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Title: YAP1 in the hippo pathway influences the risk of asthma

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Body: Asthma is an inflammatory disorder of the lungs. The main aim of this study was to identify new asthma susceptibility genes within the Hippo pathway. The Hippo pathway is responsible for organ size control, and survival and apoptosis of immune cells that play a role in asthma. The expression of seven genes in the Hippo pathway was studied on RNA isolated from induced sputum of twenty asthmatics and twelve non-asthmatics. TaqMan gene expression assays were used to find a new gene to play a role in asthma. Furthermore, six, promoter region single nucleotide polymorphisms (SNPs) of YAP1 (Yes-associated protein 1) were genotyped on 110 asthmatics and 123 controls using KASPar genotyping, in order to find a susceptibility allele within this gene. As a result, YAP1 gene expression levels were found to be significantly different between the two groups studied ($p=0.044$), hence indicating YAP1 as a novel gene in the Hippo pathway to play a role in asthma susceptibility. Additionally, correlation studies showed a significant positive correlation between YAP1 mRNA level and sputum macrophage percentages ($p=0.034$), which confirms that YAP1 gene expression increases in asthmatic progress, as well as the macrophage count increasing, leading to inflammation of the lungs in asthma. Additionally, YAP1 mRNA level also showed significant differences between the control, the mild asthmatic and the moderate to severe asthmatic groups ($p=0.035$). On the other hand, there were no significant differences in YAP1 SNP genotype counts between cases and controls. To conclude, in this study a new gene was identified within the Hippo pathway that may play a role in asthma contributing to the existing knowledge on the pathogenesis of asthma.