



International Research Journal of Engineering Science, Technology and Innovation  
Vol. 10(3) pp. 1-1, January, 2021  
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*Editorial*

## **Editorial Note on Natural Variations at FLM Splicing has Pleiotropic Effects of Modulating**

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### **EDITORIAL**

Investigating the evolution of complex phenotypes and therefore the underlying molecular bases of their variation is critical to know how organisms adapt to their environment. Applying classical quantitative genetics on a segregating population derived from a Can-OxCol-0 cross, we identify the MADS-box transcription factor Flowering Locus M (FLM) as a player of the phenotypic variation in plant growth and color. We show that allelic variation at FLM modulates plant growth strategy along the leaf economics spectrum, a trade-off between resource acquisition and resource conservation, observable across thousands of plant species. Functional differences at FLM believe one intronic substitution, disturbing transcript splicing and resulting in the build-up of non-functional FLM transcripts. Associations between this substitution and phenotypic and climatic data across Arabidopsis natural populations, show how noncoding genetic variation at one gene could be adaptive through pleiotropic effects.

Evolution may be a continuous and sophisticated process requiring coordinated changes in many traits consistent with environmental selective pressure, in theory leading to an optimal fitness during a given habitat at a given time point. Due to the various traits that require evolving co-

ordinately, mathematical models predicted that complex organisms would evolve more slowly than simple organisms toward a fitness optimum when considering mutations of same effect size. This was called the “cost of complexity” or the “cost of pleiotropy” since those models assumed that each gene is in a position to affect every trait.

Pleiotropy can have several meanings but overall states that one gene or variant controls several traits. The character of pleiotropy strongly depends on the traits measured (molecular, physiological, metabolic etc.) and therefore the level of organization considered (from cell to population). Moreover, one must take care about the relevance of the observed pleiotropy consistent with the tactic wont to assess it. As an example, studying knockout mutants might not reflect the range of mutational effects selected in nature. Additionally, when classical quantitative genetics is employed to review pleiotropy, a nontrivial point is to differentiate real pleiotropy from genetic linkage. Indeed, several independent quantitative trait loci (QTLs) within the same region may control different traits because mapping QTL in segregating populations has limited resolution with reference to the trait’s genetic architecture. Finally, many related traits could also be correlated just due to a cause-and-effect relationship, in other words an indirect effect.