## Genes or Environment?: Variability of the Brain Volume in Mexican Twins

I.M. Espinosa-Méndez<sup>1,5</sup>, D. Ramírez-González<sup>1</sup>, T.V. Román-López<sup>1</sup>, A. Piña-Hernández<sup>1,5</sup>, C.I. Sánchez-Moncada<sup>1</sup>, C.A. Domínguez-Frausto<sup>1</sup>, E.H. Pasaye-Alcaraz, A.B. García-Vilchis<sup>2</sup>, X.J. López-Camaño<sup>1</sup>, V. Murillo-Lechuga<sup>1</sup>, R. Casa-Madrid<sup>1</sup>, D. Zenteno-Morales<sup>2</sup>, Z.X. Espinosa-Valdés<sup>2</sup>, A. Tapia-Atilano<sup>2</sup>, S.A. Pradel-Jiménez<sup>2</sup>, E. Chiu-Han<sup>1</sup>, O. Aldana-Assad<sup>3</sup>, A.E. Medina-Rivera<sup>3</sup>, A.E. Ruiz-Contreras<sup>2</sup>, M. Rentería<sup>4</sup>, S. Alcauter<sup>1</sup>

<sup>1</sup>Instituto de Neurobiología, Universidad Nacional Autónoma de México, Querétaro, México; <sup>2</sup>Facultad de Psicología, Universidad Nacional Autónoma de México, Ciudad de México, México; <sup>3</sup>Laboratorio Internacional de Investigación sobre el Genoma Humano, Universidad Nacional Autónoma de México, Querétaro, México; <sup>4</sup>QIMR Berghofer Medical Research Institute, Brisbane, Australia; <sup>5</sup>Escuela Nacional de Estudios Superiores Juriquilla, Universidad Nacional Autónoma de México, Querétaro, México.

The brain undergoes constant changes throughout life. It does not finish developing before birth, it grows during childhood, and it does not finish maturing until early adulthood. Although many of these structural changes are preprogrammed in our genetics, the brain adapts and molds according to our environment and experiences. However, the extent to which genes or our environment give rise to these structural changes, such as brain growth, is not yet known. This study aims to compare different measures of the brain volume between monozygotic (MZ) and dizygotic (DZ) twins from the Mexican Twin Registry (TwinsMX). In this way, we can know if the variability between volumes has a greater genetic (greater covariance in MZ twins) or environmental load (similar covariance between MZ and DZ twins). Identical twins (MZ) share approximately 100% of their DNA, and fraternal twins (DZ) share about 50% of their DNA; in addition to sharing an environment for most of their lives. For this study, we used a sample of 92 pairs of twins (64 MZ and 28 DZ) from TwinsMX, who underwent a magnetic resonance imaging study at the Laboratorio Nacional de Imagenología por Resonancia Magnética (LANIREM). A significant correlation was found for MZ twins, but not for DZ twins, in measures of total intracranial volume (MZ  $r_s$ = 0.903, p<0.01; DZ  $r_s$ =0.172 p=0.381), relative total gray matter volume (MZ  $r_s$ = 0.808, p<0.01; DZ  $r_s$ =0.226 p=0.247), relative subcortical gray matter volume (MZ  $r_s$ = 0.820, p<0.01; DZ  $r_s$ =0.260 p=0.181), relative total white matter volume (MZ  $r_s$ = 0.836, p<0.01; DZ  $r_s$ =0.277 p=0.154), and relative total cerebrospinal fluid volume (MZ  $r_s$ = 0.742, p<0.01; DZ  $r_s$ =-0.069 p=0.726). This suggests that these structural variations are due to a greater genetic than environmental contribution. These results are the first step in evaluating the genetic and environmental contributions to brain structure; however, further analyses are required to estimate the heritability (proportion of the variance that can be attributed to genetic factors) of these phenotypes.

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