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Inflammatory response in the pathogenesis of acute mountain sickness revealed by transcriptome analysis

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Acute mountain sickness (AMS) is a common disabling condition in individuals experiencing high altitudes, which may progress to life-threatening high altitude cerebral edema. To gain further insight into the molecular underpinnings that participated in the pathophysiology of AMS. We studied paired whole blood transcriptomes from 10 individuals, 5 AMS and 5 non-AMS diagnosed by Lake Louise scoring system, comparing post-exposure to high altitude (5300 m) transcriptomes to their pre-exposure counterparts. We identified 1,164 and 1,322 differentially expressed transcripts in participants with AMS and non-AMS, respectively. Among these genes, only 328 transcripts were common in both AMS and non-AMS individuals. Moreover, immune and inflammatory responses were more enriched in participants with AMS, but not in non-AMS individuals. This study identifies that inflammatory response induced by hypoxia, may be critical in AMS pathogenesis, which is a new direction for AMS pathogenesis investigation and useful for developing pharmacological prophylaxis and treatment.

Biography

Bao Liu is an undergraduate student at Third Military Medical University, Chongqing, China. He is studying the molecular mechanisms of high altitude illness using transcriptome.

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