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computer graphics software for LinuxTuberculosis (TB) is a persistent disease and the causative agent, Mycobacterium tuberculosis (MTB), is acquired early in life and usually remains latent in the host throughout the lifetime. Despite effective TB control measures, the disease is the leading cause of death from

an infectious disease worldwide. The mechanisms that allow MTB to remain latent within its host and be reactivated at times of immunosuppression are poorly understood. Accordingly, the development of therapeutic strategies against latent MTB infection has been limited. In our recent work,

we discovered that heparan sulfate (HS), a cell surface glycoconjugate that is associated with the host response to M. tuberculosis, is required for dormancy-like survival of MTB within human macrophages. We further demonstrated that the HS biosynthetic enzyme, heparan sulfate glucosaminyl 3-O-

sulfotransferase-1 (HS3ST1), is expressed at high levels during latent infection, suggesting that it plays a role in the acquisition of latency. In this project, we will further characterize the role of HS3ST1 in the establishment and maintenance of latent infection and the

mechanisms of its biosynthesis and regulation. In Aim 1, we will determine the role of HS3ST1 in the acquisition of latency in mice that are deficient in specific immune cells using aerosol-based models of infection. In Aim 2, we will characterize the transcriptional regulation of HS3ST1 and the interaction

of its encoded protein with other bacterial factors involved in the establishment and maintenance of latent infection. These studies will provide new insights into the mechanisms of latency and the interaction of the bacteria with host tissues, and will identify new targets for the development of

treatments against latent TB.The pyruvate dehydrogenase complex is the pivotal enzyme that catalyzes the first committed step in carbohydrate metabolism by which NADH is oxidized to acetyl-CoA. It is composed of four non-identical protein components, E1, E2, E3 and the dihydrolipoamide

acetyltransferase. The E1 component is the catalytic component of the dehydrogenase complex and consists of two tightly associated, non-covalently bound, tightly bound, non-coval 2d92ce491b