

**Fig. 17.** Expression of MAIL (similar to mouse  $\text{I}\kappa\text{B}\zeta$ )-mRNA on the human ocular surface. A. RT-PCR detected MAIL-specific mRNA in the human corneal and conjunctival epithelium. Human peripheral monocytes stimulated with 100 ng/ml LPS were the positive control. (P: adherent mononuclear cells stimulated with 100 ng/ml LPS). B. Knock down of MAIL enhanced the expression of IL-6- and IL-8-specific mRNA. For the transfection of small interfering RNA (siRNA), 1  $\mu\text{g}/\text{ml}$  of the control- or targeting siRNA was transfected into primary human corneal epithelial cells using PolymagII (OZ BIOSCIENCES) according to the manufacturer's recommendations. Mag: only PolymagII, Nega siRNA: control siRNA. (\*,  $p < 0.05$ ; \*\*\*,  $p < 0.005$ ). Reprinted with permission from Ueta et al. (Ueta et al., 2005b; Ueta and Kinoshita, 2010a).

Many patients encountered by ophthalmologists present in the chronic stage of SJS/TEN; dermatologists tend to see patients with SJS/TEN in the acute stage. The differential diagnosis of SJS or TEN may be difficult in the chronic stage of SJS/TEN because at that point the vesiculobullous skin lesions present in the acute stage have healed. Thus, ophthalmologists tend to diagnose both SJS and TEN as SJS in the broad sense. Our diagnosis of SJS/TEN (SJS in the broad sense) was based on a confirmed history of acute-onset high fever, serious mucocutaneous illness with skin eruptions, and involvement of at least 2 mucosal sites including the ocular surface (Sotozono et al., 2007, 2009a; Ueta and Kinoshita, 2010a; Ueta et al., 2007c, 2008b, 2007e, 2008d; c; Ueta et al., 2007d, 2010c, 2007e, 2008d).

The pathobiological mechanisms underlying the onset of SJS/TEN have not been fully established. The extreme rarity of cutaneous and ocular surface reactions to drug therapies led us to suspect individual susceptibility (Ueta, 2008; Ueta and Kinoshita, 2010a; Ueta et al., 2007c, 2008b, 2012b, 2008d; c; Ueta et al., 2007d, 2010c, 2007e, 2012b, 2008d).

## 6.2. HLA analysis of SJS with ocular surface complications

In 1982, ophthalmologists first reported that the HLA-Bw44 antigen, a subgroup of HLA-B12, was significantly increased in Caucasian patients with SJS with ocular involvement compared with a control Caucasian population. In that study, the onset of SJS with ocular involvement was associated with putative viral syndromes or the administration of drugs (Mondino et al., 1982). Dermatologists also found that the frequency of the HLA-B12 antigen was significantly increased in French SJS/TEN patients whose disorder was clearly drug-induced compared with a French control population; the main causative agents were non-steroidal anti-inflammatory drugs (NSAIDs) (Roujeau et al., 1986).

We examined HLA-class I (HLA-A, -B, -C) antigens in Japanese SJS patients with severe ocular surface complications (Ueta et al.,

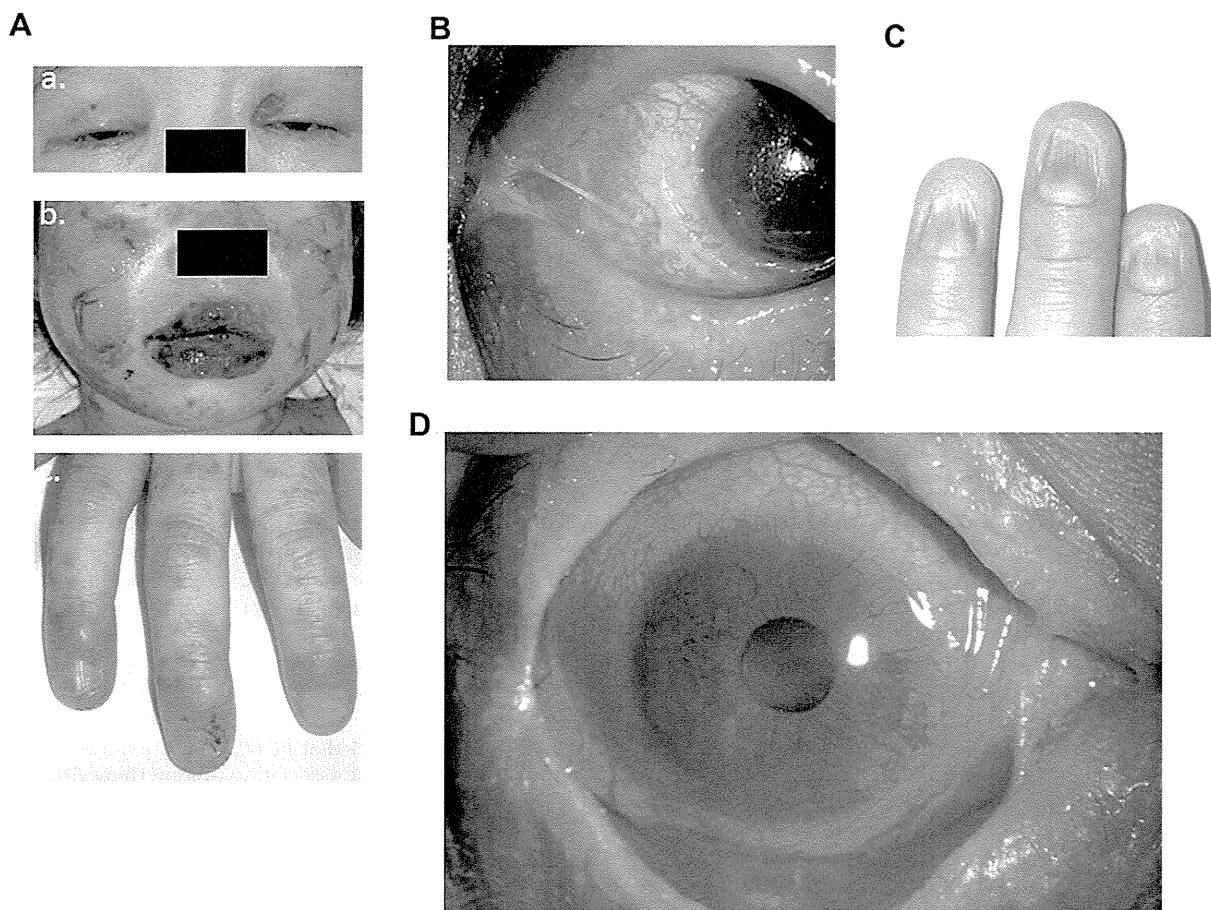
2007e, 2008d) and found that the carrier frequency of the HLA-A\*0206 antigen was significantly higher in 110 SJS patients compared to 220 Japanese controls (carrier frequency: 45.5% vs 13.6%,  $p = 0.0000000002$ , odds ratio (OR) = 5.3, gene frequency: 23.6% vs 6.8%,  $p = 0.0000000007$ , OR = 4.2). However, HLA-A\*0206, strongly associated with SJS/TEN with ocular complications in Japanese individuals, is absent in Caucasians (Ueta et al., 2007e, 2008d).

On the other hand, in our study, as in earlier reports (Mondino et al., 1982; Yetiv et al., 1980), the onset of SJS with severe ocular surface complications was associated with putative viral syndromes and/or the administration of drugs (mainly NSAIDs) (Ueta et al., 2007c, 2008b, 2007d, 2010c, 2007e). We found no association with HLA-B12 in Japanese SJS patients (Kaniwa et al., 2008; Ueta et al., 2007e, 2008d) although this antigen was significantly increased in Caucasian SJS patients (Mondino et al., 1982; Roujeau et al., 1986), probably because in Caucasians the HLA-B12 antigen is primarily coded by HLA-B\*4402 whereas in Japanese it is almost exclusively coded by HLA-B\*4403 (Tokunaga et al., 1997).

Thus, our findings suggest strong ethnic differences in the association of SJS/TEN and HLA (Ueta et al., 2007e, 2008d). Specific combinations of genes and certain environmental factors may be required for the manifestation of this rare phenotype because SJS/TEN is rare and it probably has a complex genetic inheritance background (Ueta et al., 2007e, 2008d).

In Han Chinese (Chung et al., 2004) but not in Caucasian patients (Lonjou et al., 2008, 2006) there was a strong carbamazepine-specific association between HLA-B\*1502 and carbamazepine-induced SJS/TEN. Because the allele frequency of HLA-B\*1502 is very low in the Japanese, the carbamazepine-specific association between HLA and carbamazepine-induced SJS may be specific for certain ethnic groups (Kaniwa et al., 2008; Ueta et al., 2008d).

Although an allopurinol-specific association between HLA-B\*5801 and allopurinol-induced severe cutaneous adverse reactions



**Fig. 18.** Stevens-Johnson syndrome (SJS) with severe ocular surface complications. A. Typical features of SJS/TEN in the acute stage. a. Ocular surface inflammation with conjunctivitis and eyelids swelling. b. The face manifests swollen and crusted lips, blisters, and erosion of the skin. c. Paronychia. Reprinted with permission from Ueta et al. (Ueta and Kinoshita, 2010a). B. Ocular surface inflammation of SJS: severe conjunctivitis, pseudomembrane, epithelial defect, etc. C. Transformed fingernails in the chronic stage. D. Ocular surface complications in the chronic stage; conjunctival invasion into the cornea, symblepharon, trichiasis, and dry eye.

may be a universal phenomenon in all ethnic groups (Hung et al., 2005) allopurinol-induced severe adverse cutaneous reactions may not elicit serious sequelae on the ocular surface. In fact, few SJS patients with severe ocular surface complications manifested allopurinol-related SJS/TEN (Kaniwa et al., 2008).

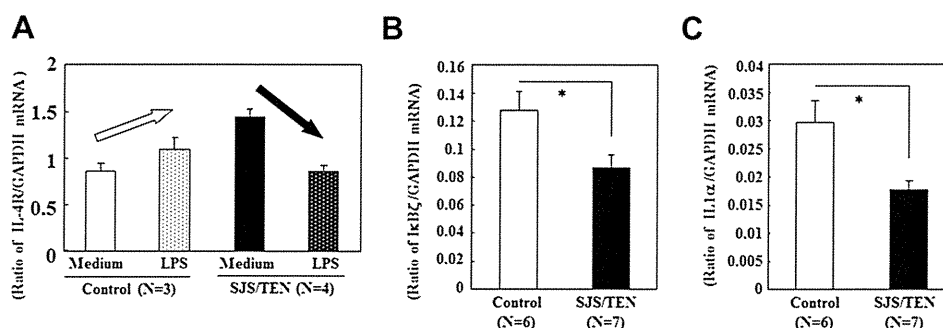
Drugs are probably the most widely accepted etiologic factors in SJS/TEN (Levi et al., 2009; Mockenhaupt et al., 2008; Roujeau et al., 1995; Wolf et al., 2005). It is worth noting that our SJS/TEN patients with severe ocular surface complications often presented with prodromata including nonspecific fever, coryza, and sore throat that closely mimic upper respiratory tract infections commonly treated with antibiotics and NSAIDs (Ueta and Kinoshita, 2010a; Ueta et al., 2007d, 2010c). More than 80% of our SJS patients developed SJS after receiving treatment for the common cold with antibiotics, cold remedies, and/or NSAIDs; only about 5% progressed to SJS after drug treatment delivered to prevent the occurrence of convulsions (Ueta et al., 2010c).

### 6.3. Gene expression analysis of SJS with ocular surface complications

We have proposed the possibility of an association between a disordered innate immune response and SJS with severe ocular surface complication. Our hypothesis was based on the observation of an association between the onset of the SJS and microbial infections, because many SJS patients with severe ocular surface complications exhibited prodromata, including non-specific fever,

coryza, and sore throat, ailments that closely mimic upper respiratory tract infections of viral or mycoplasma origin, which are commonly treated with antibiotics and NSAIDs (Ueta, 2008; Ueta and Kinoshita, 2010a; Ueta et al., 2007d, 2010c, 2012b). In addition, the SJS patients presented with opportunistic infection of the ocular surface by bacteria, especially methicillin-resistant *S. aureus* and *Staphylococcus epidermidis* (MRSA and MRSE); the detection rate of MRSA and MRSE was higher on the ocular surface of SJS/TEN patients compared to individuals with other devastating ocular surface disorders (Sotozono et al., 2002). We posit that in SJS/TEN patients, opportunistic infections of the ocular surface by bacteria are ascribable to abnormalities in their innate immunity. Moreover, SJS/TEN patients presented with persistent inflammation of the ocular surfaces harboring commensal bacteria.

Under the hypothesis of a disordered innate immune response in SJS with ocular complications, we performed gene expression analysis of monocytes, which are essential in innate immunity. We found differences in IL4R gene expression; it was down-regulated in SJS/TEN patients upon LPS stimulation and slightly up-regulated in the controls (Fig. 19A) (Ueta, 2008). We also found that in human ocular surface (corneal and conjunctival) epithelial cells IL4R-specific mRNA was down-regulated upon stimulation with PolyI:C which mimics viral components (data not shown). This observation suggests that IL4R is linked with innate immunity (Ueta, 2008). We also found that after 1-hr culture without LPS, the expression of  $\text{I}\kappa\text{B}\zeta$ - and IL-1 $\alpha$ -specific mRNA was lower in monocytes from SJS/TEN patients than normal controls (Fig. 19B, C) (Ueta,



**Fig. 19.** Gene expression analysis of monocytes (CD14<sup>+</sup> cells) from SJS with ocular complications. A: Difference in IL4R gene expression between SJS patients and normal volunteers. CD14<sup>+</sup> cells from peripheral blood were subjected to gene expression analysis. The cells were cultured for 1 h with or without LPS. B, C. Low expression of IκBζ and IL-1α by isolated monocytes from SJS patients after 1-hr culture. Quantitative RT-PCR assay confirmed that IκBζ (B) and IL-1α (C) gene expression was significantly lower in cultured monocytes from 7 SJS/TEN patients than the 6 controls. Data show the mean ± SEM. (\*,  $p < 0.05$ ; \*\*\*,  $p < 0.005$ ); evaluation was with Student's *t*-test using the Excel program. Reprinted with permission from Ueta et al. (Ueta, 2008).

2008). This suggests that the reduced expression of IκBζ and IL-1α genes may play an important role in the pathophysiology of SJS/TEN.

Possibly to prevent excessive inflammation in the presence of bacterial components, IκBζ induced by diverse pathogen-associated molecular patterns regulates NF-κB activity (Yamazaki et al., 2001). Elsewhere we documented that IκBζ gene-disrupted mice manifested ocular surface inflammation (Ueta et al., 2008a, 2005b) and that IκBζ in the ocular surface epithelium can suppress the production of pro-inflammatory cytokines such as IL-6 and IL-8 (Ueta and Kinoshita, 2010a). This suggests that the ocular surface epithelium suppresses inflammation via the expression of IκBζ (Ueta et al., 2008a, 2005b; Ueta and Kinoshita, 2010a).

We also reported that the TLR3 ligand, elicited the elevated expression of human IκBζ-specific mRNA in ocular surface epithelial cells (Ueta et al., 2005a). Because TLRs could induce the expression of IκBζ (Ueta et al., 2005a), the ocular surface inflammation seen in SJS/TEN patients may be related to innate pathogen-associated molecular pattern-amplified immune responses to microbes.

IL-1α was significantly lower and sIL-2R significantly higher in the blister fluid of TEN- than burn patients (Correia et al., 2002). We also detected a significant difference between SJS/TEN patients and the controls with respect to the expression of IL-1α by CD14<sup>+</sup> monocytes (Ueta, 2008; Ueta and Kinoshita, 2010a).

#### 6.4. Single nucleotide polymorphism (SNP) analysis of SJS with severe ocular surface complications

##### 6.4.1. The candidate gene approach

While the administration of some drugs may result in the development of SJS/TEN, not all patients taking these drugs develop SJS/TEN. As the incidence of SJS/TEN is very low, we suspected a genetic predisposition (Ueta, 2008; Ueta and Kinoshita, 2010a). We therefore performed SNP association analysis using candidate genes associated with innate immunity (Ueta, 2008; Ueta and Kinoshita, 2010a; Ueta et al., 2007d), allergy (Ueta, 2008; Ueta and Kinoshita, 2010a; Ueta et al., 2007c, 2008b), or apoptosis (Ueta et al., 2008c).

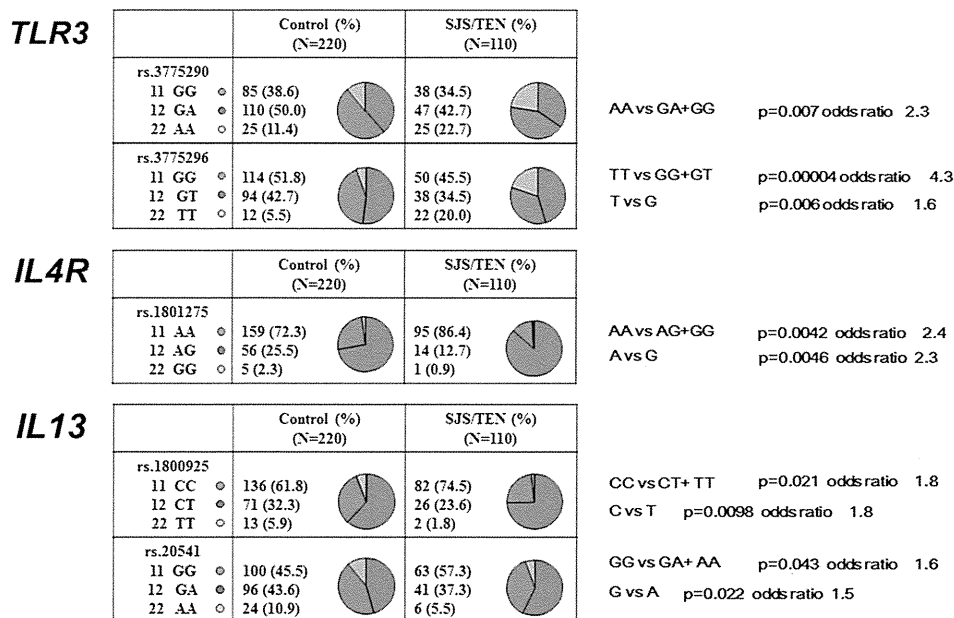
We first examined candidate genes associated with innate immunity. We investigated the IκBζ gene, which yielded different findings for SJS/TEN patients and controls in our gene expression analysis, and whose disruption results in ocular surface and skin inflammation. Another was the IL1α gene which, based on gene expression analysis, is also different in SJS/TEN patients and the controls. Other candidate genes were the TLR2 gene which is closely related to *S. aureus* and *S. epidermidis*, including MRSA and

MRSE, and the TLR3 gene which is the gene most highly expressed on ocular surface epithelium among 1–10 TLRs and which responds to the virus dsRNA-mimic polyI:C to generate pro-inflammatory cytokines and IFN-β (Ueta, 2008; Ueta and Kinoshita, 2010a; Ueta et al., 2007d).

To investigate IκBζ we analyzed 7 polymorphisms (rs.2305991, rs.622122, rs.14134, rs.3217713, rs.595788, rs.677011, rs.3821727) in the Japanese Single Nucleotide Polymorphisms (JSNP) database (Ueta, 2008). We found that in 110 SJS patients and 220 controls there was no significant association among these SNPs. Regarding IL1α, we analyzed 5 SNPs (rs.1609682, rs.1894399, rs.2071373, rs.2071375, rs.2071376) reported in JSNP. Again, we found no significant association among these SNPs (Ueta, 2008). For TLR2 we analyzed 3 SNPs (rs.3840100, rs.3840099, rs.3840097) in JSNP and found no significant association among these SNPs (Ueta, 2008). However, our analysis of 7 SNPs for TLR3 (rs.3775290, rs.3775291, rs.3775292, rs.3775293, rs.3775294, rs.3775295, rs.3775296) (Ueta et al., 2007d) revealed that in 110 SJS patients and 220 controls, SNP rs.3775296 showed a significant association under a recessive model (rs.3775296T/T vs T/G + G/G,  $p$  value = 0.00004, OR = 4.3) and a weak association with allele frequency (T vs G,  $p$  value = 0.006, OR = 1.6) and SNP rs.3775290 also showed a significant association under a recessive model (rs.3775290 A/A vs A/G + G/G,  $p$  value = 0.007, OR = 2.3) (Fig. 20). Thus, our findings suggested that polymorphisms in the TLR3 gene are associated with SJS with severe ocular surface complications in the Japanese population (Ueta et al., 2007d).

We have reported that human ocular surface epithelial cells strongly expressed TLR3 and that its ligand, polyI:C could induce various molecules such as pro-inflammatory cytokines and anti-viral- and allergy-related-molecules (Ueta et al., 2005a, 2010b; Ueta and Kinoshita, 2010a, 2010b). Elsewhere we offered the hypothesis that viral infection and/or drugs may trigger a disorder in the host innate immune response and that this event is followed by aggravated inflammation of the mucosa, ocular surface, and skin (Ueta, 2008; Ueta and Kinoshita, 2010a; Ueta et al., 2007d, 2012b).

Next we examined candidate genes associated with allergy. Our gene expression analysis had shown that with respect to the IL4R gene there are differences between SJS patients and the controls (Ueta, 2008). This gene is essential for both IL-4 and IL-13 signaling because it is a component of IL-4 and IL-13 receptors. We analyzed Gln551Arg (rs.1801275), Ile50Val (rs.1805010), and Ser478Pro (rs.1805015) polymorphisms of IL4R as they are associated with allergic diseases such as asthma (Ueta et al., 2007c, 2008b). We found no significant association between Ile50Val (rs.1805010), and Ser478Pro (rs.1805015) (Ueta et al., 2007c, 2008b). On the other hand, Gln551Arg was significantly associated with allele frequency



**Fig. 20.** Association between TLR3, IL4R, and IL13 SNPs and SJS with severe ocular surface complications. Using the candidate gene approach we identified SNPs of TLR3, IL4R and IL13 genes that were associated with SJS with severe ocular surface complications.

(A vs G,  $p$  value = 0.0046, OR = 2.3) and the dominant model (A/A vs A/G + G/G,  $p$  value = 0.0042, OR = 2.4) in the 110 SJS patients and the 220 controls (Fig. 20)(Ueta et al., 2007c, 2008b).

We also investigated IL13 and IL4, ligands of IL4R. With respect to the IL13 gene we analyzed polymorphisms of the promoter -1111C/T SNP (rs.1800925) and the Gln110Arg SNP (rs.20541); they are associated with allergic diseases such as asthma. There was a significant association of the promoter -1111C/T SNP with allele frequency (C vs T,  $p$  value = 0.0098, OR = 1.8) in all 110 SJS patients and the 220 controls; the Gln110Arg SNP exhibited a significant association with allele frequency (G vs A,  $p$  value = 0.022, OR = 1.5)(Fig. 20). We detected a significant increase in Arg110 in our SJS/TEN patients (Ueta et al., 2008b), although Gln110 was significantly increased in patients with asthma (Heinzmann et al., 2000).

With respect to the IL4 gene we analyzed polymorphisms of the promoter -590C/T (rs.2243250) related to higher IgE levels. We found no significant association between the SJS patients and the controls (Ueta et al., 2008b).

Lastly we examined FasL genes, the candidate genes associated with apoptosis; they have been reported to be increased in the serum of SJS/TEN patients in the acute stage (Abe et al., 2003). We examined 4 SNPs (rs.929087, rs.2639614, rs.2859247, rs.3830150) and found that rs.3830150 A/G (intron) showed a weak association with the dominant model (A/G + G/G vs A/A,  $p$  value = 0.015, OR = 1.8) in 110 SJS patients and 220 controls (Ueta et al., 2008c).

In summary, we found that TLR3 rs.3775296 SNP, IL4R SNP rs.1801275 (Gln551Arg), and IL13 rs.20541 (Arg110Gln) were significantly associated with SJS/TEN with ocular surface complications (Ueta, 2008; Ueta and Kinoshita, 2010a).

#### 6.4.2. Genome-wide association study (GWAS)

To elucidate the pathophysiology of SJS with severe ocular surface complications in more detail we performed GWAS of more than  $10^5$  SNPs. GWAS permits the identification of genetic loci and genes associated with complex human traits without bias or *a priori* knowledge of the function or involvement of genes in the disease pathway. GWAS detected 3 SNPs (rs1325975: chr6, rs17131450: chr1, rs11238074: chr11) that were significantly associated with SJS

with severe ocular surface complications. Because 2 of the SNPs (rs1325975 and rs11238074) were from the “gene desert” region, we focused on a SNP (rs17131450) that mapped close to the *PTGER3* gene, which is the gene of EP3 protein of human, located in the 1p31 region of the human genome (Ueta et al., 2010c).

Based on our GWAS results we performed fine-mapping analysis of the *PTGER3* region using a custom DNA array to analyze the SNPs in and near *PTGER3* gene through the two major linkage disequilibrium (LD) blocks of the HapMap Japanese (JPT) plus the Han Chinese (CHB) population. The rs17131450 SNP showing a significant association with SJS in the GWAS also showed a significant association ( $p < 0.01$ ) in our fine-mapping analysis. We also identified 5 other significantly associated ( $p < 0.01$ ) SNPs in *PTGER3* gene (rs5702, rs1325949, rs7543182, rs7555874, and rs4147114) (Ueta et al., 2010c). One of the 6 SNPs in *PTGER3* gene (rs5702) was in an exon as a silent SNP (sSNP), four (rs1325949, rs7543182, rs7555874, rs4147114) were in introns (iSNPs), and the remaining SNP (rs17131450) was a genome SNP (Ueta et al., 2010c). Lastly we assessed the association of the 6 SNPs by direct sequencing (Ueta et al., 2010c). A summary of our case-control analysis based on sequence data from 110 SJS patients and 220 control subjects is shown in Fig. 21. Based on our GWAS and direct sequencing analysis we identified 6 SNPs associated with SJS/TEN, 5 of these were located within the *PTGER3* gene (Ueta et al., 2010c).

Because EP3, which is the protein of *PTGER3* gene, is constitutively expressed in mouse conjunctival epithelial cells (Ueta et al., 2009a) we examined its expression in normal human conjunctival epithelial cells. RT-PCR assay showed that normal human conjunctival epithelial cells expressed *PTGER3* mRNA and immunohistochemistry disclosed the presence of EP3 protein (Ueta et al., 2010c, 2011d). When we looked for the expression of EP3 in the conjunctival epithelium of SJS/TEN patients with severe ocular surface complications we did not find EP3 protein. On the other hand, the protein was present in the control conjunctival epithelium from patients with conjunctivochalasis or pterygium (Ueta et al., 2010c, 2011d).

In support of the genetic association of *PTGER3* gene polymorphisms and SJS with severe ocular surface complications, we found that compared to the controls, the expression of EP3 protein

	Control (%) (N=220)	SJS/TEN (%) (N=110)	
<b>rs17131450</b>			
11 CC	193 (87.7)	84 (76.4)	CC vs CT+TT p=0.008 odds ratio 0.4
12 CT	26 (11.8)	20 (18.2)	TT vs CT+CC p=0.003 odds ratio 12.6
22 TT	1 (0.5)	6 (5.5)	T vs C p=0.00057 odds ratio 2.5
<b>rs5702</b>			
11 CC	108 (49.1)	72 (65.5)	CC vs CT+TT p=0.005 odds ratio 2.0
12 CT	95 (43.2)	28 (25.5)	C vs T p=0.04 odds ratio 1.5
22 TT	17 (7.7)	10 (9.1)	
<b>rs1325949</b>			
11 AA	104 (47.3)	76 (69.1)	AA vs AG+GG p=0.0002 odds ratio 2.5
12 AG	98 (44.5)	25 (22.7)	A vs G p=0.003 odds ratio 1.8
22 GG	18 (8.2)	9 (8.2)	
<b>rs7543182</b>			
11 GG	111 (50.5)	78 (70.9)	GG vs GT+TT p=0.0004 odds ratio 2.4
12 GT	94 (42.7)	23 (20.9)	G vs T p=0.0075 odds ratio 1.7
22 TT	15 (6.8)	9 (8.2)	
<b>rs7555874</b>			
11 GG	111 (50.5)	77 (70.0)	GG vs GA+AA p=0.0007 odds ratio 2.3
12 GA	94 (42.7)	24 (21.8)	G vs A p=0.01 odds ratio 1.7
22 AA	15 (6.8)	9 (8.2)	
<b>rs4147114</b>			
11 CC	53 (24.1)	48 (43.6)	CC vs CG+GG p=0.0003 odds ratio 2.4
12 CG	118 (53.6)	46 (41.8)	C vs G p=0.0009 odds ratio 1.8
22 GG	49 (22.3)	16 (14.5)	

**Fig. 21.** Association between *PTGER3* SNPs and SJS with severe ocular surface complications. Using the genome wide association study (GWAS) we found that 6 SNPs of the *PTGER3* gene were associated with SJS with severe ocular surface complications.

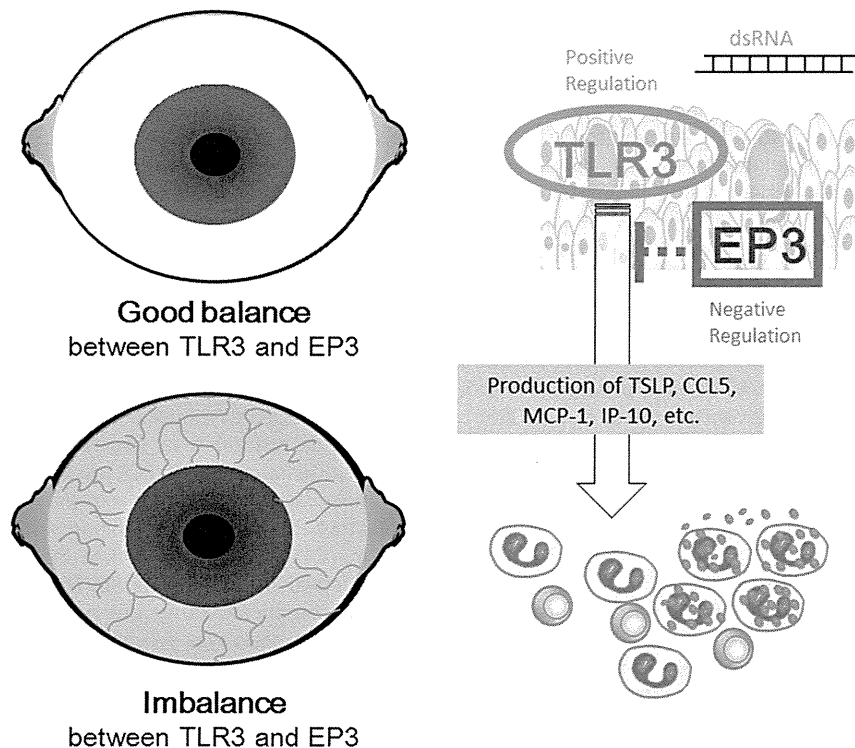
was greatly reduced in the conjunctival epithelium of these patients. This suggests that EP3 contributes functionally to the pathogenesis of SJS/TEN (Ueta et al., 2010c, 2011d).

Based on the finding that more than 75% of our SJS patients had used cold medications, possibly including NSAIDs, before the onset of their disease we posited that the observed *PTGER3* polymorphisms are associated with a NSAID-related susceptibility to SJS with severe ocular surface complications (Ueta et al., 2010c). Drugs are probably the most widely accepted etiologic factor for SJS (Roujeau et al., 1995); in fact, many patients who develop SJS with

severe ocular involvement do so after taking remedies for the common cold or NSAIDs, drugs that inhibit the production of the EP3 ligand, PGE<sub>2</sub>. This observation supports the hypothesis that EP3 is involved in the development of SJS with severe ocular surface involvement.

6.4.3. Interaction between the *TLR3* and the EP3

We reported that polymorphisms in *PTGER3*, the gene of EP3, were significantly associated with SJS with severe ocular surface complications (Ueta et al., 2010c), that PGE<sub>2</sub> is a ligand for EP3 in



**Fig. 22.** Lack of balance between *TLR3* and EP3 might trigger ocular surface inflammation.

the conjunctival epithelium, and that the PGE<sub>2</sub>-EP3 pathway down-regulates the progression of murine EAC (Ueta et al., 2009a). We also documented that TLR3 polymorphisms are associated with SJS (Ueta et al., 2007d), that the human ocular surface epithelium strongly expresses TLR3, and that cytokine production is up-regulated by polyI:C, a TLR3 ligand (Ueta, 2008; Ueta et al., 2005a; Ueta and Kinoshita, 2010a). Based on these findings we examined the function of EP3 in polyI:C-stimulated primary human conjunctival epithelial cells using an EP3 agonist. We found that the agonist significantly suppressed the production and mRNA expression of CCL5, CXCL10, CXCL11, IL-6, TSLP, and MCP-1 in polyI:C-stimulated primary human conjunctival epithelial cells, suggesting that cytokine production by conjunctival epithelial cells in response to polyI:C stimulation can be suppressed through the activation of EP3 (Ueta et al., 2011b, c; Ueta et al., 2012a).

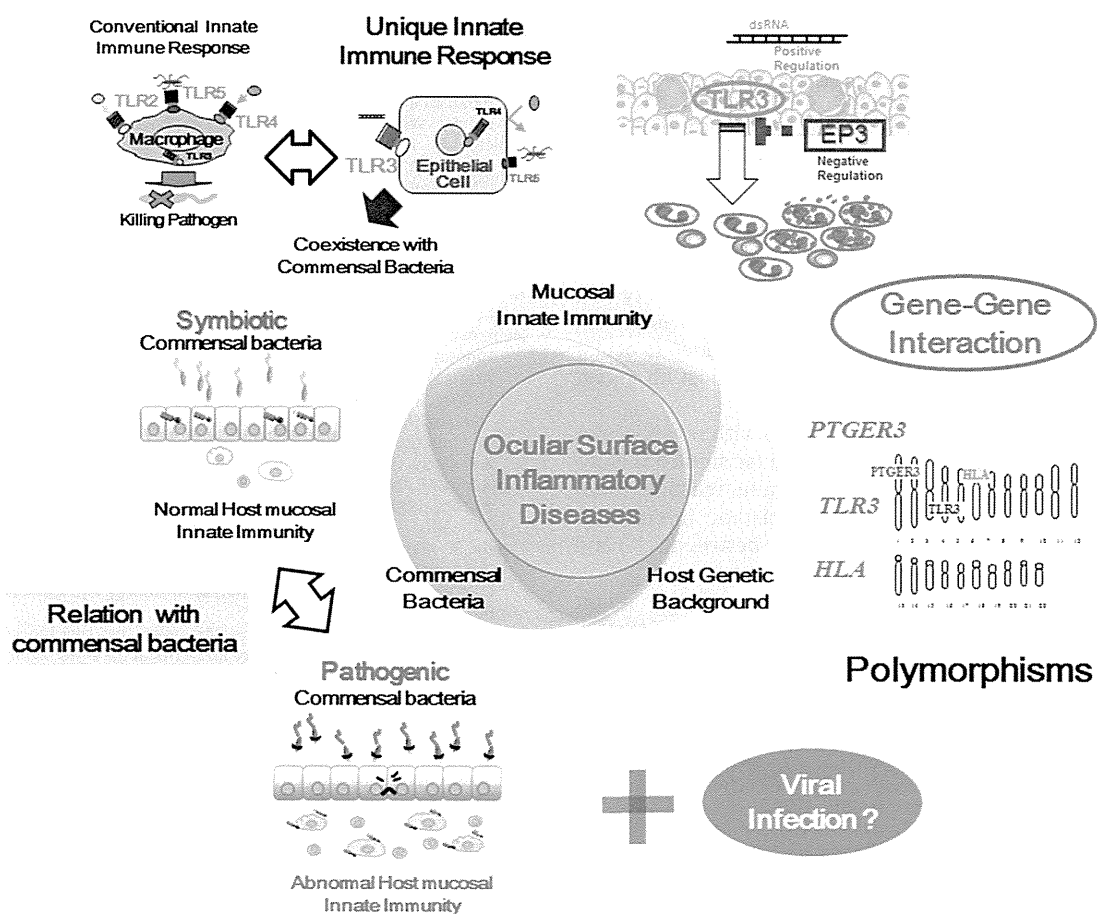
In the past decade, SNPs were widely used as genetic markers for identifying human disease-susceptibility genes. It is now apparent that gene–gene interactions should be considered in addition to major single-locus effects (Cordell, 2009). In particular, non-additive (epistatic) models for some complex diseases fit with actual observations, suggesting interactions involving multiple loci (Ritchie et al., 2001). We performed a statistical search for interactions between all possible pairs of loci by applying high-dimensional variable selection methods to the comprehensive dataset obtained from our previous studies that involved a total of 14 immune-related genes including *PTGER3* and *TLR3*. We found

a variable with susceptible effects on SJS; these effects were involved in locus-pairs of *PTGER3*-*TLR3*. The *PTGER3* rs.4147114G/C SNP and the *TLR3* rs.3775296T/T SNP exhibited a higher odds ratio (OR: 25.3,  $p = 0.000527$ ) than only *TLR3* rs.3775296T/T SNP (OR: 5.35,  $p = 0.00025$ ) or only *PTGER3* rs.4147114G/C SNP (OR: 2.66,  $p = 0.0023$ ) (Ueta et al., 2012b).

Next we focused on the epistatic interaction between *PTGER3* and *TLR3* and analyzed an additional 32 SNPs of *PTGER3* and 10 SNPs of *TLR3* (a total of 38 SNPs of *PTGER3* and 17 SNPs of *TLR3*). We found that besides the previously reported 6 *PTGER3*- and 2 *TLR3*-SNPs, 14 additional *PTGER3* SNPs and 5 additional *TLR3* SNPs were associated with SJS with severe ocular surface complications (Ueta et al., 2012b).

Elsewhere we showed that conjunctival eosinophilic infiltration in EAC was significantly more marked in EP3-KO mice (Ueta et al., 2009a) and significantly less marked in *TLR3*-KO mice than in wild-type mice (Ueta et al., 2009c). We also reported that in EP3/*TLR3*-DKO mice the number of eosinophils in the lamina propria mucosae of the conjunctiva was decreased to a level similar to that in *TLR3*-KO mice; it was significantly lower than in EP3-KO- and wild-type-mice (Ueta et al., 2012b). These findings suggest that in EAC, EP3 negatively regulates the eosinophilic infiltration induced by *TLR3* (Ueta et al., 2012b).

Thus, we provide evidence that there are functional interactions between *TLR3* and EP3 that exert susceptibility effects with respect to SJS with severe ocular surface complications and that the



**Fig. 23.** The presumed pathophysiological mechanism of the ocular surface inflammatory diseases. Ocular surface inflammatory diseases are involved with mucosal innate immunity, commensal bacteria, and host genetic background. Unique innate immune response of epithelial cells contributes to coexistence with commensal bacteria. The pathogenicity of commensal bacteria is influenced by the abnormal condition of host mucosal innate immunity. Host genetic background such as polymorphisms is involved with host mucosal innate immunity. Gene–gene interactions also contribute to pathobiological mechanisms of human ocular surface inflammatory diseases.

interactions are epistatic (Ueta et al., 2012b). Based on the findings discussed here we strongly suspect that the lack of balance between TLR3 and EP3 can trigger ocular surface inflammation (Fig. 22).

## 7. Conclusions and future directions

In this review we raise the possibility that some ocular surface inflammatory diseases are pathogenetically related with a disordered innate immune response.

Although the ocular surface epithelium is in constant contact with bacteria and bacterial products, the healthy ocular surface is not in an inflammatory state. The balance between the mucosal immunity of the ocular surface and the pathogenicity of bacteria is very important. We suspect that when the host mucosal immunity is normal, commensal bacteria are in a symbiotic relationship with their host, however, if the host mucosal immunity is abnormal, commensal bacteria may become pathogenic. Some ocular surface inflammatory diseases such as catarrhal ulcers and phlyctenular keratitis are considered to be hypersensitivity to bacteria.

We also showed that although immune-competent cells such as macrophages could recognize various microbial components through various TLRs, induce inflammation and then exclude the microbes, ocular surface epithelial cells can selectively respond to microbial components and induce limited inflammation. We suspect that the difference between ocular surface epithelial cells and macrophages lies in their dissimilarity with respect to their coexistence with commensal bacteria. The unique innate immune response machinery of the ocular surface epithelium may explain the permissive coexistence with commensal bacteria. We also document that human ocular surface epithelial cells can be induced upon stimulation with polyI:C, a ligand of TLR3, RIG-I and MDA-5, to express many transcripts including not only anti-viral innate immune response-related- but also allergy-related-genes.

We provided evidence that allergic eosinophilic infiltration of the conjunctiva can be regulated by conjunctival epithelial cells through EP3 and TLR3.

Our findings indicate that disordered innate immunity can induce ocular surface inflammation because mice in which I $\kappa$ B $\zeta$  was knocked out, expressly exhibited severe, spontaneous ocular surface inflammation with the eventual loss of almost all goblet cells.

Lastly we suggest that the pathogenesis of SJS with severe ocular surface complications, a devastating severe ocular surface inflammatory disease, is associated with innate immune reaction abnormalities, especially those related with the epistatic interactions between TLR3 and EP3. Thus, the lack of balance between TLR3 and EP3 might trigger ocular surface inflammation.

Focusing on the innate immunity of the ocular surface might help to elucidate the pathogenesis of various ocular surface diseases (Fig. 23).

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## Abbreviation

- PFGE: pulsed-field gel electrophoresis  
 TLRs: Toll-like receptors  
 IFN: interferon  
 IL: interleukin  
 TNF: tumor necrosis factor  
 PGN: peptidoglycan  
 ds: double-stranded  
 poly(I):C: polyinosine-polycytidylic acid  
 LPS: Lipopolysaccharide  
 CpG: deoxy-cytidylylate-phosphate-deoxy-guanylate  
 RT-PCR: reverse transcription-polymerase chain reaction  
 IP-10: IFN-gamma inducible protein 10  
 NLRs: nucleotide-binding oligomerization domain (NOD)-like receptors  
 RLRs: retinoic acid-inducible gene-1 (RIG-I)-like receptors  
 Mx2: myxovirus (influenza virus) resistance 2  
 Rsad2: radical S-adenosyl methionine domain containing 2  
 Cmpk2: cytidine monophosphate (UMP-CMP) kinase 2  
 Cxcl10: chemokine (C-X-C motif) ligand 10  
 Mx1: myxovirus (influenza virus) resistance 1  
 Irf44: interferon-induced protein 44  
 Irf203: interferon-activated gene 203  
 Irgp2: interferon-inducible GTPase 2  
 Rtp4: receptor transporter protein 4  
 TSLP: thymic stromal lymphopoietin  
 PG: prostaglandin  
 TX: thromboxane  
 SJS: Stevens-Johnson syndrome  
 TEN: toxic epidermal necrolysis  
 NSAIDs: non-steroidal anti-inflammatory drugs

## RESEARCH LETTERS

### Downregulation of Monocyte Chemoattractant Protein 1 Expression by Prostaglandin E<sub>2</sub> in Human Ocular Surface Epithelium

Elsewhere, we reported that in the tears and serum of patients with acute-stage Stevens-Johnson syndrome or toxic epidermal necrolysis, the levels of interleukin 6 (IL-6), IL-8, and monocyte chemoattractant protein 1 (MCP-1) were dramatically increased.<sup>1</sup> We also reported that Stevens-Johnson syndrome or toxic epidermal necrolysis with severe ocular complications was associated with polymorphism of the prostaglandin E receptor 3 (EP<sub>3</sub>) gene (*PTGER3*).<sup>2</sup>

Prostanoids are a group of lipid mediators that form in response to various stimuli. They include prostaglandin D<sub>2</sub> (PGD<sub>2</sub>), PGE<sub>2</sub>, PGF<sub>2α</sub>, PGI<sub>2</sub>, and thromboxane A<sub>2</sub>. There are 4 subtypes of the PGE receptor: EP<sub>1</sub>, EP<sub>2</sub>, EP<sub>3</sub>, and EP<sub>4</sub>. We previously reported that PGE<sub>2</sub> suppresses polyinosine–polycytidylic acid (polyI:C)–stimulated cytokine production via EP<sub>2</sub> and/or EP<sub>3</sub> in human ocular surface epithelial cells.<sup>3,4</sup> PolyI:C is a ligand of Toll-like receptor 3, which is strongly expressed in ocular surface epithelium.<sup>5</sup> We found that PGE<sub>2</sub> suppresses the production of IL-6, chemokine (C-X-C motif) ligand 10, chemokine (C-X-C motif) ligand 11, and chemokine (C-C motif) ligand 5 but not IL-8 by epithelial cells on the human ocular surface<sup>3</sup>; it remains to be determined whether it also suppresses MCP-1 production. Monocyte chemoattractant protein 1 plays a significant role in the recruitment of monocytes and lymphocytes to the site of cellular immune reactions. In this study, we investigated whether PGE<sub>2</sub> downregulates polyI:C-induced MCP-1 production.

All experiments were conducted in accordance with the principles set forth in the Declaration of Helsinki. Enzyme-linked immunosorbent assay and quantitative real-time polymerase chain reaction were performed with primary human conjunctival epithelial cells and immortalized human corneal epithelial cells using previously described methods (eAppendix, <http://www.archophthalmol.com>).<sup>3</sup>

First, we examined whether PGE<sub>2</sub> downregulated the production and messenger RNA (mRNA) expression of MCP-1 induced by polyI:C stimulation in human conjunctival and corneal epithelial cells. We found that it significantly attenuated the production of MCP-1 (**Figure A**). Quantitative real-time polymerase chain reaction confirmed that the mRNA expression of MCP-1 was significantly downregulated by PGE<sub>2</sub> (**Figure A**).

Next, we examined which PGE<sub>2</sub> receptor(s) contributed to the downregulation of polyI:C-induced MCP-1. We used the EP<sub>2</sub> agonist ONO-AE-259, the EP<sub>3</sub> agonist ONO-AE-248, and the EP<sub>4</sub> agonist ONO-AE-329. Enzyme-linked immunosorbent assay showed that the EP<sub>2</sub> and EP<sub>3</sub> agonists significantly suppressed the polyI:C-induced production of MCP-1, while the EP<sub>4</sub> agonist did not exert suppression (**Figure B**). Quantitative real-time polymerase chain reaction confirmed that the EP<sub>2</sub> and EP<sub>3</sub> agonists significantly downregulated the mRNA expression of MCP-1 (**Figure C**). Thus, our results document that PGE<sub>2</sub> attenuated the mRNA expression and production of MCP-1 via both EP<sub>2</sub> and EP<sub>3</sub>.

In human macrophages, PGE<sub>2</sub> attenuated the lipopolysaccharide-induced mRNA and protein expression of chemokines including MCP-1 through EP<sub>4</sub>.<sup>6</sup> On the other hand, we demonstrated that in human ocular surface epithelial cells, PGE<sub>2</sub> attenuated the polyI:C-induced mRNA and protein expression of MCP-1 through EP<sub>2</sub> and EP<sub>3</sub> but not EP<sub>4</sub>. Our findings suggest that EP<sub>2</sub> and EP<sub>3</sub> play important roles in the regulation of inflammation in epithelial cells, while EP<sub>2</sub> and EP<sub>4</sub> have important roles in immune cells such as macrophages.

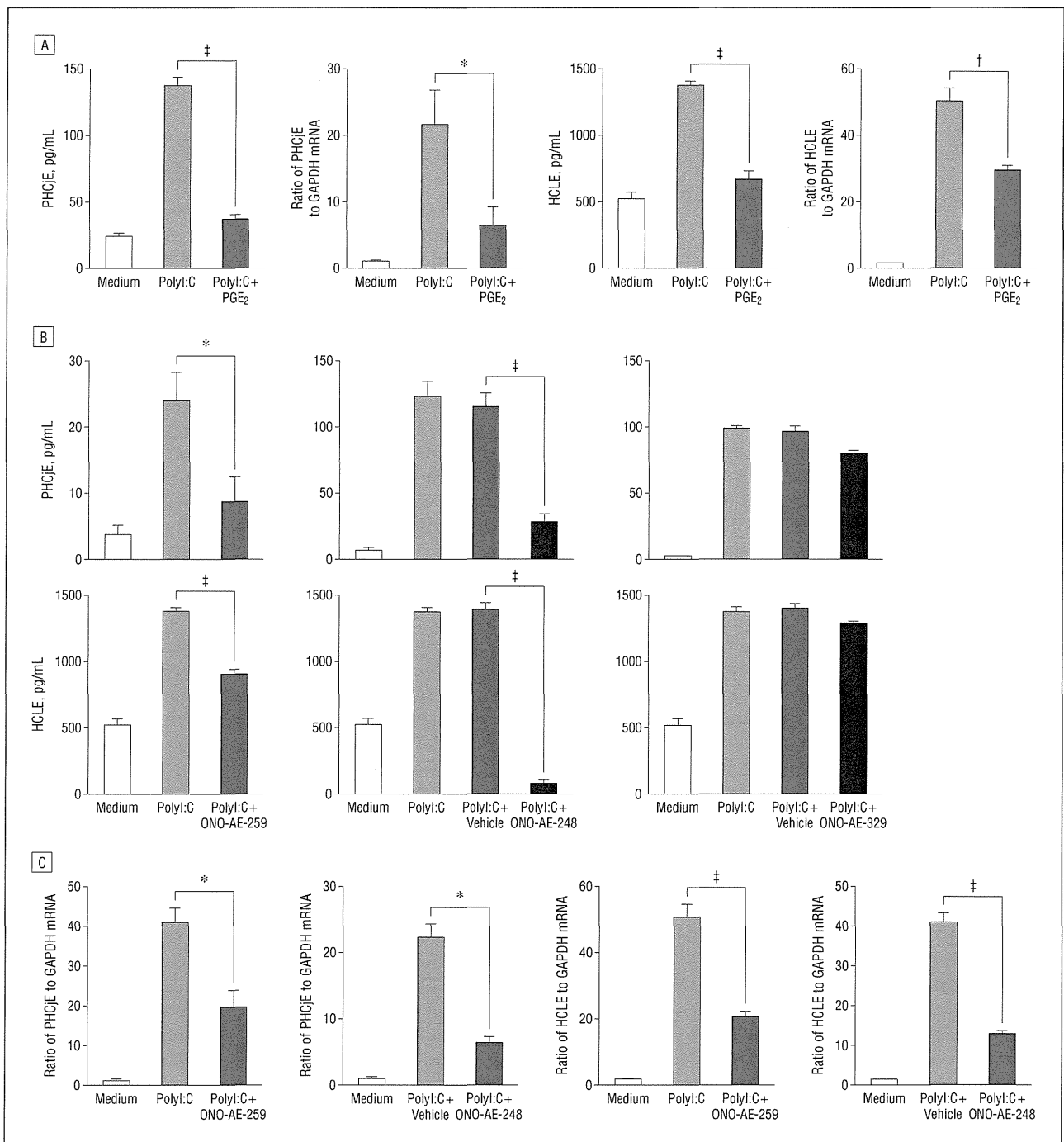
In the tears and serum of patients with acute-stage Stevens-Johnson syndrome or toxic epidermal necrolysis, the levels of IL-6, IL-8, and MCP-1 were dramatically increased.<sup>1</sup> Although IL-8 was not regulated by PGE<sub>2</sub>, IL-6 was regulated by PGE<sub>2</sub> via EP<sub>3</sub> in human ocular surface epithelial cells.<sup>3</sup> Herein, we demonstrated that MCP-1 could be regulated by PGE<sub>2</sub> via EP<sub>2</sub> and EP<sub>3</sub>. The regulation of cytokine production by PGE<sub>2</sub> may be associated with the pathogenesis of Stevens-Johnson syndrome or toxic epidermal necrolysis with severe ocular complications because it was associated with polymorphism of the EP<sub>3</sub> gene (*PTGER3*), one of the PGE receptors (EP<sub>1</sub>, EP<sub>2</sub>, EP<sub>3</sub>, EP<sub>4</sub>).<sup>2</sup>

In summary, our results show that MCP-1 produced by human ocular surface epithelial cells could be downregulated by PGE<sub>2</sub> via EP<sub>2</sub> and EP<sub>3</sub>.

Mayumi Ueta, MD, PhD  
Chie Sotozono, MD, PhD  
Norihiro Yokoi, MD, PhD  
Shigeru Kinoshita, MD, PhD

**Author Affiliations:** Research Center for Inflammation and Regenerative Medicine, Faculty of Life and Medical Sciences, Doshisha University (Dr Ueta) and Department of Ophthalmology, Kyoto Prefectural University of Medicine (Drs Ueta, Sotozono, Yokoi, and Kinoshita), Kyoto, Japan.

**Correspondence:** Dr Ueta, Department of Ophthalmology, Kyoto Prefectural University of Medicine, 465 Ka-



**Figure.** Prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) attenuated the messenger RNA (mRNA) expression and production of monocyte chemoattractant protein 1 via both prostaglandin E receptor 2 (EP<sub>2</sub>) and EP<sub>3</sub>. A, Primary human conjunctival epithelial cells (PHCjE) and human corneal-limbal epithelial cells (HCLE) were exposed to 10 μg/mL of polyinosine–polycytidylic acid (polyI:C) and 100 μg/mL of PGE<sub>2</sub> for 24 hours (enzyme-linked immunosorbent assay) or 6 hours (quantitative real-time polymerase chain reaction). GAPDH indicates glyceraldehyde-3-phosphate dehydrogenase. B and C, The PHCjE and HCLE were exposed to 10 μg/mL of polyI:C and 10 μg/mL of the EP<sub>2</sub>, EP<sub>3</sub>, or EP<sub>4</sub> agonist for 24 hours (enzyme-linked immunosorbent assay) (B) or 6 hours (quantitative real-time polymerase chain reaction) (C). Data are representative of 3 separate experiments and are given as the mean (SEM) from 1 experiment carried out in 6 to 8 wells (enzyme-linked immunosorbent assay) (B) or 4 to 6 wells (quantitative real-time polymerase chain reaction) (C) per group. \**P* < .05; †*P* < .005; ‡*P* < .001.

jiicho, Hirokoji, Kawaramachi, Kamigyoku, Kyoto 602-0841, Japan (mueta@koto.kpu-m.ac.jp).

**Author Contributions:** Dr Ueta had full access to all of the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

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**Online-Only Material:** The eAppendix is available at <http://www.archophthalmol.com>.

**Additional Contributions:** Chikako Endo provided technical assistance.

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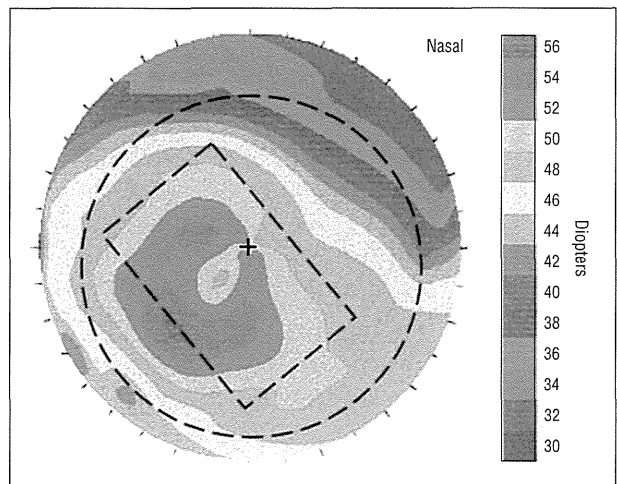
### Depth Profile Study of Abnormal Collagen Orientation in Keratoconus Corneas

In a previous study,<sup>1</sup> we used femtosecond laser technology to cut ex vivo human corneas into anterior, mid, and posterior sections, after which x-ray scatter patterns were obtained at fine intervals over each specimen. Data analysis revealed the predominant orientation of collagen at each sampling site, which was assembled to show the variation in collagen orientation between central and peripheral regions of the cornea and as a function of tissue depth. We hypothesized that the predominantly orthogonal arrangement of collagen (directed toward opposing sets of rectus muscles) in the mid and posterior stroma may help to distribute strain in the cornea by allowing it to withstand the pull of the extraocular muscles. It was also suggested that the more isotropic arrangement in the anterior stroma may play a role in tissue biomechanics by resisting intraocular pressure while at the same time maintaining corneal curvature. This article, in conjunction with our findings of abnormal collagen orientation in full-thickness keratoconus corneas,<sup>2,3</sup> received a great deal of interest from the scientific community and prompted the following question: how does collagen orientation change as a function of tissue depth when the anterior curvature of the cornea is abnormal, as in keratoconus? Herein, we report findings from our investigation aimed at answering this question.

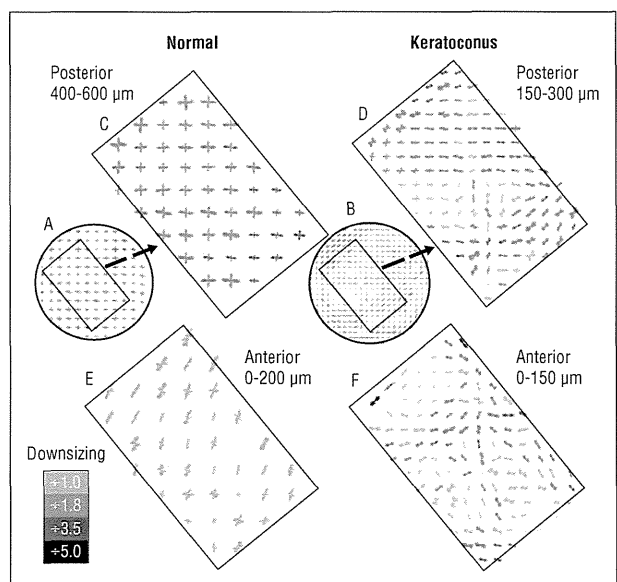
**Methods.** The Baron chamber used in our previous study<sup>1</sup> was adapted to enable corneal buttons to be clamped in place and inflated (by pumping physiological saline into the posterior compartment) to restore their natural curvature. A button diameter of 8 mm or larger was deemed necessary to ensure tissue stability during this process.

The next step, obtaining fresh, full-thickness, keratoconus buttons of sufficient diameter, proved to be problematic owing to the increasing popularity of deep anterior lamellar keratoplasty. Recently, however, the

opportunity arose to examine an 8-mm full-thickness (300-340  $\mu\text{m}$  minus epithelium) keratoconus corneal button with some central scarring and a mean power greater than 51.8 diopters (**Figure 1**). The tissue was obtained in accordance with the tenets of the Declaration of Helsinki and with full informed consent from a 31-year-old patient at the time of penetrating keratoplasty. Using techniques detailed previously,<sup>1</sup> the corneal button was clamped in the chamber and inflated. The central 6.3-mm region of the button was then flattened by the applanation cone and a single cut was made at a depth of 150  $\mu\text{m}$  from the surface using an IntraLase 60-kHz femtosecond laser (Abbott Medical Optics Inc),<sup>1</sup> thus splitting the cornea into anterior and posterior sections of roughly equal thickness. Wide-angle x-ray scattering patterns were collected at 0.25-mm intervals over each cor-



**Figure 1.** Corneal topography of the keratoconus cornea (recorded 12 years previously).<sup>3</sup> The broken lines show the 6.3-mm region of the cornea cut with the femtosecond laser (circle) and the region of greatest corneal steepening depicted in Figure 2 (rectangle).



**Figure 2.** Collagen orientation in the normal (A) and keratoconus (B) posterior stroma (central 6.3 mm). The highlighted regions of the posterior (C and D) and anterior (E and F) stroma are expanded. Large vector plots showing high collagen alignment are downsized (key).

