EPHX1 Polymorphisms, Endotoxin Exposure, and Improvement in Respiratory Health in the Shanghai Textile Worker Study.

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Objective: We investigated if *EPHX1* polymorphisms related to slow metabolism of reactive oxidative species modify the association between subsequent occupational endotoxin exposure and improvement in lung function among workers with reduced lung function before retirement in the cotton textile industry. **Methods**: Within a 25–year longitudinal study of 572 workers in the Chinese cotton textile industry, 185 subjects identified with low adjusted FEV_1 (percent predicted FEV_1 < the 25th percentile) before retirement were followed from date of diagnosis until date of recovery or end of follow–up. *EPHX1 Tyr113His* and *His139Arg* polymorphisms were genotyped by the Taqman assay on an ABI 7900 sequencer. Using Cox regression, we estimated rate ratios (RR) for recovery from low adjusted FEV_1 as a function of slow metabolism allele (0 or 1 allele as reference) in *EPHX1* and endotoxin exposure level after diagnosis adjusting for potential confounders. Models were stratified by employment status and interactions between slow metabolism allele and endotoxin exposure level were evaluated. **Results**: At end of follow–up, 112 subjects recovered from low adjusted FEV_1. Subjects with ≥ 2 slow alleles were less likely to recover in both active (RR: 0.37, 95%CI: 0.18–0.76) and retired workers (RR: 0.52, 95%CI: 0.20–1.38). In active workers, RRs (95% CI) for ≥ 2 slow alleles were 0.17 (0.03–0.91), 0.39 (0.12–1.22), and 1.43 (0.19–11.13) for high endotoxin exposure, low endotoxin exposure, and no exposure, respectively; interaction between ≥ 2 slow alleles and endotoxin level was marginally significant (LRT, 2 dfs, p=0.09). **Conclusions**: *EPHX1* polymorphisms may prevent recovery of endotoxin–related lung function loss among workers in the Chinese cotton textile industry.

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