Quantitative Population Epigenetics in Screening and Development of Regulator-Active Factors of the Farming System

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Implications

Likewise, index selection based on statistical genetic theory in plant and animal breeding the methodology "Quantitative Population Epigenetics" can be appropriated to improve efficiency in screening and development of regulator-active factors of the farming system for potential to enhance quantitative characters such as yield, standability and resistance to unfavorable environmental influences (e.g., water stress, cold temperatures, disease resistance).

For example, as was shown for an effect of monoethanolamine on yield and water use efficiency of spring barley plants (Bergmann et al. 1991).

Background and objectives

Ecological and Evolutionary Epigenetics is a new field of frontier research at the intersection between molecular genetics and evolutionary ecology. The term "Epigenetics" is used only for about ten years. Recently Stauss realized that in the 80s he basically had developed a script on "Quantitative Population Epigenetics" (Stauss 1992, Stauss 2012).

"In a strict sense, the question of whether a characteristic is hereditary or environmental has no meaning. The genes cannot cause a character to develop unless they have the proper environment, and, conversely, no amount of manipulation of the environment will cause a characteristic to develop unless the necessary genes are present." (Allard, 1960).

Optimal screening and development efficiency of regulator-active factors of the farming system obtains with 1) high environmental variability, 2) low heritability (characters for which the genotype sets a wide "norm of reaction" an environmental influences), 3) high correlation between characters under indirect selection and 4) intensity of selection.

Key results and discussion

The main application of quantitative epigenetics could be using the pattern of genetic variances and covariances to predict the response of the mean phenotype to regulator-active factors of the farming system as artificial environmental factors:

- Quantitative epigenetics aims to link phenotypic variation for complex traits to its underlying epigenetic basis in order to understand and predict better epigenetic architecture and changes within natural, agricultural, and human populations -- due to environmental factors.

- Traditionally built upon statistical abstractions of epigenetic effects (environmental, regulator-active factors of the farming system), the field could be used to reveal explicit links between epigenome and complex phenotypes, and could therefore serve as a focal point for bringing together many emerging areas of genetics, epigenetics, genomics, physiology, statistics, bioinformatics, and computational biology.

The application of statistical Quantitative Population Epigenetics to the selection and to the development of biologically active substances (e.g. plant growth regulators) is a fundamentally new approach in planning, evaluation and assessment of experiments.

- In initial screening a 'random' subpopulation of genotypes should manifest moderate expression of a target character -- resulting in low heritability.

- In testing for quantitative character enhancement, initial screening should be conducted under stress-environment conditions -- in order to obtain an optimum differentiation of farming factors (low heritability).

- To judge constancy in performance, testing should employ a random sampling of genotypes and non-stress environments -- which afford assessment of the interactions: a) factor-genotype, b) factor-environment and c) factor-genotype-environment.

- It must be possible to identify specific genotype-environment constellations from which issue 'amplifier' interactions that intensify differentiation suitability.

Hence the objective is to identify which genotype-environment constellation is the most auspicious to make use of as a 'reference combination' to achieve optimum screening efficiency.

Selection indices may be formulated in a manner similar to the optimum index of Smith and Hazel (Smith,1936; Hazel, 1943), that employs heritabilities as index weights (which weights correspond to weights from the optimum index if traits are uncorrelated), or according to the base index proposed by Williams (Williams,1962), which uses economic weights as index weights.

The statistical Quantitative Population Epigenetics theory provides basic rules for experimental designs and data analysis concerning

- experimental design: fix or random effects, size, trial conditions e.g. stress or non-stress, etc.,

- post-experimental evaluation,

- optimization of experimental designs,

- epigenotype analysis and screening of biologically active factors of the farming system with Single Nucleotide Polymorphism (SNP)-Chips and

- quantitative description of single or multiple traits designs e.g. using selection indices.

The impetus to translate this Quantitative Population Epigenetics theory into practice is weighted by a) screening sensitivity, b) time expediency, c) ease of replication, d) reliability, e) heuristic incentive, f) elimination of conjectural risks and g) financial returns.

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