

# The Impact of a Germ Free Perinatal Period on the Variation in Animal Models of Human Inflammatory Diseases – A Review

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## Summary

Bacteria prime the immune system in early life, which in the first place is relevant for the development of oral tolerance. For some disease models, such as those for inflammatory bowel disease, germ free status for an entire life span, leads to the absence of prominent disease symptoms, while for other models, such as the Type 1 diabetes-prone NOD mouse, germ free status in early life would increase the incidence to a maximum. Basically both reactions are dependent on how the immune system has been primed in early life, i.e. with which bacteria and at which age. After early life priming, the gut regulatory immunity seems to be stable and less prone to be influenced by the gut flora. However, disease development later in life will still be dependent on contact with microorganisms to induce the inflammatory response. The aim of this review is to analyze whether it is reasonable to assume that variation in animal models, and thereby reduced groups size in experiments, may be achieved if animals are reared germ free with subsequent inoculation of a standardized gut flora at a standard age.

## Introduction

The establishment of the early life intestinal microbiota is essential for the development of the immune system and variation in animal models is likely to be caused by variation in this early life priming (Tlaskalova-Hogenova *et al.*, 2004; Hansen *et al.*, 2009). However, microbiological quality assurance of laboratory animals is solely focused on eradication of specific infectious agents (Nicklas *et al.*, 2002); commonly illustrated by the use of the term *specific pathogen free (SPF)* animals. Such animals

are produced by a combination of rederivation, barrier protection and health monitoring (Hansen, 2002).

In present years there is an increasing demand for animal models for human autoimmune, inflammatory and allergic diseases, as the incidences of these diseases are rapidly increasing in developed as well as developing countries. The normal colonization of the mammalian intestine with commensal microbes is hypothesized to drive the development of humoral and cellular immune systems during neonatal life and to maintain the physiologically normal steady state of inflammation in the gut throughout life (Cebra, 1999). It is therefore also reasonable to believe that the intestinal microbiota have an impact on the development and progress of these diseases in animal models (Tian *et al.*, 2001; Hansen *et al.*, 2009). However, the systems used to produce today's labo-

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ratory animals are not aimed at standardizing the ‘normal microbiota’ of animals as these are produced in open cages in huge facilities housing frequently more than 10,000 animals. Therefore, there is a need to develop systems aimed at more standardisation in the contact made with environmental microorganisms. However, it may be complicated to maintain a standardized microbial environment in animals for an entire life-time, e.g. by isolator maintenance, while it may be less complicated to have animals born under germ free (GF) conditions and after a limited period transfer them to a more traditional barrier protected environment. The aim of this review is therefore to consider the impact that GF conditions in early life may have on animal models of autoimmune and inflammatory diseases.

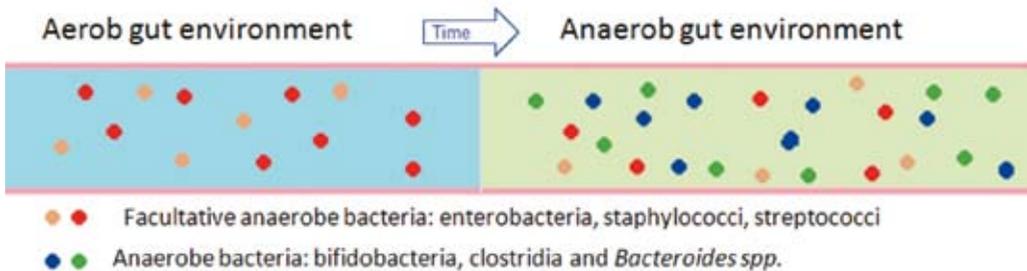
*The impact of commensal bacteria on immune system development*

The neonate gut is rapidly colonized by cutaneous, fecal and vaginal maternal bacteria initiated by facultative anaerobes, such as *Eschericia Coli*, streptococci and staphylococci inhabiting the gut, rapidly followed by anaerobic bacteria, such as *Bacteroides spp*, *Clostridium spp* and *Bifidobacterium spp*. (Ouweland et al., 2002) (Figure 1). Bacterial surfaces express ‘pathogen associated molecular pattern’ (PAMP’s), e.g. lipopolysaccharides, flaggelin and peptidoglycan, which are recognized and presented to other immune cells by antigen presenting cells (APC’s), and in the first weeks after birth ‘oral tolerance’ to food antigens and commensal microorgan-

isms develops (Tlaskalova-Hogenova et al., 2004), as gut bacteria inhibit systemic immune responses to these antigens (Moreau and Corthier, 1988; Sudo et al., 1997).

Two mechanisms are thought to be instrumental: The active suppression mediated by regulatory T-cells (CD4<sup>+</sup>CD25<sup>+</sup>T<sub>reg</sub> cells) (Fujiwara et al., 2008) and their cytokines TFG-β and IL-10, and deletion and anergy of T-cells following high doses of antigen (Tlaskalova-Hogenova et al., 2004). For example in GF mice it was only possible to induce oral T<sub>H</sub>2 mediated tolerance to ovalbumin if these were also neonatally inoculated with *Bifidobacterium infantis* (Sudo et al., 1997).

Intestinal dendritic cells (DC’s) in the lamina propria closely associated with the intestinal epithelial cells sample the antigen in the gut by one of three proposed mechanisms (Mizoguchi and Mizoguch, 2008): 1) M cells overlaying the Peyer’s patches in the gut internalize the antigen and present it to DC’s or T cells, 2) DC’s in the lamina propria extend their dendrites for direct capture of the antigen, and break it into smaller peptides to be presented by major histocompatibility class II (MHC II) molecules on the cell surface, or 3) neonatal Fc receptors (FcRn) transport IgG from the lamina propria into the gut lumen to form immune complexes with the antigen, which are transported back into the lamina propria by the FcRn to bind with DC’s. Such differences in DC stimulation decide whether the naive T cell is differentiated into various T-helper (T<sub>H</sub>) cells or alternatively into T<sub>reg</sub>. Specific pathogen free (SPF)

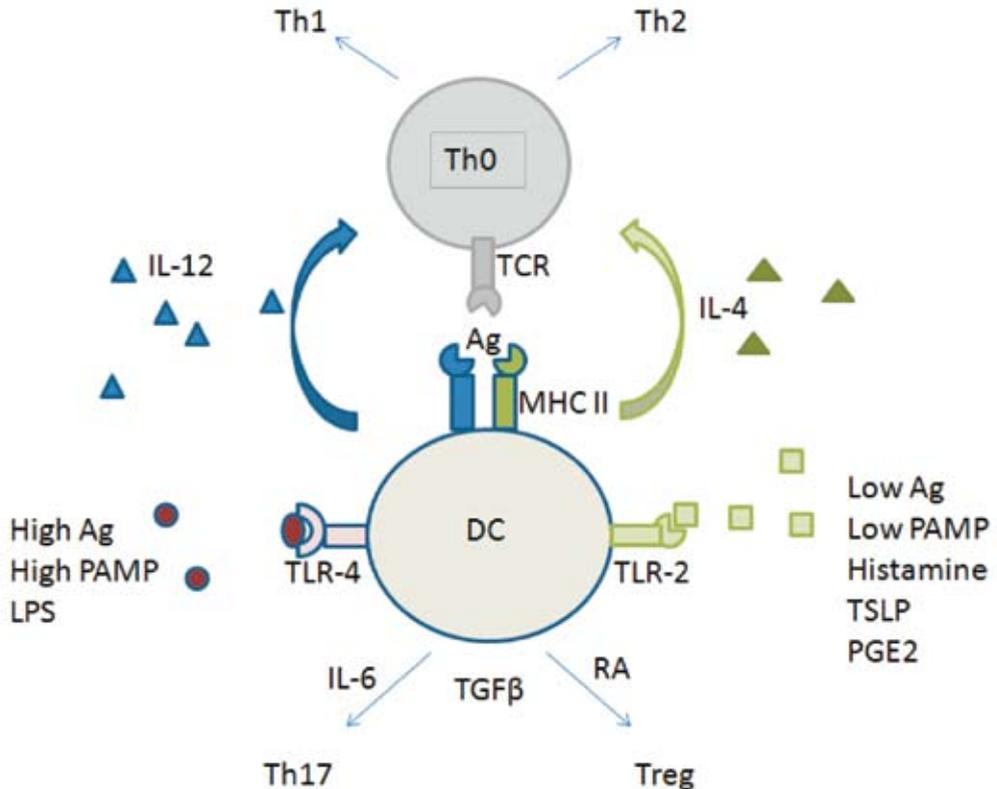


**Figure 1.** The colonization of the gut by bacteria leading to the development of an anaerobic environment suitable for the commensal flora.

and restricted flora (RF) status may shape the systemic DC population through a mechanism involving cytolytic CD8<sup>+</sup> T cells (Fujiwara *et al.*, 2008), while DC's in both SPF and GF mice are of similar phenotype and have similar in vitro antigen presenting function (Walton *et al.*, 2006).

Different toll-like receptors (TLR) present on the DC surface recognize different microbial antigens,

and mediate the antigenic stimulation (Ozinsky *et al.*, 2000). TLR's binding activates nuclear factor  $\kappa$ B (NF- $\kappa$ B), a transcription factor required for proinflammatory signalling, and mitogen-activated protein kinases (MAPK), which again stimulate the expression of a number of pro- and anti-inflammatory genes (Sartor, 2006). Immature DC's internalize the antigen, break it into smaller peptides and



**Figure 2.** Different stimulation of the dendritic cells (DCs) promotes different T cell subtypes and T regulatory cells, in the presence of different co-stimulatory molecules like interleukines (IL) or surface molecules like ICAM-1 or CD40. The DCs recognise antigen epitopes on different receptors – LPS is recognized by toll-like receptor 4 (TLR 4) and prime a T<sub>H</sub>1 cell development, whereas TLR 2 recognize Gram positive, fungal and mycobacterial components and prime a T<sub>H</sub>2 response. In the presence of TGF $\beta$  and IL-6, the development will skew towards effector T<sub>H</sub>17 and IL-23 is required to maintain the T<sub>H</sub>17. If on the other hand RA or no IL-6 are present T<sub>reg</sub> will preferentially develop. Abbreviations: DC dendritic cell, TCR T cell receptor, LPS lipopolysaccharide, PAMP pathogen associated molecular pattern, TSLP thymic stromal lymphopoietin (produced by intestinal epithelial cells), RA retinoic acid, Ag antigen, TGF $\beta$  transformin growth factor  $\beta$  (Mizoguchi and Mizoguchi 2008, Eisenbarth *et al.* 2003, Ozinsky *et al.* 2000).

**Table 1.** Factors influencing T cell development and favouring either T<sub>H</sub>1 or T<sub>H</sub>2 development. ICAM-1. Abbreviations: Inter cellular adhesion molecule, OX40L: a ligand present on the dendritic cell, interacts with OX40 on the T cell, CD 40 and B7: membrane proteins - interacts with CD40L and CD28 on the T cell respectively, STAT: signal transducer activator of transcription, IL: interleukine.

	T <sub>H</sub> 1	T <sub>H</sub> 2	References
Co-stimulatory molecules on dendritic cell	ICAM-1, OX40L, CD40, B7	OX40L, B7	Eisenbarth et al. 2003
Stimulatory IL	IL-12, IL-18, IL-27	IL-4, IL-5, IL-13	Eisenbarth et al. 2003
Transcription factors activated	STAT-4, T-bet	STAT-6, Gata 3	Shimada et al. 2006
Secrete	IFN $\gamma$ , TNF, IL-12	IL-4, IL-5, IL-10	Flohé et al. 2003 Ménard et al. 2008

present them on MHC-II. Naive T-cells that specifically recognize the antigen presented will then differentiate into the appropriate effector T-cell depending on the co-stimulatory molecules co-represented on the surface of the DC (Figure 2 and Table 1). In the steady state DC's will internalize commensals and preferentially induce T<sub>H</sub>2 and T<sub>reg</sub> response after migration to the mesenteric lymph node priming a small number of T<sub>H</sub>1 and T<sub>H</sub>17 cells as well. Furthermore, the intestinal epithelial cells produce thymic stromal lymphopoietin (TSLP) that stimulate T<sub>H</sub>2 differentiation (Coombes and Powrie, 2008). Some pathogenic bacteria present in the gut make DC's induce an inflammatory immune response dominated by T<sub>H</sub>1 and T<sub>H</sub>17 (Coombes and Powrie, 2008). Cytokines produced by the different T cell populations have stimulatory as well as inhibitory functions (Nakae et al., 2003; Eisenbarth et al., 2003; Shimada et al., 2006; Denning et al., 2007; Mizoguchi and Mizoguch, 2008). Different subsets of DC's, such as myeloid-, plasmacytoid- and CD8<sup>+</sup>DC's, also diversify the immune response to microbial antigens. Plasmacytoid DC's (pDC) have been shown to induce CD4<sup>+</sup>CD25<sup>+</sup> T<sub>reg</sub> cells or T<sub>H</sub>1/ T<sub>H</sub>2 cells depending on the antigen present (Colonna et al., 2004), and have also been proposed to play an important role in inducing tolerance via

the activation of CD4<sup>+</sup>CD25<sup>+</sup> T<sub>reg</sub> cells (Fujiwara et al., 2008). Absence of T<sub>reg</sub> suppression may cause harmful induction of T<sub>H</sub> by first time PAMP exposure later in life (Strachan, 1989; Romagnani, 2004; Hansen et al., 2009). There are at least three different types of T<sub>reg</sub> cells: CD4<sup>+</sup>CD25<sup>+</sup> T<sub>reg</sub> cells or Foxp3 T<sub>reg</sub> acting in a cell-cell mediated mechanism; Tr1 producing IL-10; and T<sub>H</sub>3 producing TGF $\beta$  (Romagnani, 2004; Shevach, 2006). There is some disagreement about whether the DC's (Coombes and Powrie, 2008) or the macrophages (Denning et al., 2007) are responsible for the induction of T<sub>reg</sub>. T<sub>H</sub>2 cell differentiation is the "default" pathway as this in the cell type most heavily represented in GF animals (Mazmanian and Kasper, 2006).

Specific bacteria have been found to preferentially prime the different T-cells. Kopitar et al. found that the commensal oral bacteria *Bacterioides fragilis*, *Streptococcus mitis* and *Propionibacterium acnes* prime human DC to induce T<sub>H</sub>1, T<sub>H</sub>2 and T<sub>reg</sub> respectively, and therefore these bacteria would also be likely to influence the development of inflammatory diseases (Kopitar et al., 2006). Microbial glycolipids are taken up by DCs and presented to natural killer T-cells (NKT) cells. These are divided into invariant NKT (iNKT or type 1 NKT) cells, defined by their reaction to  $\alpha$ -galactosyl ceramide

( $\alpha$ -GalCer), and into non-invariant NKT (non-iNKT or type 2 NKT) cells reacting with other glycolipids including the mammalian  $\beta$  forms. Glycosphingolipid molecules cannot be presented by the MHC complex, which only binds peptides. Instead, presentation is achieved through the MHC-like CD1 molecules (Porcelli and Modlin, 1999). The CD1 molecule contains a groove with two large hydrophobic pockets able to anchor the lipid tails of a glycosphingolipid (Zeng et al., 1997). The human DC's can express five kinds of CD1 molecules a, b, c, d and e, of which only c is expressed in mice. The most investigated CD1 ligand is  $\alpha$ -GalCer, which is isolated from marine sponges. There are clear indications that the development of oral tolerance is time dependent, i.e. there is an "immunological window" that plays a role in the development of autoimmune and inflammatory diseases (Sudo et al., 1997; Liu et al., 2005). It is generally assumed that this window is open sometime between birth and weaning during which period regulatory immune priming is dominant and after which adaptive reactions take over (Butler and Sinkora, 2007). However, the precise duration in different animal species and humans is not fully known.  $T_{reg}$  development seems to start already in the neonatal state (Samy et al., 2008), while later in life intestinal based regulatory immunology seems to be less influenced by microbial stimulation (Min et al., 2007).

Three checkpoints to control autoimmunity have been proposed (Darabi et al., 2004): (1) Some naive self-reactive T cells avoid negative selection, and (2) after a TLR-activating co-stimulation from a microorganism develop into pathogenic  $T_H1$  cells, which (3) due to a high serum level of cytokines from inflammation in a remote organ, e.g. the intestine, make harmful autoimmune sterile tissue injury in e.g. the beta cells.

*Immunological characteristics of germ free rodents*  
GF mice have underdeveloped intestinal lymphatic constituents, such as decreased lymphocyte number in organized and diffuse lymphatic gut tissues (Tlaskalova-Hogenova et al., 1983; Pleasants et al.,

1986; Cebra, 1999), decreased phagocyte activity and macrophage chemotaxis.  $CD4^+$  in Peyer's patches, and  $CD8^+$  or natural killer cells in intraepithelial leukocyte spaces of GF animals are quiescent. Furthermore, it has been observed that GF animals have a low concentration of IgA plasmablasts in lamina propria (Kramer and Cebra, 1995), as well as less diversified immunoglobulins and that lymphocytes react with low intensity to mitogens and polyclonal stimuli (Tlaskalova-Hogenova et al., 1983; Bos et al., 2001). Cells spontaneously secreting natural antibodies against LPS and tissue antigens appear delayed compared to conventional animals (Tlaskalova-Hogenova et al., 1983; Cebra, 1999). GF sentinels infected with *Clostridium piliforme* in young age do not produce a significant level of antibodies compared to barrier bred rats (Hansen et al., 1994). Maternal antigen experience may be thought to be instrumental in activating fetal T cells present in the gut mucosa, as in the GF maternal environment foetal  $CD3^+\beta_7^+$  T cells of both GF and bacteriologically reconstituted mice expressed the naive T cell selectin CD26L (Williams et al., 2006). These naive T cells may be involved in the induction of oral tolerance and thus are an important factor in the development of immune bias in early life and subsequent development of immune-mediated mucosal allergic and inflammatory disease (Williams et al., 2006).

It still has to be confirmed whether changes in the neonatal environment not corresponding to maternal antigen experience may result in defective regulation of the neonatal mucosal T cell repertoire and immune biasing (Williams et al., 2006). GF status has been shown to favour the development of a  $T_H2$  bias (Mazmanian and Kasper, 2006). Bacterial polysaccharide A (PSA) contains both positive and negative charges, thereby being of a different composition to other bacterial polysaccharides which are normally either neutral or negatively charged. *Bacillus fragilis* PSA will stimulate the normal development of  $T_H1$  vs.  $T_H2$  cells and thereby correct the imbalance in  $T_H1/T_H2$  that arises in GF animals. It will also correct the systemic T cell deficiency and direct lymphoid organogenesis (Mazmanian et al.,

2005), as mice inoculated with *B. fragilis* with the PSA gene proceeded to develop the immune system normally, whereas mice inoculated with *B. fragilis* without the PSA gene did not support the same differentiation of the immune system, and did not differ from the GF mice (Mazmanian *et al.*, 2005).

*Germ free disease models*

The importance of maternal antigen experience and development of fetal T cells has also been proposed as a factor in the development of harmful inflammatory responses later in life (Williams *et al.*, 2006). As GF status favours the development of a T<sub>H</sub>2 bias it is most likely to assume a lower incidence of T<sub>H</sub>1 dependent inflammatory diseases such as Type 1 diabetes (T1D) or T<sub>H</sub>1 mediated colitis (a model for Crohn’s disease) and a higher incidence of T<sub>H</sub>2 dependent inflammatory diseases such as allergies in GF animal models. This is, however, more complicated (Table 2).

*Type 1 diabetes (T1D) models*

Functional mediators of β-cell destruction in T1D are thought to be pro-inflammatory T<sub>H</sub>1 cells (Tian *et al.*, 2001). Incidence in female NOD mice is about 60-80% in barrier bred colonies but frequently less than half in conventional colonies (Pozzilli *et al.*, 1993). The incidence is influenced by the environment and the occurrence of infection with Coxsackievirus B early in life will exert a protective effect (Drescher *et al.*, 2004). Animals reared under GF conditions have higher cumulative incidence, up to 100% in females (Tlaskalova-Hogenova *et al.*, 2004). Treatment with the anti-Gram positive antibiotic fusidic acid (Buschard *et al.*, 1992), and a shift to a less Gram positive microflora induced by a gluten free diet have an incidence lowering effect (Hansen *et al.*, 2006), which is accompanied by an increase in intestinal T<sub>reg</sub> (Ejsing-Duun *et al.*, 2008). On the other hand, treatment with *Lactobacilli* later in life also reduces T1D incidence (Tabuchi *et al.*, 2003). Brugman *et al.* showed that the intestinal

**Table 2.** Summary of the effect of germ free status on the disease incidence in animal models. Abbreviations: T1D Type 1 diabetes, IBD Inflammatory bowel disease, RA rheumatoid arthritis, MS multiple sclerosis, KO knock-put, TG trans-gene, EAE experimental allergic encephalomyelitis. ? = no studies have been performed, but the fact that when injecting the CNS antigen, co-injection of adjuvant is what starts the inflammation, bacterial status might be less important than in other models. Adapted from Hansen *et al.* 2009.

Dis-ease	Organ specificity	T- cell	Animal model	Impact of germ free status on incidence	References
T1D	β-cells	T <sub>H</sub> 1	NOD mouse,	Higher	Suzuki <i>et al.</i> 1987
			BB rat	Same	Like <i>et al.</i> 1982
IBD	Bowel	T <sub>H</sub> 1 or T <sub>H</sub> 17	IL-2, IL-10 KO mice HLA-B7 TG rats	Lower	Taurog <i>et al.</i> 1994 Song <i>et al.</i> 1999
		(T <sub>H</sub> 2)	TCRα		Contractor <i>et al.</i> 1998
RA	Joints	T <sub>H</sub> 1	Collagen-/adjuvant Induced arthritis	Lower	Taurog <i>et al.</i> 1994 Lu <i>et al.</i> 1999 Bigazzi 2005
MS	CNS	T <sub>H</sub> 1	EAE	?	Darabi <i>et al.</i> 2004

microbiota were an influencing factor in the development of diabetes (Brugman *et al.*, 2006). They found that the faecal microbiota differed before the onset of diabetes and that those animals developing diabetes had a higher binding to a *Bacteroides*-specific probe than the rats that did not develop diabetes. Furthermore there was a protective effect in the groups treated with antibiotics, an effect improved by feeding a hydrolysed casein diet, reducing the observed incidence of diabetes in this study from approx. 90% to 0%. Both SJL and NOD mice have defects in NKT cell development and/or function (Yoshimoto *et al.*, 1995; Gombert *et al.*, 1996), and in humans with autoimmune diseases NKT cell numbers are reduced (van der Vliet *et al.*, 2001).  $\alpha$ -GalCer-specific activation of NKT cells protects against diabetes in NOD mice (Sharif *et al.*, 2001; Hong *et al.*, 2001), providing strong evidence that CD1d-reactive NKT cells suppress autoreactive T cells. Overexpression of NKT cells protects transgenic NOD mice against diabetes (Lehuen *et al.*, 1998), whereas a shortage of NKT cells in CD1d knock-out mice leads to exacerbation of Type 1 diabetes (Shi *et al.*, 2001). Finally, upregulation of CD1d expression within the beta cells restores the immunoregulatory function of NKT cells and prevents diabetes in NOD mice (Falcone *et al.*, 2004).

#### *Inflammatory bowel disease (IBD) models*

Both  $T_H1$ / $T_H2$  and more recently  $T_H17$  have been demonstrated to be involved in the pathogenesis of IBD. The role of a given molecule in the development of IBD in the many different animal models of IBD varies greatly depending on several factors, including the mechanism of disease induction, the target cell type, phase of disease and the environment (Mizoguchi and Mizoguchi, 2008). The presence of commensals in the gut are an important factor in the pathogenesis of IBD (Blumberg *et al.*, 1999). Tolerance mechanisms, such as active suppression by  $T_{reg}$  (Fujiwara *et al.*, 2008), prevent inappropriate responses to non-pathogenic, commensal bacteria in the gut lumen, and loss of these may lead to the development of IBD (Brimnes *et al.*, 2001).

IBD-associated CD4<sup>+</sup>T cells from diseased SCID mice did not react to faecal extracts from GF mice, nor to extracts from food antigens, indicating that bacterial antigens are responsible for activating the CD4<sup>+</sup>T cells (Brimnes *et al.*, 2001). If reared under GF conditions knockout (KO) mice for IL-10, IL-2 and TCR $\alpha$ , HLA-B7 transgenic rats and SAMP1/Yit mice (a spontaneous model for IBD) will not develop mucosal inflammation (Taurog *et al.*, 1994; Contractor *et al.*, 1998; Song *et al.*, 1999). On the other hand, GF IL-2-deficient mice in the absence of clinical symptoms histologically showed mild focal intestinal inflammation at 13 weeks of age, suggesting that the mechanisms behind IBD were present in GF mice, but exacerbated in SPF or conventional mice (Schultz *et al.*, 1999). In HLA-B7 transgenic rats, which develop not only intestinal inflammation, but skin, joint and genital inflammatory lesions, a GF state prevented IBD and peripheral joint lesions, but not skin and genital inflammation (Taurog *et al.*, 1994; Contractor *et al.*, 1998). When the animals were treated with a bacterial flora, IBD occurred, but no joint inflammation developed in the relatively short observation period of this study (Taurog *et al.*, 1994). The Gram positive flora including *Lactobacilli* seems to be protective against IBD (Schultz *et al.*, 2002).

#### *Pristane (tetramethylpentadecane) induced murine lupus and rheumatoid arthritis (RA) model*

The pristane model is primarily a model of human systemic lupus erythematosus in SLE mice, while in BALB/c, CBA and DBA mice, inflammatory joint disease (pristane-induced arthritis, PIA), which makes this an interesting model for rheumatoid arthritis (RA) (Lu and Holmdahl, 1999). The development of PIA is dependent on contact with microorganisms, as animals reared in GF environment do not develop PIA (Bigazzi, 2005).

#### *Experimental allergic encephalomyelitis (EAE) multiple sclerosis model*

Injection of neuroantigen in a TLR-activating adjuvant is enough to induce a vigorous neuroantigen

specific  $T_H1$  response in EAE susceptible mice. However, in other murine models there is also the need for pertussis toxin (PTX) to be co-injected in order to develop EAE (Darabi *et al.*, 2004). PTX promotes the  $T_H1$  differentiation, and in addition, it is also thought to break down the blood-brain-barrier and thereby grant the autoantigen-specific  $T_H1$  access to the brain (Darabi *et al.*, 2004). In these models the impact of the commensal intestinal flora would seem redundant as the method for inducing the disease is entirely dependent on the injection of antigen, adjuvant and other co-stimulatory molecules like PTX. However, according to checkpoint 3 as described by (Darabi *et al.*, 2004) and mentioned previously, the presence of inflammation in the intestine could influence the development of EAE by massive serum IL-12, which would also make PTX unnecessary. Treatment of mice with sulfated galactosyl ceramide (sulfatide) prevents EAE, which seem to involve an increase in the number of  $T_{reg}$  (Jahng *et al.*, 2004).

### Discussion

It seems to be clear that bacteria prime the immune system in early life during which microbial contact with  $T_{reg}$ , DC and NKT cells is important. In the first place this is relevant for the development of oral tolerance. For some disease models, such as those for IBD, GF status leads to the absence of prominent disease symptoms, which in most cases would invalidate their use as animal models (Taurog *et al.*, 1994; Contractor *et al.*, 1998; Schultz *et al.*, 1999; Song *et al.*, 1999). For other models, such as the T1D-prone NOD mouse, GF status in early life would increase the incidence to a maximum (Tlaskalova-Hogenova *et al.*, 2004).

However, both model reactions may be explained from the 'hygiene hypothesis' (Strachan, 1989): contact with microorganisms in early life primes the immune system in a regulatory direction, while contact with microorganisms later in life primes the immune system in a more inflammatory direction. IBD-prone transgenic mice and NOD mice are both examples of genetically based models, in which the

genetic drive towards disease is very strong. However, early life priming in IBD mice is not strong enough to prevent IBD from developing when direct exposure to bacteria is encountered in the intestine. Furthermore, it is also evident that in some mice subclinical symptoms develop even in the GF state (Schultz *et al.*, 1999), while  $T_{reg}$  probably are the only defence against T1D in NOD mice and responsible for the absence of the disease in those 20 % of the mice not developing T1D. Therefore the lack of early life priming removes the last defence against the genetic inevitability also in these mice.

After early life priming the gut regulatory immunity seems to be stable and less prone to be influenced by the gut microbiota (Min *et al.*, 2007). However, disease development later in life will still be dependent on contact with microorganisms to induce the inflammatory response (Darabi *et al.*, 2004). Hence it is reasonable to hypothesize that disease development in animal models will be enhanced by early life GF status reliant on the reduced regulatory immune response, followed by a strong microbial contact later in life. Variation in this contact is very likely to induce variation in the development of disease and thereby increase the group sizes needed to achieve statistical significance (Hansen *et al.*, 2009).

Several authors have introduced pro- and pre-biotics in potential preventive therapies against allergies and autoimmune diseases, and the Gram positive flora, including *Lactobacilli*, indeed seems to be protective/preventive against IBD (Schultz *et al.*, 2002), reduce T1D incidence (Tabuchi *et al.*, 2003) and ameliorate symptoms of RA (Nenonen *et al.*, 1998). The explanation may be that the presence of e.g. microaerophilics, suppress those bacteria, which express the PAMP's that induce the inflammatory response, and it underlines that variation in bacterial contact may lead to variation in disease expression. It is reasonable to assume that the impact that different groups of bacteria will have on the immune system is very much age-dependent, so microaerophilics may have another impact if given at another age. Therefore, the lowest variation in the model may be achieved if GF status is com-

bined with inoculation with a standardized flora at a standardized age. However, which flora to use for a high disease incidence is a complicated matter.

In conclusion, it is likely to assume that early life GF status combined with subsequent inoculation of a standardized gut flora would be an applicable tool to reduce variation in animal models, but the questions still need further elucidation to be applied in practice.

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