Study unveils new clonal relations in the mouse brain

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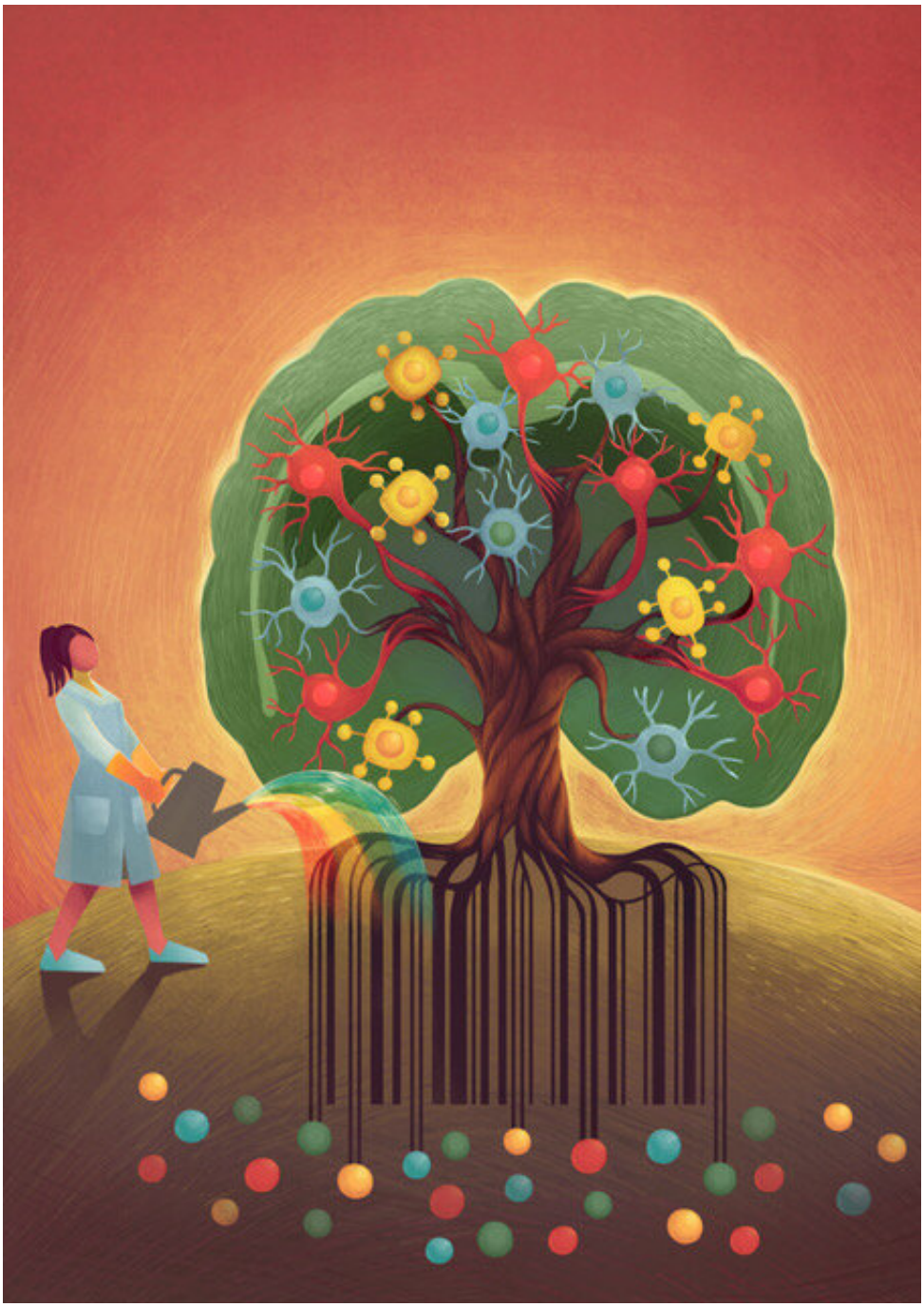

Cover art that illustrates “next-generation clonal tracing”: genetic barcodes and high-throughput sequencing can be used to reveal how “simple” cells (spheres in the ground) develop into a range of ”complex” cell types (leafs in the tree) of the brain. Image credit: Lesya Adamchuk (Ella Maru Studio, Inc.).

The human brain and the brain of other mammals contain numerous populations of specialized cells with unique functions, molecular structures and characteristics. These cells originate from a thin layer of neuroepithelial progenitor cells, cells that can divide themselves into specific populations of neurons and glial cells.

In recent years, technological advances have allowed neuroscientists to study the diverse cell populations in the brain more in depth. While this has shed light on the function of some cell populations and their molecular composition, the relationship between mature cell populations and progenitor cells is still poorly understood.

Researchers at Karolinska Institute, KTH Royal Institute of Technology and Stockholm University have recently carried out a study aimed at better understanding the clonal relations between cells in the mouse brain. Their findings, published in *Nature Neuroscience*, were collected using a new approach they developed that combines single-cell and spatial transcriptomics with clonal barcoding, two different methods used to conduct neuroscience studies.

"Our lab studies the potential of neural stem cells to generate a wide variety of cell types, which is important to understand normal brain development and could be exploited to regenerate lost cells in neurological diseases," Michael Ratz, one of the researchers who carried out the study, told Medical Xpress.

To better understand the potential of stem cells as generators of different cell populations, the researchers used an approach known as "fate mapping" or "clonal tracking." This is a powerful technique that allows scientists to identify the "progeny" of a single cell and to reconstruct its developmental history (i.e., ancestry).

"These methods have led to fundamental insights about tissue

development and have been used for many years, but they are limited in their ability to study many cells at the same time due to their reliance on microscopy which can only distinguish a few colors (usually