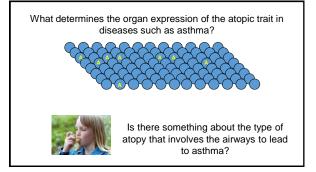
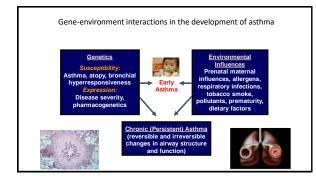
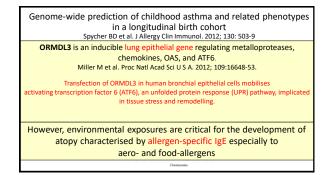


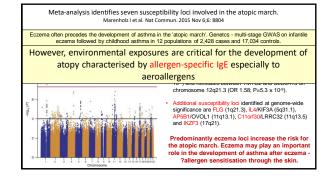
Overwhelming evidence that atopy is among the strongest driver of asthma in childhood

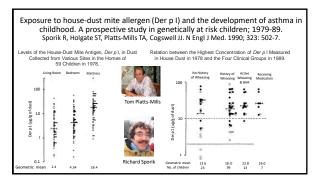
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- two-year follow-up of wheeze and atopic status. Am J Respir Crit Care Med. 2002; 165: 176-80

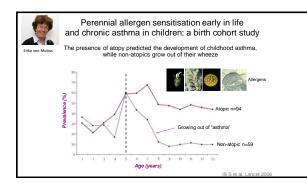




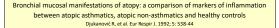








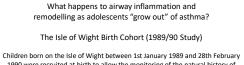




- Endobronchial biopsies in 13 symptomatic atopic asthmatics, 10 atopic nonasthmatics and 7 normals.
- Numbers of mast cells in submucosa no different between groups, but e.m. showed
 mast cell degranulation, although less marked in atopic non-asthmatics, was a feature
 of atopy in general.
- Numbers of eosinophils greatest in asthmatics, low or absent in normals and intermediate in atopic non-asthmatics.
- Subepithelial basement membrane thickness on e.m. thickest in asthmatics, intermediate in atopic non-asthmatics and thinnest in normals.
- Airways eosinophilia, degranulation of eosinophils and mast cells and increased subepithelial collagen are a feature of atopy in general and that the degree of change may determine the clinical expression of this immune disorder.

14

Djukanovi

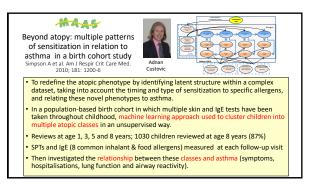


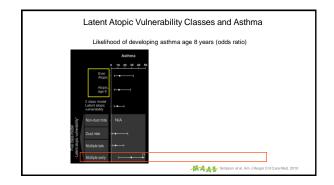
Children born on the isle of Wight between 1st January 1989 and 2sth February 1990 were recruited at birth to allow the monitoring of the natural history of asthma and allergies.

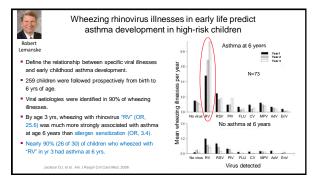
The children were followed up at one, two, four, 10 and 18 years of age.

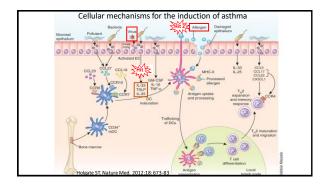


	Asthma	transitior	from age 10-1	8 years
Asth	ma char	nges betw	een age 10 and	18 years
	Number		Total	Percent
Persistent	125	181 (asthma	at age 10 yrs.)	69.06%
Remission	56	181 (asthma	at age 10 yrs.)	30.94%
New onset	56	198 (asthma	ta age 18 yrs.)	28.28%
Salbutamol reversibility	versibility			=0.015 Tissue
	bility		_ 1	=0.015 Tissue
25	p = 0.032	-	⁸⁰ 1	p <0.001 eosinophils
(%) 20-	FEV		E	T
uu 15	4			
EV1 Differe	* *	÷.	iii 20.	
E .		÷.	_	
Persistent	Asthma	No	Persistent	Asthma No Remission asthma



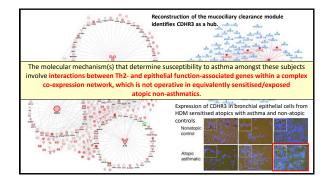


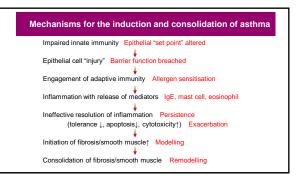






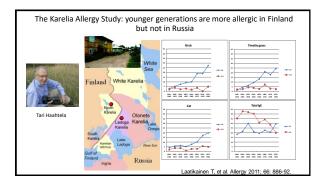
- Vast majority of atopics do not develop asthma-related wheeze, despite ongoing exposure to aeroallergens to which they are strongly sensitised, indicating that additional pathogenic mechanism(s) operate in conjunction with Th2 immunity to drive asthma pathogenesis.
- Systems analyses to identify gene networks operative at baseline in sputum-derived RNA from HDM-sensitised subjects with/without wheezing history; identify networks characteristic of the ongoing asthmatic state.
- HDM sensitised-nonwheezers displayed baseline gene expression in sputum including IL-5, IL-13 and CCL17.
- HOM sensitized wheezers showed equivalent expression of these dassical Th2-effector genes, but their overall baseline sputum signatures were more complex, comprising hundreds of Th2-associated and epithelialassociated genes, networked into two separate co-expression modules:
- The first module was connected by the hubs EGFR, ERBB2, CDH1 and IL-13.
- The second module was associated with CDHR3, and contained genes that control mucociliary clearance.



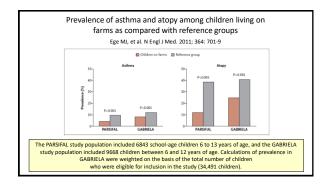


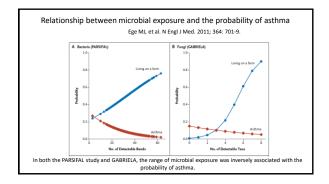
Changing worldwide trends in asthma

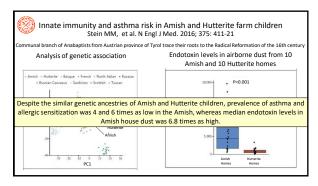
- Asthma and related allergic diseases have increased markedly in Western countries over the past 50 years, and this has been attributed to urbanization and associated changes to diet and lifestyle^{1.}
- The urban-rural gradient in prevalence demonstrated most strongly in children who grow up in environments with a wide range of microbial exposures (e.g. traditional livestock farms or in families who have adopted a more 'naturalistic' diet and lifestyle), who are protected from childhood asthma and atopy in proportion to their level of exposure to bacterial and fungal microbes².
- This protective effect against the onset of asthma in children is even more apparent if the microbial exposure (for example, working with animals or drinking unpasteurized milk)³ occurred throughout the mother's pregnancy⁴.
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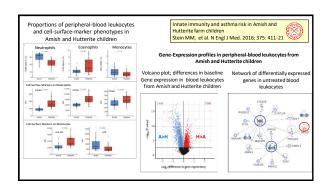


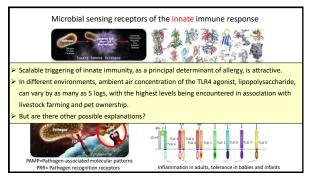


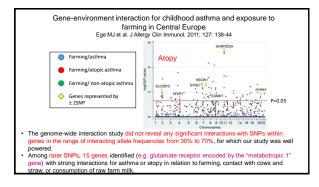


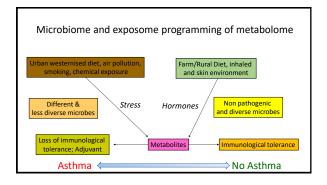












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Destructive factors	es lesses	
Microbiome diversity ↓		
Microbiome diversity ↓		