participants had 29 PExs that met criteria for randomization but were not randomized; parent or participant discomfort with randomization was the most common reason (45% of eligible PExs that were not randomized).

Among the 33 participants randomized to the "tailored therapy" arm, 23 (70%) were not treated with oral antibiotics within 28 days of randomization. Across both arms, 35% returned to clinical care: 13 (43%) in the "early antibiotic" arm and 9 (27%) of the "tailored therapy" arm. Failure to improve within 7 days and incomplete recovery within 14 days of randomization were the most common reasons. Nineteen participants reported 31 adverse events (AEs). The majority were mild and unrelated to study procedures.

Conclusions: The STOP PEDS pilot study met its primary objectives by demonstrating that a single mild PEx in a selected population could resolve without oral antibiotics in 70% of the cases, and by demonstrating the feasibility of enrollment, identification of PEx through weekly texts, randomization of PEx treatment, and adherence to study measures. A definitive clinical trial is necessary to evaluate the short- and long-term safety and efficacy of this approach for repeated PEx events.

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**TRANSLATION**

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**Bronchoalveolar lavage proteome identifies pathways of disease that segregate lung transplant recipients with and without bronchiolitis obliterans syndrome**

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**Background:** Lung transplantation (LTx) is a treatment option for many end-stage lung diseases, including cystic fibrosis (CF). Proteomic analysis of bronchoalveolar lavage (BAL) fluid from LTx recipients has not been performed to identify potential biomarkers or pathways associated with bronchiolitis obliterans syndrome (BOS). We hypothesized that determining the differences between patients with and without BOS might shed light on the molecular underpinnings of disease.

**Methods:** We analyzed BAL fluid from 31 adult LTx recipients with (n = 15, 2 female) and without (n = 16, 3 female) BOS. Samples were collected from patients who underwent LTx for idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, or alpha 1 antitrypsin deficiency. Whole BAL protein was precipitated with acetone, resolubilized, fractionated using sodium dodecyl sulfate gel electrophoresis, in-gel trypsin digested, and subjected to mass spectrometer–based proteomic analysis.

**Results:** Our liquid chromatography mass spectrometry proteomic approach identified 4908 protein isoforms that were present in at least half of either cohort, with 227 isoforms (p < 0.01, false discovery rate (FDR) <0.1) distinguishing LTx recipients with and without BOS. Pathway analysis of differentially expressed proteins reveal vascular permeability (p < 0.003), proliferation and migration (p < 0.06), protein localization to ciliary membrane (p < 0.001), and prostaglandin E2 immune response (p < 0.049) (Figure 1). A more stringent percolator-decoy analysis identified 9 isoform differences and reveals changes in platelet degranulation (p < 0.001, FDR = 6.09e-6), kalikrein-kinin driven inflammation (p < 0.001, FDR = 3.37e-3), lectin-induced complement pathway (p < 0.001, FDR = 6.09e-6), blood coagulation (p < 0.001, FDR = 4.567e-5), and IL-6 mediated inflammation (p < 0.004, FDR = 9.96e-3). Disease associations of identified differences included connective tissue diseases (p < 0.001, FDR = 3.26e-3), wounds and injuries (p < 0.001, FDR = 3.26e-3), and autoimmune disease (p < 0.001, FDR = 3.26e-3). Strong signals antigen presentation and immunoglobulin mediated immune response (p < 0.001) and viral transcription (p < 0.001) were also observed in the BOS cohort.

**Conclusions:** The data suggest that antiviral, antimicrobial, complement inhibition, and antigen presentation are features of disease in LTx patients who developed BOS. Therapies that target these pathways may be of benefit. Furthermore, our proteomic approach may offer an additional tool for the diagnosis of BOS in LTx recipients.

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**Figure 1.** Pathway analysis of differential bronchoalveolar lavage protein expression in lung transplant (LTx) recipients with and without bronchiolitis obliterans syndrome (BOS). MetaCore by Clarivate, version 22.1, build 70 800 pathway analysis software was used to analyze differentially expressed proteins in LTx subjects with and without BOS.

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**Computed tomography body composition and clinical outcomes after lung transplantation in cystic fibrosis**

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**Background:** Low muscle mass is common in patients undergoing lung transplantation and may be linked to worse post-transplantation outcomes, but existing studies assessing muscle mass and post-transplantation outcomes include few patients with cystic fibrosis (CF). To address this limitation, we identified a cohort of people with CF and examined the relationship between pre-transplantation muscle mass measured using computed tomography (CT) and post-transplantation outcomes.

**Methods:** Between May 1993 and December 2018, of 152 adults with CF who underwent lung transplantation at our institution, 83 met inclusion criteria and had usable CT scans. Using Cox proportional hazards regression, we evaluated the association between pre-transplantation thoracic skeletal muscle index (SMI) and our primary outcome of death after lung transplantation. Secondary outcomes, including days to post-transplantation extubation and post-transplantation hospital and intensive care unit (ICU) length of stay, were assessed using linear regression. We also examined associations between thoracic SMI and post-transplantation pulmonary function and 6-minute walk distance.

**Results:** There was no association between pre-transplantation thoracic SMI and death after lung transplantation (HR 1.025; 95% CI, 0.948–1.109), days to post-transplantation extubation, or post-transplantation hospital...