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EDITORIAL

Special issue on "The relationship between genotype and phenotype: new insight into an old question"

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The term "genotype–phenotype (GP) relationship", or "genotype–phenotype map", can be understood in different ways. It was first defined by Richard Lewontin (1974) as the evolutionary interplay in a population between the *average* genotype and the *average* phenotype, which is determined by different evolutionary forces acting on phenotypic space—migration, mating, and natural selection—and genotypic space—mutation and recombination. This historical definition is not so common nowadays. In the most common sense of the term, the GP relationship refers to the correspondence between genotype and phenotype in an *individual*. But how should we understand the word "relationship"? In the reductionist paradigm of molecular biology and genomics, it is often implicitly interpreted in terms of the mechanisms by which genotypic information is processed to build a phenotype through development in a given environment. The extreme complexity of these mechanisms and their emergent properties can only be tackled using high-throughput technology and/or a systems biology approach. This is not the editorial line we chose for this special issue. From an evolutionary point of view, which is also the one that prevailed at the dawn of genetics, the term GP relationship implies a directed relationship whereby changes at the genotypic level induce changes at the phenotypic level. Because of pervasiveness of genetic polymorphisms and epistasis, and given the role of biotic and abiotic factors in phenotypic expression, this relationship is far from simple and its study requires the use of a combination of experimental, theoretical and conceptual tools. In this special issue, we focus mainly on the conceptual issues.

The Introduction by de Vienne and the final article by Pontarotti et al. cover the history and epistemology of GP distinction and of the GP relationship. Vasseur et al. address the question of the hierarchy of phenotypic levels and suggest that allometric models could provide us with equations that describe the relationship between trait variations at different scales of organization. Shah focuses on what might be called the epigenotype–phenotype relationship, and compares the relative contribution of epimutations and mutations to phenotypic diversity. Fisch questions the reliability of genome-wide investigations to detect the causal variants of complex traits in humans and discusses the use of the endophenotype concept. Also in human genetics, Robette et al. warn against the misuse of the concept of heritability, which raises many medical and ethical issues. Finally, Chevin et al. show how the plasticity of gene expression could be related to phenotypic plasticity to detect the causal genes of trait variation, even in the absence of genetic polymorphisms.

We hope that the ideas expressed in this issue will stimulate new research on what is one of the most important questions in biology.

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