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Title: LSC 2013 abstract - MicroRNA based biomarkers for early risk assessment of asthma

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Body: Introduction: Asthma is difficult to diagnose in children below 5 years of age because lung function testing is difficult in this age group and because asthma-like symptoms can be provoked by respiratory tract viral infections. Early asthma diagnosis is mandatory to initiate anti-inflammatory therapy to attenuate the airway remodelling process and preserve lung function. MicroRNAs (miRs) are attractive candidates for biomarker development because they are highly stable in serum and evolutionary conserved allowing the use of translational animal models. Objectives:To identify miR-based biomarkers predictive for paediatric asthma in murine models and to test translational feasibility in serum samples from asthmatic children. Methods: MiR profiling was performed in serum samples from a) the ovalbumin model of allergic asthma, b) Tbx21-/- mice as a genetic model of spontaneous asthma development. To address different disease states, Tbx21-/- were studied at different ages (nursling to adult). Results: Serum profiling in the ovalbumin model was performed in 3 experimental groups: "asthmatic" (ova/ova), "atopic" (ova/pbs) and control (pbs/ova) mice. 108/132 miRNA were detectable and passed quality control. After adjustment for multiple testing, 23 miRs were differentially regulated (FC>|1.5|, p-adj.<0.05) between "asthma" and control and 7 miRs between "asthma" and "atopy". Conclusion: Serum-miRs are differentially regulated between "asthma", "atopy" and control in the ovalbumin model of murine asthma. These will be further evaluated for asthma biomarker development.