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Researchers prove hypothesis in population genetics

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Taiwan researchers prove hypothesis in population genetics

Singapore: A research team led by Dr Jun-Yi Leu, an associate research fellow at the Institute of Molecular Biology in Taiwan, has validated the long-standing hypothesis in population genetics: that high mutation rates are selected against in adapted mutator populations. These studies are fundamentally important to the study of the role of cells that mutate at a high rate in cancers. The study was published in the journal *Current Biology* on July 10, 2012.

Mutation is the source of both beneficial adaptive variation, and harmful genes. Cells that mutate at a high rate, known to biologists as "mutators", are thought to be involved in the rapid emergence of dangerous pathogens and invasion of tumor cells. Population geneticists have hypothesized for many years that low mutation rates must be restored in natural populations, however, up until now the theory has not been observed experimentally.

Using an experimental evolution approach, the research team found that mutators significantly reduce their mutation rate after 6,700 generations of evolution. Genomic analyses using microarrays revealed two plausible mechanisms by which mutation rates are reduced. To understand how mutator populations deal with accumulated harmful mutations, the researchers treated all the derived populations with an anti-cancer drug that can enhance the harmful effects of accumulated mutations. The results indicated that mutator cells follow different evolutionary trajectories suggesting that the clinical application of the anti-cancer drugs may become ineffective due to the existing genetic variation in mutator populations.