

Tertiary lymphoid tissue develops during normal aging in mice and humans

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One Sentence Summary: Mice develop bladder tertiary lymphoid tissue (bTLT) during aging that is dependent on TNF α and independent of urinary tract infection.

1 **ABSTRACT**

2 Aging has multifaceted effects on the immune system in the context of systemic responses
3 to specific vaccines and pathogens, but how aging affects tissue-specific immunity is not well-
4 defined. Chronic bladder inflammation is highly prevalent in older women, but mechanisms by
5 which aging promotes these pathologies remain unknown. Here we report distinct, age-
6 associated changes to the immune compartment in the otherwise normal female (but not in male)
7 mouse urinary bladder and parallel changes in older women with chronic bladder inflammation.
8 In aged mice, the bladder epithelium became more permeable, and the homeostatic immune
9 landscape shifted from a limited, innate immune-predominant surveillance to an inflammatory,
10 adaptive immune-predominant environment. Strikingly, lymphoid cells were organized into tertiary
11 lymphoid tissues, hereafter named bladder tertiary lymphoid tissue (bTLT). Analogous bTLTs
12 were found in older women, many of whom had a history of recurrent urinary tract infection (UTI).
13 Aged mice responded poorly to experimental UTI, experiencing spontaneous recurrences at
14 higher rates than young mice. However, bTLT formation was dependent on aging and
15 independent of infection. Furthermore, bTLTs in aged mice played a role in *de novo* antibody
16 responses and urinary IgA production by recruitment of naive B cells that form germinal centers
17 and mature into IgA-secreting plasma cells. Finally, TNF α was a key driver of bTLT formation, as
18 aged TNF $\alpha^{-/-}$ mice lacked bTLTs. Both aged TNF $\alpha^{-/-}$ and wild type mice exhibited increased
19 bladder permeability, suggesting that epithelial dysfunction may be an upstream mediator of
20 chronic, age-associated bladder inflammation. Thus, bTLTs arise as a function of age and may
21 underlie chronic, age-associated bladder inflammation. Our model establishes a platform for
22 further investigation of age-association tissue inflammation and translation to new treatment
23 strategies.

24 INTRODUCTION

25 Immune dysfunction during aging is characterized by chronic, low-grade inflammation
26 coupled with ineffective responses to pathogens. Aging is also the strongest risk-factor for
27 numerous chronic diseases, including cardiovascular disease, neurodegeneration, osteoarthritis,
28 and cancers. While these diseases are all linked by chronic inflammation, immune responses vary
29 by tissue, resulting in tissue-specific inflammation and dysfunction. Older women (50+) are highly
30 susceptible to bladder disorders including overactive bladder/urge incontinence (OAB), interstitial
31 cystitis/bladder pain syndrome (IC/BPS), and recurrent urinary tract infections (rUTIs) (1-5).
32 These disorders all have a chronic inflammatory component as well as overlapping symptoms,
33 known as lower urinary tract symptoms (6, 7). How and why bladder disorders and bladder
34 inflammation become more prevalent with aging is not currently understood (8). Since aging is
35 characterized by chronic, low-grade systemic inflammation, termed inflamm-aging (9), the
36 common association of bladder disorders with both aging and chronic inflammation suggests that
37 an underlying driver of pathology may be age-associated inflammation (10, 11).

38 The bladder is a storage organ with a mucosal barrier that provides protection from both
39 urinary wastes and pathogens (12, 13). In contrast to the epithelial barriers of other mucosal
40 tissues, such as the intestinal epithelium, the multi-layered bladder epithelium (known as the
41 urothelium) must be watertight and highly impermeable to solutes, metabolites, and toxic wastes
42 present in the urine (13). Large superficial facet cells, the outer layer of the urothelium, form this
43 barrier via synthesis of surface uroplakins and tight junctions that limit exposure of the underlying
44 cells to urine. These superficial cells also have cell-autonomous defenses such as exfoliation and
45 rapid regeneration in response to injury or infection (12, 14). Other epithelial barriers, including
46 the intestine, lung, and eye, exhibit increased permeability with aging that is thought to stimulate
47 age-associated inflammation (15, 16). In the bladder, disruption or dysfunction of the urothelial
48 barrier leads to chronic inflammation and disorders such as IC/BPS and rUTIs (7, 14, 17). Whether
49 urothelial barrier function is affected by aging is not known.

50 In contrast to other mucosal tissues, the bladder contains a relatively sparse repertoire of
51 resident and patrolling immune cells (12, 18). During homeostasis, bladder immune cells consist
52 of ~70% antigen-presenting macrophages and dendritic cells, ~10% T cells, and smaller numbers
53 of NK cells, mast cells, eosinophils, and patrolling monocytes (19, 20). The bladder lacks
54 dedicated mucosal secondary lymphoid organs (SLOs) that form during development like the
55 Peyer's patches of the small intestine. However, non-lymphoid tissues may form ectopic SLO-like
56 structures, known as tertiary lymphoid tissues (TLTs), in response to chronic inflammation and
57 antigen exposure (21, 22). Aging affects the size, presence, and functionality of TLTs in several
58 tissues (23-26). For example, isolated lymphoid follicles (intestinal TLT) in aged mice have altered
59 cellular compositions and produce more IgA compared to young mice (27), and inducible
60 bronchus-associated lymphoid tissue (lung TLT) forms more robustly in response to cigarette
61 smoke in aged mice compared to young mice (28). Whether aging affects immunity in the bladder
62 mucosa is not known. Since both infectious and non-infectious chronic bladder inflammation is
63 highly prevalent in older women, age-associated disruption of immune homeostasis in the bladder
64 may mediate inflammatory pathology and lower urinary tract symptoms.

65 Here, we report that bladders from aged mice exhibit transcriptional signatures enriched
66 in immune-mediated responses and a cellular repertoire skewed towards an expansion of
67 lymphoid populations relative to bladders from young mice. Furthermore, we identify lymphoid
68 cells organized into TLTs that we term bladder tertiary lymphoid tissues (bTLTs). bTLTs are found
69 predominantly in females and analogous bTLTs are found in bladders of older women, many of
70 whom had a history of rUTI. While aged mice similarly have a higher frequency of UTI recurrences
71 than young mice, we demonstrate that bTLT form in an age-dependent manner that is
72 independent of infection. We further demonstrate that bTLTs are capable of producing IgA⁺
73 plasma cells that form within germinal centers and secrete IgA into the urine. Moreover, we
74 identify that TNF α is a major driver of bTLT formation, as TNF α -deficient mice lack bTLTs at any
75 age. Finally, both aged wild type (WT) and TNF α ^{-/-} mice have increased urothelial permeability.

76 Thus, age-dependent TNF α responses to urothelial barrier dysfunction may ultimately drive
77 chronic inflammation resulting in organized bTLTs in elderly women.

78

79 **RESULTS**

80 *Adaptive immune networks distinguish bladders of aged mice from those of young mice*

81 Since chronic, age-related bladder inflammation primarily affects women, we assessed
82 how aging affects the global environment of the female bladder by performing RNA-sequencing
83 on bladder tissue from young (3-4 month [mo]) and aged (18-22 mo) female mice. Compared to
84 the transcriptome of bladders from young mice, bladders from aged mice had at least a 2-fold
85 (FDR-adjusted $P < 0.05$) increase in expression of 417 genes and decrease in expression of 59
86 genes (**Fig. 1A**). We then performed gene set enrichment analysis using the KEGG pathway
87 database and identified 13 up-regulated pathways and 1 down-regulated pathway enriched in the
88 bladder transcriptome of aged mice compared to those of young mice (**Fig. 1B**). Notably, the up-
89 regulated pathways included B- and T-cell receptor signaling, antigen presentation, and IgA
90 production pathways (**Fig. 1B**), which strongly suggested that the predominant age-associated
91 changes to the bladder were immune-mediated responses.

92 To determine if there were corresponding changes on a cellular level, we examined the
93 immune compartment of bladders from young and aged mice by flow cytometry. Aged mice had
94 higher numbers of immune cells in their bladders than young mice (**Fig. 1C**). Since macrophages
95 are usually the largest immune cell population in the bladder and act as key sentinels that respond
96 to infection and injury (19, 20, 29, 30), we examined whether bladder macrophages in aged mice
97 differ from those in young mice. Despite the overall increase in immune cell numbers, there was
98 a surprising decrease in the frequency of F4/80⁺CD64⁺ macrophages in bladders from aged mice
99 compared to those from young mice (**Fig. 1D**). While the majority of bladder macrophages from
100 both young and aged mice were the resident, Ly6C⁻ type, bladders from aged mice had a higher
101 frequency of Ly6C⁺ macrophages, which are inflammatory monocyte-derived macrophages

102 recently infiltrated into the tissue (**Fig. 1E**) (19, 20, 31). Since macrophages were no longer the
103 predominant immune cell within the bladders of aged mice, we searched for expanded numbers
104 of other immune cell types. Examining the lymphoid compartment, we found that bladders from
105 aged mice were comprised of higher frequencies of T cells compared to those from young mice
106 (**Fig. 1F**). Among both total immune cells and total T cells, bladders from aged mice had higher
107 frequencies of CD4⁺ and CD8⁺ T cells than young mice (**Fig. 1G, S1**). Furthermore, the ratio of
108 CD4⁺ T cells to CD8⁺ T cells was lower in aged mice than in young mice (**Fig. 1H**); this shift
109 towards increased numbers of CD8⁺ T cells is a characteristic feature of age-associated
110 inflammation, suggesting that the bladder mucosa may be affected by inflamm-aging (32).
111 Whereas B cells are essentially absent in bladders from young mice, there was a substantial
112 number of CD19⁺ B cells in bladders from aged mice (**Fig. 1I**). Thus, in aged mice, the expansion
113 of lymphocytes displaces macrophages as the predominant immune cell within bladder tissue and
114 may be a sign of age-associated inflammation in the bladder.

115

116 *Lymphocytes organize into tertiary lymphoid tissues in bladders of aged female mice and older* 117 *women*

118 Since bladder tissue differs between sexes, and females are known to develop more
119 pronounced inflammatory phenotypes with age, we examined bladder tissue from young and
120 aged mice of both sexes to localize the expanded lymphoid compartment observed by flow
121 cytometry. Surprisingly, lymphoid cells in bladders from aged female mice were concentrated in
122 large, dense aggregates throughout the bladder (**Fig. 2A**); in contrast, bladders from aged male
123 mice rarely contained these structures and did not exhibit signs of tissue inflammation (**Fig. S2**).
124 These findings mirror the epidemiology of chronic bladder inflammation; OAB, IC/BPS, and rUTIs
125 are highly prevalent among older women and rarely found in older men. Since bladders from aged
126 female mice, but not those from aged male mice, exhibited a dramatic inflammatory phenotype,

127 we further studied age-associated inflammation in the female bladder as a model of what is seen
128 in human populations.

129 The morphologic feature of the lymphoid infiltrates found in aged female bladders and the
130 altered cell populations observed by flow cytometry (**Fig. 1F-I**) suggested that bladders from aged
131 mice may contain tertiary lymphoid tissues (TLTs), which resemble the composition and structure
132 of the secondary lymphoid organs (SLOs), but form ectopically in chronically inflamed tissues (21,
133 22). Nearly all of the B and T cells were localized to the lymphoid aggregates by
134 immunofluorescence (**Fig. 2B**). B and T cells were segregated into distinct zones, forming an
135 organized structure characteristic of TLTs. Other structural features of TLTs that are otherwise
136 only found in dedicated lymphoid tissues include specialized high endothelial venules (HEVs),
137 which permit the extravasation of migrating naive lymphocytes, and follicular dendritic cell (FDC)
138 networks, which support the formation and maintenance of the B cell follicle by secretion of
139 chemokines and capture of antibody via complement receptors (33, 34). We identified both HEVs,
140 marked by co-expression of platelet endothelial cell adhesion molecule (PECAM; CD31⁺) and
141 peripheral node addressin (PNAd⁺), and FDC networks, marked by complement receptor 1 (CR1;
142 CD35^{hi}), within large lymphoid aggregates (**Fig. 2C-D**), indicating that bladders from aged female
143 mice contained *bone fide* TLTs. Together, our data demonstrate that B and T cells in bladders
144 from aged mice localize to distinct aggregates with the organization and specialized structures
145 characteristic of TLTs. Hereafter, these structures are termed bladder tertiary lymphoid tissues
146 (bTLTs).

147 Small clinical case series occasionally report lymphoid aggregates or follicles in the
148 bladder (35-37), but their relation to aging and outcome of chronic bladder inflammation remains
149 unknown. Small, raised, reddish-yellow nodules can be grossly visualized by bladder endoscopy
150 (cystoscopy) in some women with chronic bladder inflammation (**Fig. 2E**) (39); however, the
151 significance of these nodules is not clear. Since aging is associated with high rates of chronic
152 bladder inflammation in women, we sought to determine if bTLTs could be found in symptomatic

153 women undergoing cystoscopy with possible biopsy. Since chronic bladder inflammation is most
154 prevalent in older women, we hypothesized that these nodules are similar to bTLTs found in aged
155 mice. Thirteen women with nodular lesions visualized by cystoscopy (**Fig. 2E**) were biopsied for
156 pathologic diagnosis. Eleven of the 13 biopsies were read by a clinical pathologist and reported
157 to have chronic inflammation with no malignant or pre-malignant changes. Furthermore, 7 of the
158 11 (64%) biopsies were noted in pathology reports to contain distinct lymphoid follicles in the
159 lamina propria (**Fig. 2F**). Since some biopsies were too small to identify distinct lymphoid follicles
160 by routine histology, we further analyzed separate biopsies obtained simultaneously for research.
161 In biopsies from 12 of the 13 patients (92%), we identified distinct B and T cell organization (**Fig.**
162 **2G**) and FDC networks within follicles (**Fig. 2H**) similar to bTLTs found in aged mice. Since
163 biopsies of healthy bladder tissue or bladders without visible lesions are not clinically indicated, it
164 is impossible to determine if aging alone plays a role in the formation or enlargement of bTLTs
165 from our cohort; however, it is notable that the median age of the patients with bladder biopsies
166 was 64 years old (range 27-87). Women could develop bTLTs as a consequence of aging or may
167 be predisposed to developing grossly-visible bTLTs in response to chronic bladder inflammation
168 caused by rUTIs, IC/BPS, or OAB. Considering the striking similarity of bTLTs found in older
169 women and aged mice, they may share underlying molecular drivers that could be further
170 elucidated in this mouse model.

171

172 *Aged mice are susceptible to recurrent UTIs, but bTLTs form independent of infection*

173 Ten out of the 13 women with bladder biopsies reported a history of recurrent UTIs (rUTIs),
174 defined as at least 2 culture-positive UTIs in the past 6 months or 3 culture-positive UTIs in the
175 past year. However, since biopsies are taken when there is not an acute infection, bTLTs in these
176 patients represent a long-term inflammatory response in the bladder. In mice, chronic bladder
177 inflammation can result in long-term changes to the mucosa that predisposes to further infections
178 (38, 40, 41); thus we hypothesized that age-associated bTLTs may be associated with increased

179 susceptibility to rUTIs. To determine if aged mice with bTLTs were similarly susceptible to rUTIs,
180 we infected young and aged mice with uropathogenic *E. coli* and monitored urine bacterial titers
181 over 14 days post infection (dpi). Young and aged mice were equally infected, as determined by
182 urine bacterial titers at 6 hours post infection (**Fig. S3**). Over the first 3 dpi, young and aged mice
183 cleared UPEC from their urine at equal rates; however, similar to older women, aged mice had
184 more spontaneous recurrences of bacteriuria than young mice between 7 and 14 dpi (**Fig. 2I**).
185 Histologically examining the bladders from aged mice, we found no difference in the proportion of
186 mice that had bTLTs before and after infection (84% uninfected vs. 76% infected, $p=0.5854$, **Fig.**
187 **2J**). These findings suggested that, while aged mice are more susceptible to recurrent UTIs than
188 young mice, bTLTs likely form due to age-associated inflammation rather than infection-induced
189 inflammation. To determine when during the lifespan bTLT form in mice, we examined bladders
190 from mice ranging from 3 to 24 mo of age. While no bTLTs (well-defined aggregates $\geq 10^4 \mu\text{m}^2$)
191 were found in mice 6 mo or younger, bTLTs were found in bladders beginning at 9 mo, and nearly
192 all bladders contained bTLTs by 15 mo (**Fig. 2K**). While the number of bTLTs found in the bladder
193 increased over time, the average size of each individual bTLT not significantly (**Fig. S3**). Thus, in
194 mice, bTLTs form during normal aging beginning around 9 mo of age and increase in number,
195 but not size, over time.

196

197 *bTLTs contain germinal centers that support local B cell maturation and IgA production*

198 In SLOs, the homeostatic lymphoid chemokines CXCL12, CXCL13, CCL19, and CCL21
199 attract naïve lymphocytes and organize their characteristic follicular structure (34, 42, 43). Ectopic
200 expression of one or more of these chemokines is sufficient to induce TLTs in a permissive tissue
201 environment (44, 45). Given that bTLTs are found in bladders from aged mice, we anticipated that
202 one or more of the homeostatic chemokines may be acting in the bladder. Indeed, *Cxcl13* was
203 identified by RNA-seq as one of the most highly upregulated genes (17.8-fold change, FDR-
204 adjusted $P=0.0125$) in bladders from aged mice. Consistent with TLTs found in other mucosal

205 tissues, both *Cxcl13* (13.2-fold change) and *Ccl19* (10-fold change) were both highly upregulated
206 in bladders from aged mice compared to those of young mice, as measured by qRT-PCR (**Fig.**
207 **3A**). *Cxcl12* and *Ccl21* expression were not higher in bladders from aged mice (**Fig. S4**). Since
208 these chemokines use overlapping receptors and have some functional redundancies, it is
209 possible that CXCL13 and CCL19 are sufficient to recruit and organize bTLTs in aged mice while
210 CXCL12 and CCL21 are dispensable (42, 43).

211 Since the homeostatic chemokines recruit naïve B and T cells to SLOs and TLTs, we
212 hypothesized that bTLTs recruited naïve lymphocytes and generated *in situ* adaptive immune
213 responses (46, 47). The majority of B cells within bTLTs stained positive for the naïve B cell
214 marker IgD (**Fig. 3B**). After activation via antigen recognition, B cells may form germinal centers
215 (GCs) within follicles, where they undergo somatic hypermutation, affinity maturation, and class
216 switch recombination (48). If this were the case in the bladder, we would anticipate evidence of
217 multiple isotypes of immunoglobulin (Ig) heavy chains. Indeed, RNA-seq analysis of bladders from
218 young and aged mice revealed that the most highly upregulated genes in aged bladders were Ig
219 constant genes, with IgM and IgA being the most significantly-upregulated (**Fig. 3C**). Since IgA is
220 a class-switched isotype that is often produced in mucosal lymphoid tissues, we hypothesized
221 that bTLTs supported local GCs that produce IgA-secreting plasma cells. Locally active GCs were
222 identified within bTLTs by the highly-specific GC marker GL-7 (**Fig. 3D**), and CD138⁺IgA⁺ plasma
223 cells were found localized to the edges of bTLTs (**Fig. 3E**). Furthermore, aged mice had 10-fold
224 higher urine IgA concentrations than young mice (**Fig. 3F**), suggesting a role for bTLT in urinary
225 IgA production. To determine if the increase in urine IgA was locally produced in the bladder, we
226 cultured bladders from young and aged mice *ex vivo*. Bladders from aged mice secreted over 45
227 ng/mL more IgA than bladders from young mice (**Fig. 3G**), indicating that the increase in urine
228 IgA was likely due to increased local production and secretion. The frequency of plasma cells in
229 bladders from aged mice was also higher than those from young mice by flow cytometry (**Fig.**
230 **3H**), and IgA⁺ plasma cells were primarily localized to bTLT (**Fig. 3E**). These data further support

231 a role for bTLTs in aged mice play in the local antibody responses and IgA production that is
232 transported across the urothelium into the urine.

233

234 *Aging impairs urothelial barrier function and requires TNF α for bTLT formation*

235 Both animal and human studies demonstrate an age-dependent loss of epithelial integrity
236 in the gastrointestinal tract, lung, eye, and skin (15). Given the urothelium's distinct role as a
237 water- and solute-tight barrier to urinary wastes (13, 49), we hypothesized that aging impairs
238 urothelial barrier integrity, which could stimulate chronic inflammation and bTLT formation in
239 bladders from aged mice and older women. To test this hypothesis, we transurethrally instilled
240 FITC-dextran into the bladders of young and aged mice (50). In bladders from both young and
241 aged mice, FITC-dextran accumulated in the outermost, superficial urothelial cells (**Fig. 4A, white**
242 **arrowheads**) that exclude urinary contents from underlying urothelial cells and tissue. However,
243 FITC-dextran also penetrated into the intermediate and basal urothelial layers (**Fig. 4A, red**
244 **arrows**) in aged mice but not in young mice. Furthermore, fluorescence from FITC-dextran that
245 had been absorbed through the urothelial basement membrane was higher in aged mice than in
246 young mice (**Fig. 4B**). Thus, aged mice have increased penetration of urinary contents into the
247 underlying bladder tissue, which could damage host proteins to stimulate bladder inflammation in
248 an age-dependent manner (49).

249 TNF α is a major pro-inflammatory cytokine involved in promoting inflamm-aging and its
250 pathological consequences (16, 51). RNA-seq data indicated that *Tnf* was a top, locally-
251 upregulated cytokine in bladders from aged mice (7.2-fold change, FDR-adjusted P=0.0035),
252 which we confirmed by qRT-PCR (**Fig. 4C**). In the colon, age-associated TNF α has been shown
253 to lead to epithelial permeability that permits increased translocation of bacterial products into the
254 circulation, stimulating further age-associated inflammation via a positive feedback loop (16, 52).
255 To test whether TNF α induces age-associated urothelial permeability, we transurethrally instilled

256 FITC-dextran into the bladders of young and aged WT and $\text{TNF}\alpha^{-/-}$ mice. Aged $\text{TNF}\alpha^{-/-}$ had
257 urothelial barrier defects similar to aged WT mice, thus $\text{TNF}\alpha$ was not required for age-associated
258 urothelial permeability (**Fig. 4D**). However, bladders from aged $\text{TNF}\alpha^{-/-}$ mice rarely contained
259 bTLT compared to age-matched WT mice (**Fig. 4E**), and these bTLT were significantly smaller
260 than those found in WT mice (**Fig. 4F**). In contrast to the increased $\text{TNF}\alpha$ -dependent permeability
261 in the aging gut (16), these data demonstrate that in the bladder, urothelial permeability increases
262 in an age-dependent manner, while bTLT formation requires $\text{TNF}\alpha$ -dependent inflammatory
263 responses.

264 **DISCUSSION**

265 Postmenopausal and elderly women have increased susceptibility to bladder disorders
266 involving chronic inflammation, including overactive bladder (OAB), interstitial cystitis/bladder
267 pain syndrome (IC/BPS), and recurrent UTIs (rUTIs) (1, 3, 4); however, the underlying
268 mechanisms predisposing older women to bladder inflammation have remained unclear (10).
269 Here, we show the first characterization of age-induced changes to the immune system in the
270 urinary bladder. Most strikingly, bladders from aged female mice, but not those from aged male
271 mice, frequently contain large aggregates of lymphoid cells with a composition and organization
272 consistent with tertiary lymphoid tissues (TLTs) (21, 22, 33, 34), thus we termed them bladder
273 tertiary lymphoid tissues (bTLTs). We show that bTLTs develop with age in the absence of any
274 experimental trigger, indicating that age itself is a risk factor for an increased inflammatory milieu
275 in the bladder. bTLTs are not considered a normal finding in the bladder and are not found in
276 healthy, young mice; thus bTLTs are a sign of chronic inflammation and perturbed homeostasis
277 in this tissue (36, 39, 53). Furthermore, our finding that aging is also associated with urothelial
278 barrier dysfunction and increased production of secretory IgA could shift the approach to studying
279 and treating age-associated bladder inflammation. We also identified the key, age-associated
280 inflammatory cytokine $TNF\alpha$ as a driver of bTLT formation in the aging bladder. These findings
281 reveal a new target that could be used in the management of chronic bladder inflammation in
282 older women. Furthermore, age-associated inflammation may promote bTLT formation and age-
283 related susceptibility to chronic bladder inflammation.

284 Adaptive immune responses in lower urinary tract infections (e.g. cystitis without
285 pyelonephritis) are reportedly limited, inadequate, and actively inhibited by the innate immune
286 response to infection (12, 19, 54). Cellular characterization of aged bladders prior to infection
287 revealed an influx of $CD4^+$ and $CD8^+$ T cells, naïve and activated B cells, and IgA^+ plasma cells,
288 all localized to organized bTLTs. Global bladder transcriptomes indicate that classical lymphoid
289 neogenesis signaling pathways, including $TNF\alpha$, lymphotoxin, and the homeostatic lymphoid

290 chemokines, likely play a role in orchestrating the organization of these lymphocytes in aged
291 bladders (21, 22, 33, 34). Young bladders do not contain substantial numbers of these cellular
292 populations, particularly those of the B cell lineage (12, 19). T cell influx has been reported in
293 young mice given multiple UTIs with uropathogenic *E. coli* (55), and aggregates of CD45⁺ cells
294 have been observed in a subset of C3H/HeN mice with persistent bacteriuria, chronic cystitis, and
295 pyelonephritis (40). Whether the adaptive immune cells that do infiltrate the bladder after infection
296 remain resident in the tissue in the absence of on-going inflammation and antigenic stimulation
297 hasn't been addressed. Further studies will be needed to establish whether bladder lymphoid
298 aggregates under these conditions are also organized bTLT that can support germinal center
299 reactions and become a permanent feature of the bladder mucosae.

300 Since mucosal B cells and TLTs in other tissues can play both protective and pathogenic
301 roles, it remains to be determined whether age-associated bTLTs are harmful or helpful (21, 47,
302 56-60). Here, we present evidence that bTLTs are active sites of naïve B cell recruitment, germinal
303 center formation, and B cell maturation into plasma cells, suggesting that bTLTs serve as local
304 antigen-processing centers in the bladder. Considering the association of bTLTs with aging and
305 susceptibility to recurrent infection, we speculate that formation of age-associated bTLTs may
306 exacerbate inflammatory pathology triggered by infection or other inflammatory insults in the
307 bladder. While bTLTs have been observed in urothelial cancer specimens and correlated with
308 advanced stages of disease (61), bladder cancer is less common in women than in men, and
309 patients in our study had no evidence of malignancy or pre-malignant changes. TLTs associated
310 with autoimmune diseases like rheumatoid arthritis typically propagate pathogenic auto-
311 antibodies. Successful treatment with immune modulators such TNF α inhibitors can lead to TLT
312 regression and reduction of pathology in rheumatoid arthritis patients (56, 62, 63). On the other
313 hand, in other cancers, TLTs generally correlate with improved outcomes, implying that they aid
314 in effective immune responses against tumor cells (21, 65). While adaptive immune responses
315 from TLTs would intuitively be protective against infections, their association with chronic

316 infections suggests that they are not always sufficient to eradicate such infections. In chronic
317 hepatitis C virus infection, TLTs are associated with inflammatory pathology and autoimmune
318 complications such as cryoglobulinemia (64). TLTs in the lung are associated with control and
319 latency of *Mycobacterium tuberculosis* and thus thought to protect against reactivation of latent
320 *M. tuberculosis* in this chronic infection (66-68). In chronic *Helicobacter pylori* gastroenteritis,
321 TLTs have not been associated with specific infection outcomes, but these gastric TLTs have the
322 potential to become mucosa-associated lymphoid tissue lymphomas (69-71). Interestingly, these
323 gastric TLTs, both benign and malignant, frequently regress after eradication of *H. pylori* with
324 antibiotics. The transient nature of *H. pylori*-associated gastric TLTs suggests that adaptive
325 responses in this tissue may not be permanent. Thus, specific pathogens, tissue locations, and
326 the nature of the immune responses occurring within TLTs impact whether TLTs are considered
327 protective or pathogenic.

328 In the elderly, excessive inflammation in response to infection coupled with a lack of
329 protective adaptive responses may indicate that TLTs associated with infection in this population
330 could be pathogenic (72). TLTs in the elderly may also represent their inability to clear chronic
331 infections and control latent infections (73). Given the high prevalence of UTIs among elderly
332 women and the known mechanisms of uropathogenic *E. coli* persistence and recurrence, our
333 discovery of age-associated bTLTs warrants further investigation from both a clinical and
334 mechanistic perspective.

335 Mechanistically, we demonstrate that age-associated TNF α promotes the formation of bTLTs
336 over the lifespan of mice. TNF α is a well-established marker of age-associated inflammation and
337 likely has many roles in pathogenic changes that arise during older age (11, 16). Both aging and
338 TNF α increase permeability in the intestinal epithelium (16, 52), but this phenomenon had not
339 previously been demonstrated in the bladder epithelium. Given the critical importance of the
340 bladder epithelium to serve as an impermeable barrier to urinary contents, increases in urothelial

341 permeability have adverse consequences. For example, urothelial barrier defects are frequently
342 found in interstitial cystitis/bladder pain syndrome (IC/BPS) patients, which is most often
343 diagnosed in women over 40 (3). In an IC/BPS mouse model, urine exposure was required to
344 induce permeability-mediated inflammation (49), and in another model, ectopic expression of
345 $\text{TNF}\alpha$ in the bladder resulted in heightened pain sensitivity reminiscent of IC/BPS (74). In our
346 studies, both aged WT and $\text{TNF}\alpha^{-/-}$ mice exhibited increased urothelial permeability, suggesting
347 that age is the primary driver of epithelial dysfunction in the bladder. Since bladders from aged
348 $\text{TNF}\alpha^{-/-}$ mice rarely contained bTLT, urothelial permeability is likely to be upstream of a $\text{TNF}\alpha$ -
349 mediated inflammatory cascade. The cycle of age-induced epithelial permeability, urine exposure
350 in the underlying tissue, and $\text{TNF}\alpha$ -mediated inflammatory responses may thus lead to or
351 exacerbate bTLT formation. $\text{TNF}\alpha$ also plays a role in promoting the maturation of TLTs and
352 germinal center reactions in SLOs (75), and could thus be a downstream factor limiting the
353 formation of age-associated bTLTs. Further mechanistic studies are needed to fully define the
354 exact role that $\text{TNF}\alpha$ plays in this process, which could lead to future improvement in the care
355 and therapy of elderly women with chronic bladder inflammation.

356 As the global population ages, we must continue to assess how advanced age
357 influences homeostasis and inflammatory responses. The newly recognized connection
358 between aging, inflammation, epithelial permeability, and TLT formation could be a common
359 theme affecting many mucosae and their age-related pathologies.

360

361 **Materials and Methods**

362 *Mice*

363 All experimental procedures were approved by the animal studies committee of Washington
364 University in St. Louis School of Medicine (Animal Welfare Assurance #A-3381-01) and McMaster
365 University's Animal Research Ethics Board. 3- to 24-month-old C57B6/J mice were obtained from
366 the National Institute of Aging. Mice were maintained under specified pathogen-free conditions in
367 a barrier facility under a 12 h light-dark cycle. *Tnfa*^{-/-} and WT mice (originally from Jackson
368 Laboratories) were bred and aged to 18-24 months at McMaster University (Theverajan 2017).
369 To account for environmental factors, experiments with *Tnfa*^{-/-} mice were compared to WT mice
370 raised in the same facility.

371

372 *Mouse Urinary Tract Infection*

373 UTI89, a clinical UPEC isolate from a patient with recurrent cystitis was grown statically for 17 h
374 in Luria-Bertani broth (Tryptone 10 g/L, Yeast extract. 5 g/L. and NaCl 10g/L) at 37°C prior to
375 infection. Mice were anesthetized and inoculated via transurethral catheterization with 10⁷ colony
376 forming units (CFUs) of UTI89 in phosphate-buffered saline (PBS; Sigma-Aldrich, D8537). Urines
377 were collected at indicated time points and spotted onto LB-agar plates to measure bacterial titers.

378

379 *Histological and Immunofluorescence analysis*

380 Bladders were aseptically removed, cut along the anterior-posterior axis, and fixed in 10% neutral
381 buffered formalin or methacarn (60% methanol, 30% chloroform, 10% acetic acid), embedded in
382 paraffin, stained with hematoxylin and eosin (7211, Richard-Allen Scientific) and imaged on a
383 Nanozoomer 2.0-HT system (Hamamatsu). Matching anterior or posterior bladder halves were
384 compared within groups. Number and area of bTLTs were determined in 5 sections spaced 150
385 μm apart using NDP,view2 software (Hamamatsu). Compact aggregates $>10,000 \mu\text{m}^2$ were
386 considered bTLTs. For immunofluorescence analysis, bladders were embedded in OCT

387 Compound (4583, Tissue-Tek) and flash frozen. 7 μ m sections were fixed with 1:1 methanol-
388 acetone, rehydrated in PBS, and blocked with Avidin/Biotin Blocking Kit (SP2001, Vector
389 Laboratories) followed by 1% BSA in PBS. Primary antibodies against B220 (13-0452,
390 eBioscience), CD3 (14-0031-82, eBioscience) PNA^d (120803, BioLegend), CD31 (ab28364,
391 Abcam), CD138 (142511, BioLegend), CD35 (558768, BD Biosciences), GL7 (13-5902-81,
392 eBioscience), and IgD (1120-01, SouthernBiotech) were incubated overnight at 4° and detected
393 with streptavidin-conjugated and species-specific secondary antibodies followed by Hoechst dye.
394 Slides were covered slipped with Prolong Gold antifade (P36930, Invitrogen) and imaged on a
395 Zeiss Axio Imager M2 microscope with a Hamamatsu Flash4.0 camera using Zeiss Zen Pro
396 software.

397

398 *Urothelial permeability assay*

399 50 μ L of 10 mg/mL 10 kD FITC-dextran (D1821, Invitrogen) was transurethrally inoculated into
400 mice as previously described (Shin 2011). After 90 minutes, bladders were embedded in OCT
401 Compound (4583, Tissue-Tek) and flash frozen. 7 μ m sections were briefly dipped in 1:1
402 methanol-acetone and PBS, then cover-slipped with Prolong Diamond Antifade with DAPI
403 (P36971, Invitrogen). Images were acquired using a fixed exposure set to detect fluorescence in
404 young WT bladders. Stromal fluorescence was quantified by averaging the mean gray value for
405 FITC channel in 6 random squares from 2 separate images for each mouse using ImageJ
406 software. Values were combined for each mouse and used for statistical analysis.

407

408 *Organ culture and IgA ELISA*

409 Bladders were aseptically removed, rinsed with PBS, bisected, and both halves cultured together
410 in 500 μ L RPMI-1640 with 10% FBS, Pen/Strep, 10 mM HEPES, and glutamax. Supernatants
411 were removed after 24 hrs and cleared of debris by centrifugation. IgA concentration in urines

412 and culture media was determined by ELISA according to manufacturer protocol (88-50450-22,
413 Invitrogen).

414

415 *Flow cytometry*

416 Bladders were aseptically removed, minced with scissors, and digested at 37° for 30 minutes in
417 RPMI-1640 with 10mM HEPES, collagenase D (C5318, Sigma-Aldrich), and DNase
418 (10104159001, Sigma-Aldrich). Bladders were forced through a 70 µm cell strainer (352350,
419 Corning) and washed with 5% FBS in PBS. Single cell suspensions were stained with anti-CD45-
420 eFluor450 (48-0451-82, eBioscience), anti-CD3-APC (17-0032-82, eBioscience), anti-CD19-PE
421 (115511, BioLegend), anti-CD4-FITC (100405, BioLegend), anti-CD8-PE/Cy7 (100721,
422 BioLegend), anti-CD138-BrilliantViolet605 (142515, BioLegend), and 7-AAD (420404,
423 BioLegend). Data was acquired on LSR II flow cytometer (BD) and analyzed with FlowJo software
424 v10.0. Gates were determined with isotype antibodies in bladder suspensions from young mice.

425

426 *RNA-sequencing*

427 RNA was purified from snap frozen, homogenized bladders with RNeasy Mini Kit (74101,
428 Qiagen) and RNase-free DNase digestion kit (79254, Qiagen). Libraries were prepared with
429 Ribo-Zero rRNA depletion kit (Illumina) and sequenced on HiSeq3000 (Illumina). Reads were
430 aligned to the Ensembl top-level assembly with STAR version 2.0.4b. Gene counts were derived
431 from the number of uniquely aligned unambiguous reads by Subread:featureCount version
432 1.4.5. Transcript counts were produced by Sailfish version 0.6.3. Sequencing performance was
433 assessed for total number of aligned reads, total number of uniquely aligned reads, genes and
434 transcripts detected, ribosomal fraction, known junction saturation and read distribution over
435 known gene models with RSeQC version 2.3. All gene-level and transcript counts were
436 then imported into the R/Bioconductor package EdgeR and TMM normalization size factors
437 were calculated to adjust samples for differences in library size. Ribosomal features as well as

438 any feature not expressed in at least the smallest condition size minus one sample were
439 excluded from further analysis and TMM size factors were recalculated to create effective TMM
440 size factors. The TMM size factors and the matrix of counts were then imported into
441 R/Bioconductor package Limma and weighted likelihoods based on the observed mean-
442 variance relationship of every gene/transcript and sample were then calculated for all samples
443 with the `voomWithQualityWeights` function. Performance of the samples was assessed with a
444 spearman correlation matrix and multi-dimensional scaling plots. Gene/transcript performance
445 was assessed with plots of residual standard deviation of every gene to their average log-count
446 with a robustly fitted trend line of the residuals. Generalized linear models were then created to
447 test for gene/transcript level differential expression. Differentially expressed genes and
448 transcripts were then filtered for False Discovery Rate (FDR)-adjusted p-values less than or
449 equal to 0.05. Pathways analysis was performed using results imported into the R/Bioconductor
450 packages GAGE and Pathview.

451

452 *RT-qPCR*

453 Bladders were flash frozen or stabilized in RNA Save (01-891-1A, Biological Industries) and RNA
454 extracted using TRIzol reagent (15596018, Invitrogen) according to manufacturer protocol
455 followed by gDNA digestion with TURBO DNA-free kit (AM1907, Invitrogen). cDNA was
456 generated using Superscript III Reverse Transcriptase (18064014, Invitrogen). qPCR was
457 performed with SsoAdvanced Universal SYBR Green Supermix (1725275, Bio-Rad) on a CFX96
458 Touch Real-Time PCR Detection System (Bio-Rad). Fold-changes were calculated using $\Delta\Delta C_t$
459 method and normalized internally to 18S expression.

460

461 *Tissue analysis of human bladder biopsy samples*

462 Cystoscopic pinch biopsies were obtained from patients undergoing gynecologic surgery with
463 previous findings of bladder nodules from the Women's Genitourinary Tract Specimen

464 Consortium at Washington University in St. Louis School of Medicine (IRB#201810094)
465 biorepository. Biopsies (approx. size 1 mm³) were fixed in 10% neutral buffered formalin,
466 embedded in paraffin, stained with hematoxylin and eosin. Images were acquired with Olympus
467 DP71 software. Sections were stained with antibodies to CD20 (14-0202-80), CD3 (ab5690,
468 Abcam), and CD21 (NBP1-22527, Novus Biological) and imaged as above.

469

470 *Statistical analyses*

471 Statistical tests were performed in GraphPad Prism 8. Data sets were evaluated for normality
472 and lognormality with Anderson-Darling, D'Agostino-Pearson, Shipiro-Wilk, and Kolmogorov-
473 Smirno tests. Lognormal distributions were log-transformed and analyzed as a parametric
474 distribution. Unpaired t-tests (with Welch's correction where appropriate) or two-way ANOVA
475 with Bonferroni post-tests were used for parametric data and Mann-Whitney U test or Kruskal-
476 Wallis with Dunn's multiple comparison tests were used for non-parametric data. P<0.05 was
477 considered significant. Data points represent individual animals. Lines represent the mean for
478 normal distributions, geometric mean for log-normal distributions, or median for non-parametric
479 distributions. Error bars represent SEM.

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Author contributions

Conceptualization MML, CW, IUM. Methodology MML, CW, IUM, DMEB. Investigation MML, CW, CS, END. Data curation ZJ. Data analysis MML. Resources JLL, DMEB. Supervision CW, DMEB, JLL, IUM. Funding IUM, DMEB. Visualization MML. Writing--original draft MML, IUM. Writing--review & editing MML, CW, DMEB, IUM

Competing Interests

The authors have no financial interests to disclose.

Data and materials availability

All sequencing data will be deposited in an appropriate public repository.

Figures

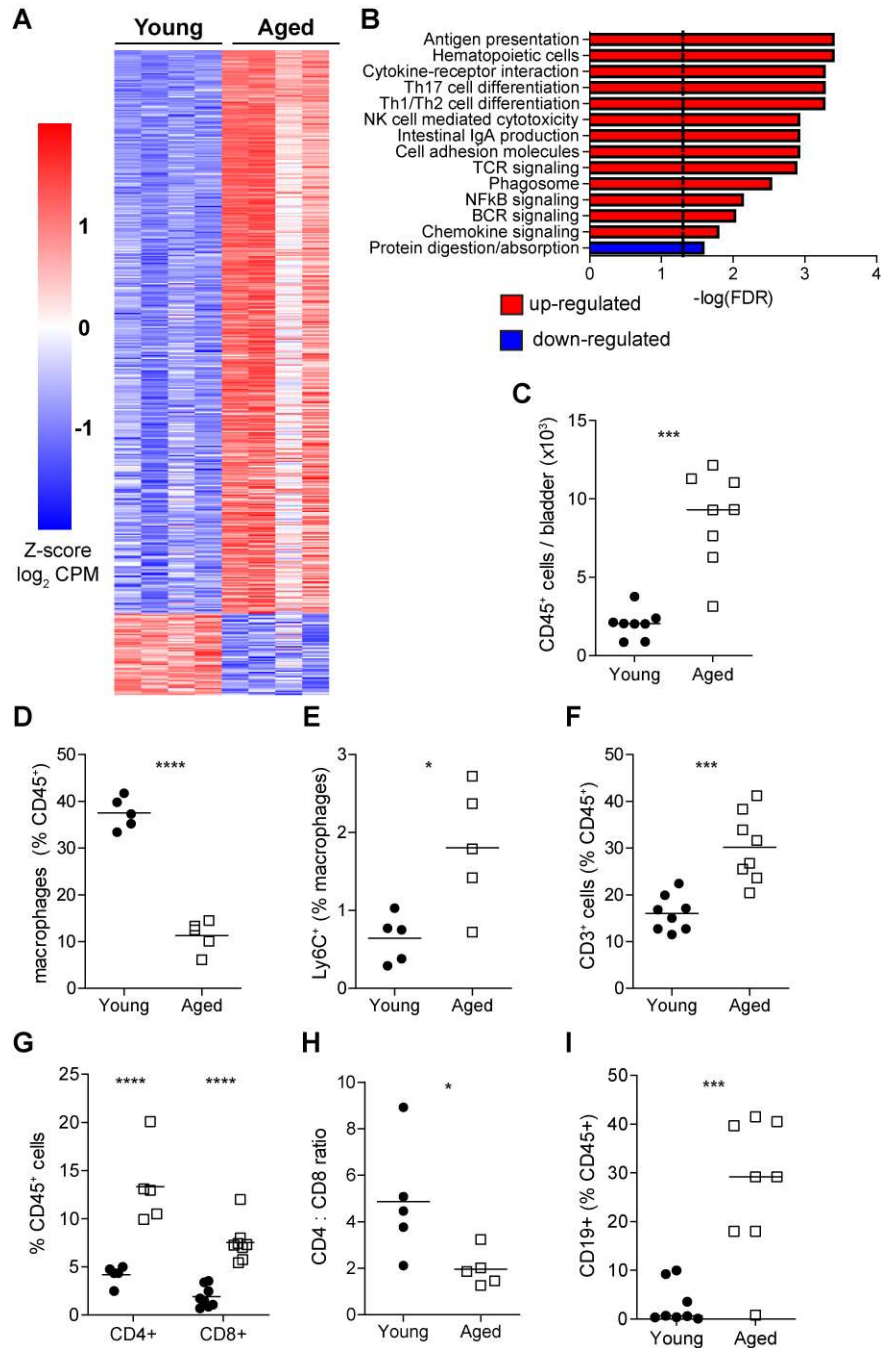


Fig. 1. Immune processes and lymphocyte populations are expanded in bladders from aged mice. (A) Relative gene expression of whole bladder from young (3 mo, n=4) and aged mice (22 mo, n=4) showing genes with at least a 2-fold change (FDR-adjusted $p < 0.05$). (B) Gene set enrichment analysis of KEGG pathways with FDR-adjusted p-values for up- (red) or down-regulated (blue) pathways. (C) Total number of live CD45⁺ cells in bladders (n=7 young, n=8 aged). Data are combined from 3 independent experiments. (D) Frequency of F4/80⁺CD64⁺ macrophages among total CD45⁺ cells in bladders (n=5/group). Data are combined from 2 independent experiments. (E) Frequency of Ly6C⁺ macrophages from bladders in (D). (F) Frequency of CD3⁺ T cells in bladders (n=8/group). Data are combined from 3 independent experiments. (G) Frequency of CD4⁺ and CD8⁺ T cells in bladders (n=5/group for CD4⁺ cells, n=8/group for CD8⁺ cells). Data are combined from 2 independent experiments. (H) Ratio of CD4⁺ T cell frequency to CD8⁺ T cell frequency in bladders (n=5/group). Data are combined from 2 independent experiments. (I) Frequency of CD19⁺ B cells in bladders (n=8/group). Data are combined from 3 independent experiments. **** $p < 0.0001$, *** $p < 0.001$, ** $p < 0.01$, * $p < 0.05$ by Mann-Whitney U-test shown with median (C, H, I), unpaired t-test shown with mean (D, E), unpaired t-test of log-transformed data shown with geometric mean (F), or two-way ANOVA with Bonferroni post-test (G).

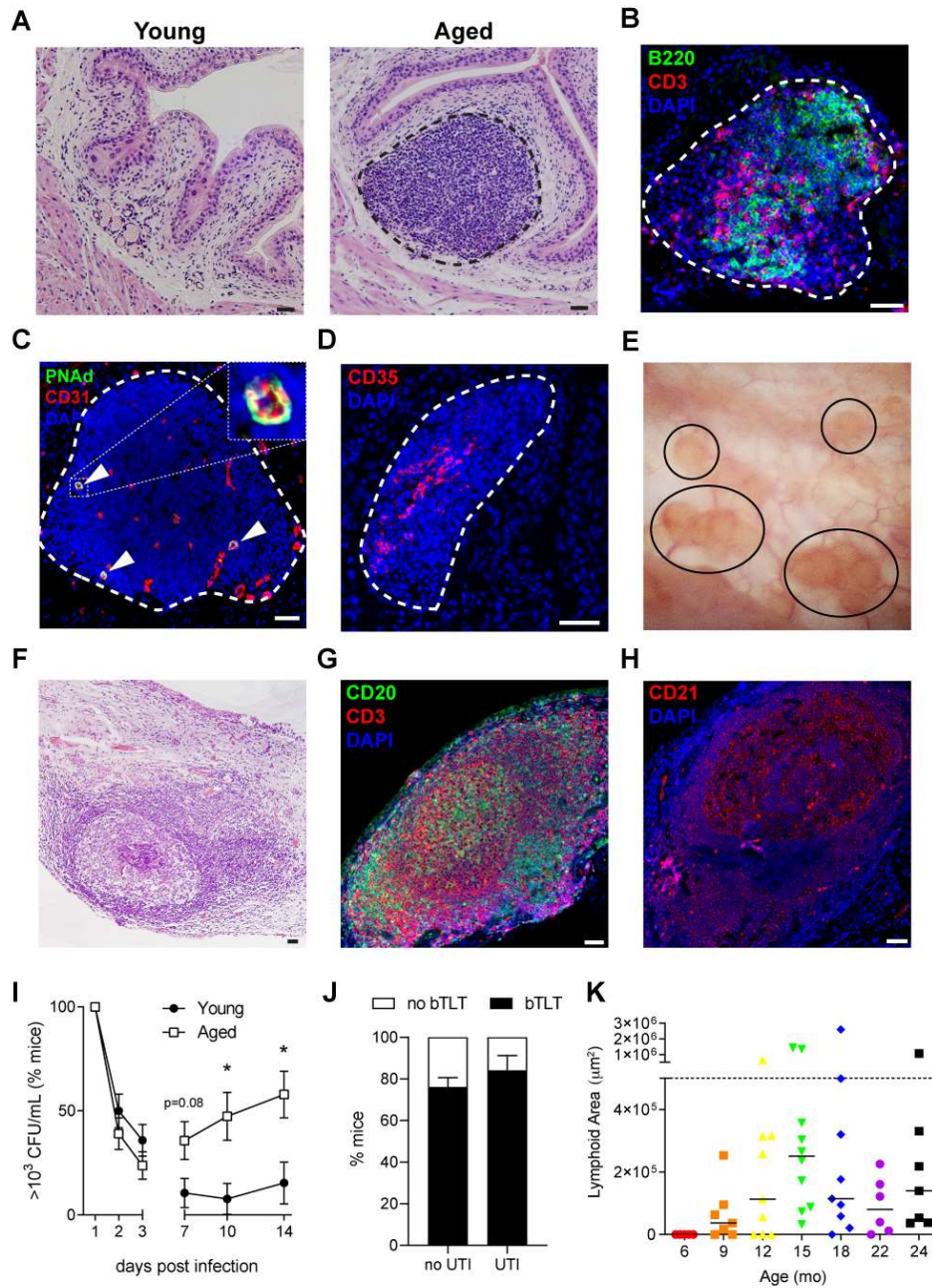


Fig. 2. Bladder tertiary lymphoid tissue (bTLT) is found in aged mice and older women with a history of recurrent urinary tract infection. (A) Hematoxylin and eosin (H&E) image of bladder tissue from young (3 mo) and aged (18 mo) mice with an example of well-formed bTLT in aged mice. (B) Immunofluorescence (IF) image of B cells (B220, green) and T cells (CD3, red) within bTLT of aged mice. (C) IF image of high endothelial venules marked by peripheral node addressin (PNA^d, green) and CD31 (red). (D) IF image of follicular dendritic cell (FDC) network marked by CD35 (red). (E) Cystoscopic image of nodules (black circles) in a chronically inflamed bladder that was biopsied. (F) H&E image of a well-formed lymphoid follicle in a bladder biopsy. (G) IF image of B cells (CD20, green) and T cells (CD3, red) in a bladder biopsy. (H) IF image of FDC network marked by CD21 (red) in a bladder biopsy. (I) Proportion of mice with urine titer $>10^3$ CFU/mL uropathogenic *E. coli* at given time points (n=19-42 mice/group/time point). (J) Proportion of mice with bTLT before (no UTI, n=88) or after (UTI, n=25) infection. (K) Total area of bTLTs from mice of different ages (n=5-10 mice/age). Mouse images are representative of at least 5 mice. Human images are representative of n=12 patients. Dashed lines encircle bTLTs. All nuclei are stained blue with DAPI. Scale = 50 μm . * $p<0.05$, ** $p<0.01$ by Fisher's exact test shown with percentage and SEM (I) or Kruskal-Wallis with Dunn's multiple comparison test shown with median.

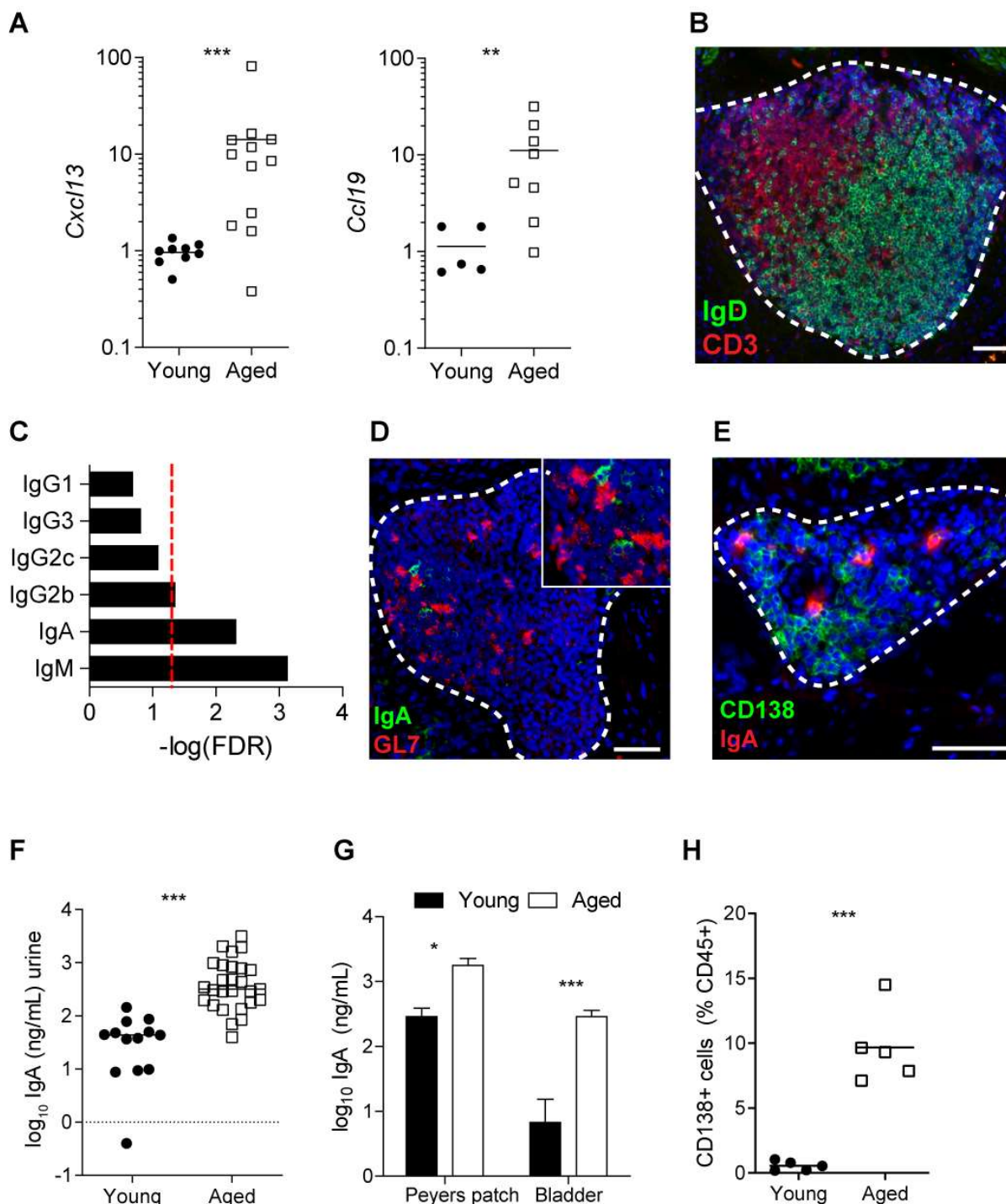


Fig. 3. bTLTs in aged bladders generate local B cell responses. (A) Bladder gene expression of *Cxcl13* and *Ccl19* relative to young mice (n=6 young, n=12 aged). (B) Immunofluorescence (IF) image of T cells (CD3, red) and naive B cells (IgD, green) within bTLT from aged mice. (C) Enrichment of immunoglobulin (Ig) heavy chain constant genes in bladders from aged mice compared to those from young mice (n=4/group) in RNA-sequencing analysis. Red dashed line marks FDR-adjusted p=0.05. (D) IF image of bTLT with germinal center (GL7, red) containing IgA+ (green) cells. (E) IF image of plasma cells (CD138, green) within bTLT. (F) Urine IgA concentration (n=13 young, n=27 aged). (G) IgA concentration after 24 hours *ex vivo* organ culture (n=5/group). Data are combined from 3 independent experiments. (H) Frequency of CD138⁺ plasma cells among total CD45⁺ cells in bladders (n=5/group). Data are combined from 2 independent experiments. All images are representative of at least 5 aged mice. Dashed lines encircle bTLTs. All nuclei are stained blue with DAPI. All scale bars are 50 μ m. ****p<0.0001, ***p<0.001, **p<0.01, *p<0.05 by Mann-Whitney U-test shown with median (A, F, H) or 2-way ANOVA with Bonferroni post-test (G).

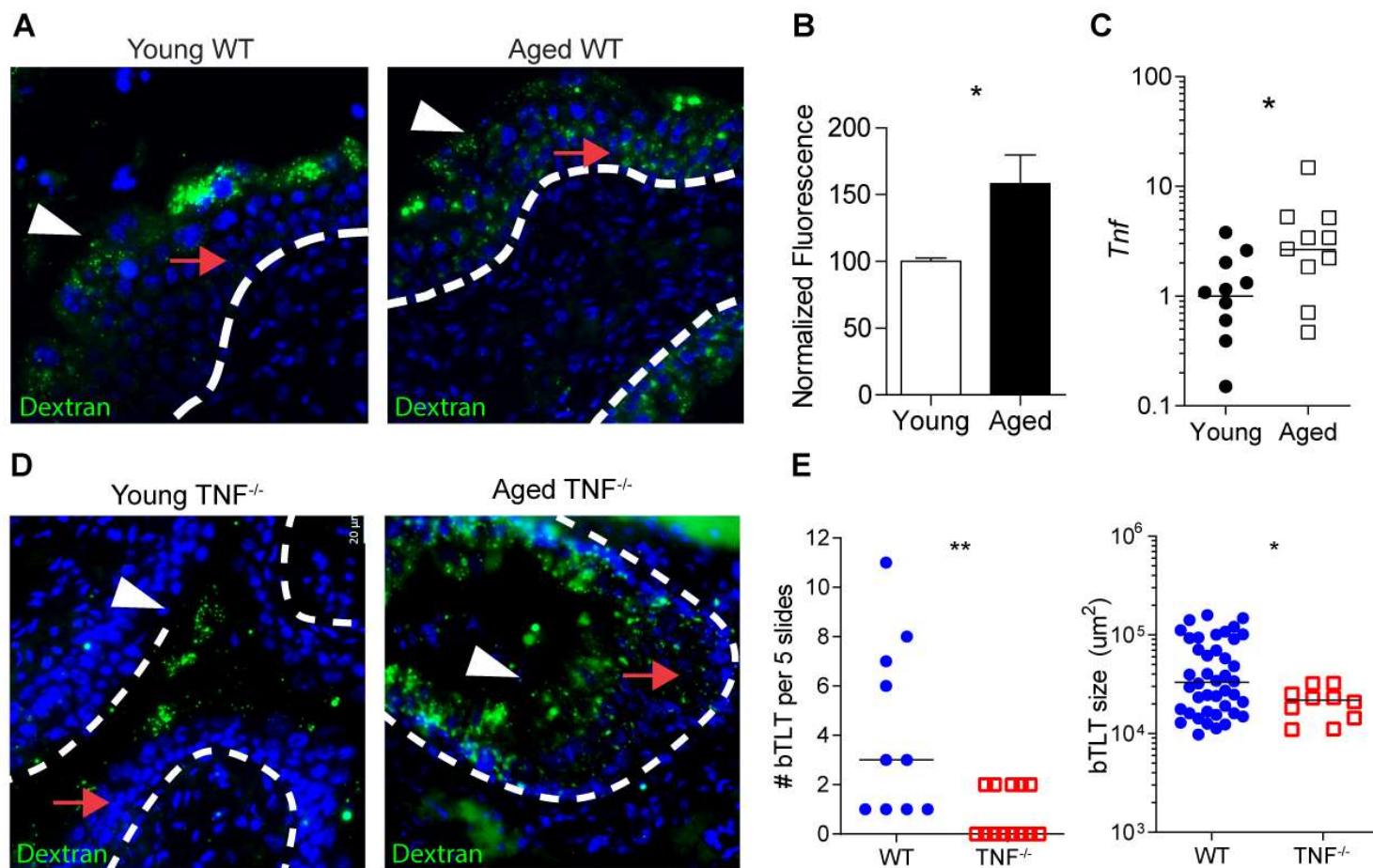


Fig. 4. Aged $TNF\alpha^{-/-}$ mice lack bTLT but retain age-associated urothelial barrier defects. (A) FITC-dextran permeability in urothelium of young and aged mice. White arrowheads identify superficial umbrella cells with intracellular FITC-dextran. Red arrows identify basal and intermediate cell layers. (B) Mean gray value of stroma in mouse bladders treated with FITC-dextran (n=4/group). Values are normalized to the average value from young mice. Data are combined from 2 independent experiments. (C) Relative expression of *Tnf* in mouse bladder tissue (n=10/group)). (D) FITC-dextran permeability in urothelium of $TNF\alpha^{-/-}$ mice (n=2 young, n=3 aged) as in (A). (E) Number (left) and size (right) of bTLT in 5 bladder sections (n=10 WT, n=11 $TNF\alpha^{-/-}$). Images are representative of 2 independent experiments. All nuclei are stained blue with DAPI **p<0.01, *p<0.5 by Mann-Whitney U-test shown with median (B, E) or unpaired t-test of log-transformed data shown with geometric mean (C).