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RESEARCH AREA

Cancer is the leading cause of death in the developed world. According to estimates from the International Agency for Research on Cancer, there were 8.2 million cancer deaths in 2012 worldwide. Cancer research began as early as at the end of the 19th century, indicating the social efforts to control this devastating disease. In recent years, the tremendous advances reached in molecular biology and genomics has given further impetus to the development of this field. Among other things, the recently developed high-throughput sequencing technology platforms have generated massive amounts of genetic variation data from a huge number of cancer samples. The collected data support the concept that cancer is a disease of our genome, because in the majority of tumors tens or even hundreds of thousands of mutations have been detected. These data also show that the spontaneous mutation rate observed in normal cells is not sufficient to account for the high number of mutations found in cancers. The key feature of cancer cells, allowing them to rapidly evolve more and more new mutations, is the instability of their genetic material.

The long-term objective of our laboratory is to explore genetic alterations fuelling malignant transformation by undermining the stability of the genome.

TECHNIQUES AVAILABLE IN THE LAB

Basic molecular biological methods, involving isolation manipulation and analysis of DNA, RNA and proteins, standard mammalian tissue culture techniques, basic mouse colony management techniques, gene knockout and gene knockdown techniques, advanced gene delivery methods used in tissue culture and in animal models.

SELECTED PUBLICATIONS

Kopasz A.G., Pusztai D.Z., Karkas R., Hudoba L., Abdullah K.S.A., Imre G., Pankotai-Bodó G., Migh E., Nagy A., Kriston A., Germán P., Bakné Drubi A., Molnár A., Fekete I., Dani V.É., Ocsovszki I., Puskás L.G., Horváth P., Sükösd F., **Mátés L.** (2022) A versatile transposon-based technology to generate loss- and gain-of-function phenotypes in the mouse liver. **BMC Biology 20:** 74

Katter, K., Geurts, A.M., Hoffmann, O., **Mátés, L.,** Landa, V., Hiripi, L., Moreno, C., Lazar, J., Bashir, S., Zideke, V., Popova, E., Jerchowc, B., Beckerc, K., Devarajc, A., Walterj, I., Grzybowksib, M., Corbettb, M., Filhol, A.R., Hodgesb, M.R., Baderc, M., Ivics, Z., Jacob, H.J., Pravenec, M., Bősze, Z., Rülicke, T., Izsvák, Z. (2013) Transposon-mediated Transgenesis, Transgenic Rescue, and Tissue-specific Gene Expression in Rodents and Rabbit. **FASEB J 27:** 930-941.

Xue, X., Huang, X., Nodland, S.E., **Mátés, L.,** Ma, L., Izsvak, Z., Ivics, Z., LeBien, T.W., McIvor, R.S., Wagner, J.E., Zhou, X. (2009) Stable gene transfer and expression in cord blood-derived CD34+ hematopoietic stem and progenitor cells by a hyperactive Sleeping Beauty transposon system. **Blood 114:** 1319-1330.

Mátés, L., Chuah, M.K., Belay, E., Jerchow, B., Manoj, N., Acosta-Sanchez, A., Grzela, D.P., Schmitt, A., Becker, K., Matrai, J., Ma, L., Samara-Kuko, E., Gysemans, C., Pryputniewicz, D., Miskey, C., Fletcher, B., VandenDriessche, T., Ivics, Z., Izsvak, Z. (2009) Molecular evolution of a novel hyperactive Sleeping Beauty transposase enables robust stable gene transfer in vertebrates. **Nature Genet 41:** 753-761.

Ivics, Z., Li, M.A., **Mátés, L**., Boeke, J.D., Nagy, A., Bradley, A., and Izsvak, Z. (2009) Transposon-mediated genome manipulation in vertebrates. **Nat Methods 6:** 415-422.