Gene expression signature to predict sepsis mortality

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Meet the Inventors

Tsalik, Ephraim
Ginsburg, Geoffrey
Henao Giraldo (Henao), Ricardo
Woods, Chris

Contact For More Info

Thomas, Dennis
919-681-7580
dennis.thomas@duke.edu

Department

Department of Medicine (DOM)(Dept. & CRU)

Improved risk stratification and prognosis in sepsis is a critical unmet need. Clinical severity scores and available assays such as blood lactate reflect global illness severity with suboptimal performance, and do not specifically reveal the underlying dysregulation of sepsis. Here three scientific groups were invited to independently generate prognostic models for 30-day mortality using 12 discovery cohorts (N=650) containing transcriptomic data collected from primarily community-onset sepsis patients. Predictive performance was validated in 5 cohorts of community-onset sepsis patients (N=189) in which the models showed summary AUROCs ranging from 0.765-0.89. Similar performance was observed in 4 cohorts of hospital-acquired sepsis (N=282). Combining the new gene-expression-based prognostic models with prior clinical severity scores led to significant improvement in prediction of 30-day mortality (p