Somatic copy number variation is an important mechanism of regulation of miRNA and miRNA biogenesis genes *DICER1* and *DROSHA* in cancer

Piotr Kozlowski
European Centre of Bioinformatics and Genomics (ECBiG), Institute of Bioorganic Chemistry, Polish Academy of Sciences
Noskowskiego 12/14, 61-704 Poznan, Poland
Phone: +48 616653100
Email: kozlowp@yahoo.com; kozlowp@ibch.poznan.pl

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ABSTRACT

Cancer initiation and development are associated with the accumulation of numerous genetic alterations. The accumulation of such variations in a particular gene may be an indicator of its role in cancer, either as a tumor suppressor or oncogene. A growing body of evidence indicates that miRNAs may be a class of genetic elements that play an important role in cancer.

We analyzed the somatic copy number variation of 14 miRNA genes frequently found to be either over- or underexpressed in lung cancer, as well as two miRNA biogenesis genes, *DICER1* and *DROSHA*, in non-small-cell lung cancer (NSCLC).

Our analysis showed that most analyzed miRNA genes undergo substantial copy number alteration in lung cancer. The most frequently amplified miRNA genes include the following: *miR-30d*, *miR-21*, *miR-17* and *miR-155*. We also showed that both *DICER1* and *DROSHA* are frequently amplified in NSCLC and that their copy number variation correlates well with their expression and survival of NSCLC and other cancer patients.

In conclusion, our results show that copy number variation is an important mechanism of upregulation/downregulation of miRNAs in cancer and strongly suggest an oncogenic role for *DROSHA*. Acknowledgements:

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