanding of plant growth and improve yields.

### 4. Declaration

Ethical Approval and Consent to participate: Not applicable  
 Consent for publication: I as corresponding author declare that we abide by the guideline of the journal and obey publication ethics of the journal.

Availability of data and materials: All data were acknowledged and included in this manuscript.

Funding: There is no funding

Competing interests: I, the corresponding author verified that there is no competing interest in this manuscript.

Authors' contributions: both authors contributed equally

Acknowledgements: N/A

### 5. References

- Athar HR, Ashraf M. Strategies for crop improvement against salinity and drought stress: An overview. In *Salinity and water stress* (pp. 1-16). Springer, Dordrecht, 2009.
- Bailey-Serres J, Parker JE, Ainsworth EA, Oldroyd GE, Schroeder JJ. Genetic strategies for improving crop yields. *Nature*. 2019; 575(7781):109-118.
- Bar M, Ori N. Leaf development and morphogenesis. *Development*. 2014; 141(22):4219-4230.
- Bartel DP. MicroRNAs: genomics, biogenesis, mechanism, and function. *Cell*. 2004; 116(2):281-297.
- Burke MB, Lobell DB, Guarino L. Shifts in African crop climates by 2050, and the implications for crop improvement and genetic resources conservation. *Global Environmental Change*. 2009; 19(3):317-325.
- Chen R, Tong H, Shi B, *et al.* Control of grain size and rice yield by GL2-mediated brassinosteroid responses. *Nature Plants*. 2015; 2:15195.
- Dagang J, Weiting C, Jingfang D, *et al.* Overexpression of miR164b-resistant OsNAC2 improves plant architecture and grain yield in rice. *Journal of Experimental Botany*. 2018; 69(7):1533-1543.
- Dunwell JM, Moya-León MA, Herrera R. Transcriptome analysis and crop improvement : ( A review). *Biological research*. 2001; 34(3-4):153-164.
- Egal F. Review of the State of Food Security and Nutrition in the World, 2019. *World Nutrition*. 2019; 10(3):95-97.
- Ellis RP, Forster BP, Robinson D, Handley LL, Gordon DC, Russell JR, Powell W. Wild barley: a source of genes for crop improvement in the 21st century? *Journal of Experimental Botany*. 2000; 51(342):9-17.
- Kumsa F. Factors affecting in vitro cultivation of grape (*Vitis Vinifera* L.): a review. *International Journal of Agricultural Research, Innovation and Technology IJARIT*, 9(2355-2020-1330), 2020, 1-5.
- Francis CA, Callaway MB. Crop improvement for future farming systems. *Crop Improvement for Sustainable Agriculture*, 1993, 1-18.
- Gao F, Wang K, Liu Y, *et al.* Blocking miR396 increases rice yield by shaping inflorescence architecture. *Nature Plants*. 2015; 2:15196.
- Gou J, Ma C, Kadmiel M, Gai Y, Strauss S, Jiang X, Busov V. Tissue-specific expression of Populus C19 GA 2-oxidases differentially regulates above-and below-ground biomass growth through control of bioactive GA concentrations. *New Phytologist*. 2011; 192(3):626-639.
- Hamblin MT, Buckler ES, Jannink JL. Population genetics of genomics-based crop improvement methods. *Trends in Genetics*. 2011; 27(3):98-106.
- Horigome A, Nagasawa N, Ikeda K, Ito M, Itoh JJ, Nagato Y. Rice OPEN BEAK is a negative regulator of class 1 Knox genes and a positive regulator of class B floral homeotic gene. *The Plant Journal*. 2009; 58(5):724-736.
- Horton P. Prospects for crop improvement through the genetic manipulation of photosynthesis: morphological and biochemical aspects of light capture. *Journal of experimental botany*, 51(suppl\_1), 2000, 475-485.
- Hu J, Jin J, Qian Q, Huang K, Ding Y. Small RNA and degradome profiling reveal miRNA regulation in the seed germination of ancient eudicot *Nelumbo nucifera*. *BMC genomics*. 2016; 17(1):684.
- Hu J, Zeng T, Xia Q, Qian Q, Yang C, Ding Y, Wang W. Unraveling miRNA regulation in yield of rice (*Oryza sativa*) based on a differential network model. *Scientific reports*. 2018; 8(1):8498.
- Jain SM. Tissue culture-derived variation in crop improvement. *Euphytica*. 2001; 118(2):153-166.
- Jiang D, Fang J, Lou L, Zhao J, Yuan S, Yin L, Li X. Characterization of a null allelic mutant of the rice NAL1 gene reveals its role in regulating cell division. *PloS one*. 2015; 10(2):e0118169.
- Kharkwal MC, Pandey RN, Pawar SE. Mutation breeding for crop improvement. In *Plant breeding, 2004*, (pp. 601-645). Springer, Dordrecht.
- Kozłowski TT, & Pallardy SG. *Growth control in woody plants*. Elsevier, 1997.
- Kuhlemeier C, Green PJ, Chua NH. Regulation of gene expression in higher plants. *Annual Review of Plant Physiology*. 1987; 38(1):221-257.
- Lauria M, Molinari F, Motto M. Genetic strategies to enhance plant biomass yield and quality-related traits for renewable fuel and chemical productions. In *Tech*, 2015.
- Mathan J, Bhattacharya J, Ranjan A. Enhancing crop yield by optimizing plant developmental features. *Development*. 2016; 143(18):3283-3294.
- Mba C, Guimaraes EP, Ghosh K. Re-orienting crop improvement for the changing climatic conditions of the

- 21st century. *Agriculture & Food Security*. 2012; 1(1):7.
28. Miflin B. Crop improvement in the 21st century. *Journal of experimental botany*. 2000; 51(342):1-8.
  29. Moose SP, Mumm RH. Molecular plant breeding as the foundation for 21st-century crop improvement. *Plant Physiology*. 2008; 147(3):969-977.
  30. Padulosi S, Hodgkin T, Williams J, Haq N, Engles JMM, Rao VR, Jackson M T. 30 underutilized crops: trends, challenges, and opportunities in the 21st century. *Managing plant genetic diversity*, 2002, 323.
  31. Saroja R, Suppl PG, Goldshmidt A, Efroni I, Floyd SK, Eshed Y, Bowman JL. Differentiating Arabidopsis shoots from leaves by combined YABBY activities. *The Plant Cell*. 2010; 22(7):2113-2130.
  32. Sharma HC, Crouch JH, Sharma KK, Seetharama N, Hash CT. Applications of biotechnology for crop improvement: prospects and constraints. *Plant Science*. 2002; 163(3):381-395.
  33. Shleizer-Burko S, Burko Y, Ben-Herzel O, Ori N. Dynamic growth program regulated by LANCEOLATE enables flexible leaf patterning. *Development*. 2011; 138(4):695-704.
  34. Si L, Chen J, Huang X, *et al.* OsSPL13 controls grain size in cultivated rice. *Nature Genetics*. 2016; 48:447-456.
  35. Singh YP, Nayak AK, Sharma DK, Gautam RK, Singh RK, Singh R, Ismail AM. Farmers' participatory varietal selection: A sustainable crop improvement approach for the 21st century. *Agroecology and sustainable food systems*. 2014; 38(4):427-444.
  36. Tang J, Chu C. MicroRNAs in crop improvement: fine-tuners for complex traits. *Nature plants*. 2017; 3(7):17077.
  37. Wang L, Sun S, Jin J, Fu D, Yang X, Weng X, Zhang Q. Coordinated regulation of vegetative and reproductive branching in rice. *Proceedings of the National Academy of Sciences*. 2015; 112(50):15504-15509.
  38. Wang Y, Cheng X, Shan Q, Zhang Y, Liu J, Gao C, Qiu JL. Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. *Nature Biotechnology*. 2014; 32(9):947
  39. Yu X, Zeng T, Wang X, Li G, Chen L. Unraveling personalized dysfunctional gene network of complex diseases based on differential network model. *Journal of translational medicine*. 2015; 13(1):189.
  40. Zhang YC, Yu Y, Wang CY. Overexpression of microRNA OsmiR397 improves rice yield by increasing grain size and promoting panicle branching. *Nature Biotech*. 2013; 31:848-852.