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Title

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Permalink

<https://escholarship.org/uc/item/6g46v1g2>

Journal

FASEB JOURNAL, 28(1)

ISSN

0892-6638

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Publication Date

2014

Peer reviewed

Sphingolipid biosynthesis and inflammatory signaling in asthma (605.21)

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Abstract

Objective– SNPs located within human chromosomal region 17q21 are strongly associated with the incidence of inherited asthma and have been correlated by others to elevated transcript levels of nearby genes, including *ORMDL3*. Studies in yeast have identified the yeast *ORMDL3* orthologs, as negative regulators of the serine palmitoyl–CoA transferase (SPT) enzyme complex. This study investigates the role of mammalian *ORMDL3*. **Methods and Results**– To further understand the function *ORMDL3*, a stable doxycycline–inducible human embryonic kidney (HEK) cell line was developed that overproduces *ORMDL3* up to 40–fold compared to control cells. SPT activity in *ORMDL3* overexpressing cells was reduced to 40–60% compared to that of control cells. Sphingolipidomic analysis revealed that all sphingolipid species, were reduced in these cells, consistent with significant inhibition of SPT activity. Conversely, combined RNAi–mediated knockdown of all *ORMDL* isoforms resulted in higher SPT activity and increased sphingolipids. However, knockdown of any single *ORMDL* isoform did not alter SPT activity, suggesting that they serve a redundant function in inhibiting SPT. Additionally, individual knockdown of the two, different, small non–catalytic subunits of SPT_ *SPTSSA* and *SPTSSB* _did not alter *ORMDL3*–mediated inhibition of SPT. Furthermore, to attempt to determine the consequence of increased *ORMDL3* expression in asthma, LPS–induced TLR4 endocytosis was measured in RAW macrophages overproducing *ORMDL3*. There was a very modest increase in the fraction of cells displaying cell surface TLR4 in the *ORMDL3* overexpressing macrophages as compared to control cells. This result may due to inefficient transfection of the cell population. **Conclusions**– Taken together, these findings suggest that, although *Ormdl3* demonstrably impacts sphingolipid biosynthesis at the level of SPT, overproduction *ORMDL3* does not dramatically affect at least one arm of the innate immune response.