



Inhibition of the mevalonate pathway affects epigenetic regulation in cancer cells

Heidrun Karlic^{a,*}, Roman Thaler^{b,1}, Christopher Gerner^c, Thomas Grunt^{a,d,e}, Katharina Proestling^{d,e,f}, Florian Haider^b, Franz Varga^b

^a Ludwig Boltzmann Cluster Oncology, Vienna, Austria; ^b Ludwig Boltzmann Institute of Osteology at the Hanusch Hospital of Social Health Insurance Vienna (WGKK) and Austrian Social Insurance for Occupational Risks (AUVA) Trauma Centre Meidling, 1st Medical Department, Hanusch Hospital, Vienna, Austria; ^c Institute of Analytical Chemistry, Faculty of Chemistry, University of Vienna, Vienna, Austria; ^d Signaling Networks Program, Division of Oncology, Department of Medicine I, Medical University Vienna, Vienna, Austria; ^e Comprehensive Cancer Center, Medical University Vienna, Vienna, Austria; ^f Department of Obstetrics and Gynecology, Medical University of Vienna, Vienna, Austria

The mevalonate pathway provides metabolites for post-translational modifications such as farnesylation, which are critical for the activity of RAS downstream signaling. Subsequently occurring regulatory processes can induce an aberrant stimulation of DNA methyltransferase (*DNMT1*) as well as changes in histone deacetylases (HDACs) and microRNAs in many cancer cell lines. Inhibitors of the mevalonate pathway are increasingly recognized as anticancer drugs. Extensive evidence indicates an intense cross-talk between signaling pathways, which affect growth, differentiation, and apoptosis either directly or indirectly via epigenetic mechanisms. Herein, we show data obtained by novel transcriptomic and corresponding methylomic or proteomic analyses from cell lines treated with pharmacologic doses of respective inhibitors (i.e., simvastatin, ibandronate). Metabolic pathways and their epigenetic consequences appear to be affected by a changed concentration of NADPH. Moreover, since the mevalonate metabolism is part of a signaling network, including vitamin D metabolism or fatty acid synthesis, the epigenetic activity of associated pathways is also presented. This emphasizes the far-reaching epigenetic impact of metabolic therapies on cancer cells and provides some explanation for clinical observations, which indicate the anticancer activity of statins and bisphosphonates.

Keywords Mevalonate pathway, statins, bisphosphonates, epigenetics, cancer metabolism

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For more than 100 years, it has been known that cholesterol may accumulate in cancerous tissues (1) and plays a critical role in cancer progression, thus emphasizing the therapeutic potential of lowering cholesterol and downregulating the mevalonate pathway in cancer prevention and treatment (2). The mevalonate pathway converts acetyl-coenzyme A (acetyl-CoA) to isoprenoids, thus supplying key metabolites for cholesterol and steroid synthesis. It comprises a series of

enzymatic reactions that occur in the endoplasmic reticulum. The rate-limiting step is catalyzed by 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase, which converts HMG-CoA to mevalonate. This reaction is inhibited by statins, whereas bisphosphonates target more downstream reactions in this pathway, such as farnesylation and geranylgeranylation.

Meanwhile, there exists an increasing amount of data, which indicate that statins, as well as bisphosphonates, target the three most important epigenetic levels: DNA methylation, histone deacetylation, and microRNAs (Figure 1).

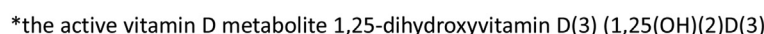
The best-described epigenetic roles of statins and bisphosphonates result from a reduction of the membrane anchoring from RAS and associated signaling toward DNA

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* Corresponding author.

E-mail address: heidrun.karlic@meduniwien.ac.at

¹ Current affiliation: Mayo Clinic, Rochester MN, USA.



In this study, simvastatin was chosen as a representative statin for transcriptomic studies, because a large-scale investigation was already performed with this drug and it was the first statin drug used extensively in clinical practice for control of elevated cholesterol. Epigenetic studies with simvastatin emphasize its role as a direct inhibitor of HDAC1 and HDAC2 (6) or as an inducer of respective microRNAs (19–21). Ibandronate was selected as a representative bisphosphonate, because it is already known for its epigenetic impact (3).

One day after splitting, 32 μ M simvastatin (Sigma-Aldrich) or 150 μ M ibandronate (Sigma-Aldrich) were added to the culture

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