Individualized training as a biopsychosocial challenge – interlinking epigenetics, social sciences and psychology in sport scientific research

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To cite this article: Ansgar Thiel & Barbara Munz (2018) Individualized training as a biopsychosocial challenge – interlinking epigenetics, social sciences and psychology in sport scientific research, European Journal for Sport and Society, 15:3, 211-215, DOI: 10.1080/16138171.2018.1500116

To link to this article: https://doi.org/10.1080/16138171.2018.1500116

Published online: 08 Nov 2018.
Individualized training as a biopsychosocial challenge – interlinking epigenetics, social sciences and psychology in sport scientific research

In recent years, the individualization of training in both elite sports and health-promoting exercise has steadily gained importance. Research has shown that people react to the same training stimuli in different degrees; consequently, individually tailored training strategies are required. However, the mechanisms of training adaptation are very complex. The acute physiological reaction to a training stimulus, which eventually triggers adaptation, is not only influenced by genetic factors, but also by the subjective–affective experience of training and the psychosocially conditioned training motivation (Bryan et al., 2011). In order to better understand training adaption, but also initiation, acceptance and maintenance of training, researchers and experts in the field increasingly emphasize the need for interdisciplinary research strategies.

Genetics, epigenetics and training adaptation

However, such ‘holistic’ perspectives are still the exception in training research. Recently, studies on the mechanisms of training adaptation have mostly focused on the molecular level. Today it is known that the genetic make-up is highly responsible for whether an untrained individual will perform better or worse in a certain sporting task. Furthermore, we know that the genetic make-up has an influence on how the individual reacts to certain training stimuli, more precisely, how well the organism can adapt to a specific form of physical training, i.e. how ‘trainable’ it is (Hargreaves, 2015). Molecular biology research has also provided a number of insights into the physiological adaptation of the body to training stimuli, not least due to the development of ‘omics’ technologies. This technology enables researchers to obtain a comprehensive and detailed characterization of transcriptomes and proteomes associated with training. For example, endurance and strength training cause different specific changes in gene expression patterns in the skeletal muscles. While adaptation to strength training tends to stimulate the expression of genes that promote glycolytic metabolism and muscle hypertrophy combined with an increased protein synthesis rate, endurance training promotes the expression of genes associated with aerobic metabolic pathways. These different adaptive responses are controlled by molecular signals that are triggered by the physical activity itself and differ depending on the type of training.

Training experience and epigenetic conditioning

Recently, there have been several research findings that individual trainability can change during the life course due to external factors such as nutrition or stress. This is where the still young research field of epigenetics comes into play. Epigenetics deals with processes that specifically and robustly alter gene expression patterns without affecting the base
sequence of the DNA itself. The DNA sequence is largely stable and can only be altered by non-targeted mutations that have been ‘tested’ over many generations and over long periods of time by natural selection. Epigenetic changes, on the other hand, can be rapid and targeted, enabling an individual (not just a species) to adapt efficiently to changing environmental conditions. Environmental stimuli such as physical training or nutrition can cause epigenetic changes that subsequently influence how the individual reacts to other stimuli, such as a new training session (for a detailed description, see Munz & Thiel, 2018).

Epigenetic characteristics could not only function as specific training markers, but also as predictors for the degree of training adaptation. For example, it is conceivable that so-called ‘non-responders’ to physical activity may feature characteristic epigenetic patterns in different tissues, such as skeletal muscle, cardiovascular, or respiratory system. Moreover, specific training forms, such as MICE (Moderate Intensity Continuous Exercise), or HIIT (High-Intensity Interval Training), might induce characteristic epigenetic changes, or, vice versa, an individual’s epigenetic characteristics might determine his or her reaction to a specific training regimen. At the same time, movement-induced epigenetic modifications can have lifelong positive effects. A very interesting assumption in this context can be derived from a review by Alegria-Torres, Baccarelli, and Bollati (2011). The authors report, for example, that elderly people whose peripheral blood lymphocytes show a high degree of methylation in certain areas of the DNA have a lower incidence of and mortality due to ischemic heart disease and stroke. According to the authors, a higher degree of methylation of these regions is also associated with a higher level of physical activity. In the future, it would therefore be interesting to analyze whether there is a causal relationship between the degree of methylation of the corresponding regions and the reduction of the cardiovascular risk profile through physical activity (Alegria-Torres et al., 2011).

In any case, there are many indications that earlier training episodes could induce a kind of ‘epi-memory’ (Sharples, Stewart, & Seaborne, 2016). This memory subsequently influences the molecular response of a cell, for example, a muscle fibre, to a later training stimulus, even if this stimulus occurs a long time later. According to various studies, it might even be speculated that training stimuli could cause epigenetic changes that are ‘biologically remembered’ in the epigenetic make-up of a person’s offspring (Sharples et al., 2016).

‘Social epigenetics’ as a biopsychosocial research perspective

Molecular biology research on the organism’s training adaptation has made great progress in recent years. Today, it is commonly known that the physiological response to physical activity is not determined solely by temporally stable genetic conditions, hence more attention must be paid to epigenetic mechanisms (Bloch & Zimmer, 2012). However, epigenetics should actually be more than molecular biology research only. Outside the field of sports science, this point is being increasingly discussed. Some researchers emphatically demand to complement molecular biology research with sociological and psychological models. The fear is that epigenetic research, which actually promised a less essentialist understanding of nature (Griffiths & Stotz, 2013) and thus a substantial progress in the Nature–Nurture controversy could get stuck in a new form of (biological) reductionism (Meloni, 2014).

In particular, the collaboration between epigenetics and sociology promises interesting new insights into the genesis of many health-related phenomena, such as the link between social disadvantages in childhood and the state of health in later life. Sociology would explain this connection, for example, with the assumption that children from families with
little education and poor economic status are socialized into living conditions that are characterized by unhealthy lifestyles, which, later on in life, lead to chronic degenerative diseases. Epigenetics, on the other hand, studies ‘semi-stable molecular states (e.g. life-long and transmissible over a limited number of generations) that influence physiology in subtle ways during development, in physiological conditions and in the establishment of several diseases’ (Loi, Del Savio, & Stupka, 2013). In this sense, epigenetics would address the changes in gene expression and phenotype.

Putting both perspectives together: Genes have a relatively stable but not a deterministic influence on behaviour since the biological systems have the flexibility to react to environmental influences and ‘learn’ in a rudimentary manner (Loi et al., 2013). Unhealthy environmental conditions early in life could lead to a pattern of early epigenetic programming which may have a negative impact on both health behaviour and health-related outcomes throughout an individual’s lifetime (Loi et al., 2013).

The combination of epigenetics and sociology could also give explanations for the transgenerational transmission of poor health that go beyond mere biological descriptions. From this perspective, the inheritance of unhealthy lifestyles is to a certain extent the product of an unconscious (social) learning of unhealthy lifestyles. Children learn the unhealthy lifestyle from their parents who already learned this lifestyle from their parents. The constant exposure to an unhealthy lifestyle is subsequently biologically reflected by epigenetic programming and even passed on to future generations (Loi et al., 2013).

One of the many indications that support such explanations is given by nutrition research. Researchers assume that nutrition in early life causes metabolic structures at the molecular level, which have an effect on nutritional physiology in adults (Landecker, 2011). The way nutrition is provided in early childhood in-turn depends on the attitudes of parents, socio-economic conditions, education, infrastructure, etc.

Recent research therefore shows that social structures and social regulation are directly and causally linked to genome structures and gene regulation (Landecker & Panofsky, 2013). This finding is particularly interesting for sports science research, not least because genes that are epigenetically influenced by nutrition also seem to be influenced to a considerable degree by physical activity and its metabolic correlates (Sanchis-Gomar et al., 2012). Recent epigenetic work even suggests that fostering the enjoyment of physical activity (for e.g. through a motivating sports programme or exercise-friendly environments) could be an important long-term factor in the prevention of serious illnesses in later life. It is believed that positive stress associated with physical activity acts as an epigenetic modulator that reduces the risk of obesity and chronic degenerative diseases by means of epigenetic changes (Sanchis-Gomar et al., 2012).

**Dynamics of the ‘biopsychosocial identity’ in the context of training adaptation**

For future interdisciplinary work in the field of individualized training, the challenge is to integrate epigenetics, sociology and psychology into reasonable research programmes. In this context, concepts such as the model of the fluid bio-social identity (Wiese, Escobar, Hsu, Kulathinal, & Hayes-Conroy, 2018) offer helpful starting points. Wiese et al. (2018) postulated that ‘in congruence with social and psychological understandings of identity, biological identity is much more dynamic than any static genome can represent’. Moreover, according to Wiese et al. (2018), the dynamic of an individual’s biological identity always has a biographical background. It is not only that the human body changes over time, but in particular that
the body becomes unique through the singular, constantly changing relationships with the world in which the individual is located (Wiese et al., 2018).

One methodological research problem to be solved in this context is the systematic recording of the effect of diverse, chaotic and therefore ultimately unpredictable environmental influences on the trajectory from genotype to phenotype. Against the background of this high degree of disorder, Relton and Davey Smith (2012) rightly emphasize that it makes little sense to characterize generative mechanisms of epigenetic variation at the level of the individual. Rather, systematization at a group level should be sought to identify key biopsychosocial determinants of health and disease development.

In the relationship between the biological and the social, many questions remain open, e.g. the relationship between early-life events and adult epigenetic drift, the relative contribution of environmental mediation of the epigenome at different life stages, and importantly, the reversibility of all these epigenetic changes (Landecker & Panofsky, 2013).

If epigenetic parameters are regarded as biomarkers of a ‘brute luck disadvantage’ (Loi et al., 2013), i.e. the disadvantage for which one is not responsible, then it is particularly important to identify the systematic conditions of such disadvantages. The relevance of such a biopsychosocial research perspective is extremely high, not least because the plasticity of the epigenome suggests that epigenetic changes may also be reversible. This perspective opens up completely new therapeutic possibilities. It is conceivable, for example, that an early epigenetic diagnosis of ‘socially inherited’ health problems not only provides starting points for early pharmacological interventions to avoid long-term health problems, but also provides indications for targeted intervention in the lives of adolescents (Loi et al., 2013).

Such a research perspective is also a challenge for sports science. An individualized training strategy that wants to do justice to the peculiarities of individuals to which training programmes are to be tailored will have to deal with the central question for environmental epigenetics: How are social structures and social regulation causally connected with genome structures and gene regulation (Landecker & Panofsky, 2013)? In sports science training research, however, we are still a long way from tackling such comprehensive questions and finding corresponding methodological approaches.

Note


Disclosure statement

No potential conflict of interest was reported by the authors.

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