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Health, Development and Epigenetic Characteristics of Institutionalized Children: A Preliminary Study based on a Small Cohort

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Abstract

To date, researcheshave show that a variety of diseases and developmental delays, overrepresented in institutionalized children, are associated with deprivation conditions of baby homes. The epigenome appears to be a molecular mediator that regulates the interaction between the environment and the phenotype. Our preliminary comparative study examined indicators of physical development, health status and epigenetic profiles of institutionalized children with typical and delayed development from two organizationally different baby homes. The results showed that delayed physical and cognitive development is accompanied by changes in the epigenomes of children.

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*Keywords:*Institutionalization, Development delay, Epigenetics

1. Introduction

Well-established epidemiological findings indicate that children living in institutional care demonstrate developmental delays, and that various developmental diseases and disorders are overrepresented in this subpopulation of children. About 25% of institutionalized childrenin the first year of lifehave disabilities.Congenital anomalies and birth defects, genetic abnormalities and nervous system disorders are most prevalent among the causes of disability[1]. Children living in institutional care are characterized by both low

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indicators at entry (e.g., elevated frequencies of medical and social risk factors) and negative health trajectories (e.g., elevated frequencies of infectious and other diseases and developmental delays). Such poor health and subnormal developmental trajectories are typicallyassociatedwith various facets of deprivation experienced by children residing in baby homes. To date, literature has provided plenty of evidence of a wide range of maladaptive outcomes in children who experience early institutionalization, such as delays in physical development, deficiencies in cognitive functioning and social-emotional adjustment(see e.g., [2, 3]).At the same time, research in the field indicates that these negative effects on children's development and well-being can be partly neutralized byenvironmental enrichment through the placement in a family environment[4, 5] or by improving the institutional environment[6, 7].

Althoughthe dynamic association between early social environment and children's health and development has been well-established, the molecular mechanisms that may underlie this association, or mediate this dynamic link between environment and phenotype, are still poorly understood. Epigenetic regulation appears to be one of such molecular mechanisms. It is known that the epigenome (the combined mechanism of DNA methylation and chromatin modification that programs gene expression) mediates the genome's response to environmental signals, modulating the interaction between environmental factors, genetic factors, and phenotype, including health outcomes. To date, it has been shown that the epigenome is a dynamic structure that is highly involved in human development and aging[8, 9], and the early developmental stages of a child's epigenetic status may have a profound impact on health and well-being in later life[10-12]. Studies connecting the epigenome and environment have indicated that epigenetic states might be changed in response to early social experiences, especially stressogenic ones[13-15]. Despite the long-term stability of environment-driven epigenetic changes, there is evidence that some of these changes might be reversible through the epigenome-environment interplay during development[16].

This considerable findings on early social environment, specifically the institutional environment and its role in child development, allows us to frame the following hypotheses. First, we predict that social environment may influence the developmental trajectories and, as a consequence, may affect developmental outcomes, including the health and physical development of children. Second, we assume that such environment-driven changes in development might be accompanied by perturbations in the system of epigenetic regulation. Third and finally, the institutional environment per se, being heterogeneous in terms of its social-emotional atmosphere, might be a good model for investigating groups of children living in different environments.Here we report the results of a preliminary comparative study of children from two organizationally different baby homes based on characteristics of their physical development and health (the structure and the prevalence of diseases), and epigenetic states (DNA methylation patterns).

2. Method

2.1. Participants

The study was conducted in two baby homes (BH) in St. Petersburg that differ in how the living and social spaces of the children are organized, and on the workload distribution and responsibilities of the BH personnel. It has been argued that these changes influence the broader social-emotional atmosphere of baby homes, approximating the environment of a family. Specifically, BHA is a BH that reformed itself to resemble a family setting with a sizable sibship, where BHB is a BH that still practices pre-reform policies. There were 69 children (39 boys and 30 girls) aged 5-59 months, of which 38 resided in BHA (20 boys and 18 girls) and 31—in BHB (19 boys and 12 girls). The groups did not differ on the distribution of boys and girls. In terms of their developmental profiles, the participants represented three groups: (1) typically developing children (TD group; N= 23, mean age 20,78 ± 11,4 mos; 56,5 % of girls.), (2) children with a developmental delay, or children with special needs, which had a severe delay in the development of speech, social skills and cognitive functions (SN group; N= 26, mean age 22,12 ± 13mos; 42,3 % of girls), and (3) children with delayed development related to