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Phosphatase PP2A is essential for $T_H 17$ differentiation

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Short title: PP2A is essential for T_H17 differentiation

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23 Abstract

24 Phosphatase PP2A expression levels are positively correlated to the clinical severity of systemic lupus 25 erythematosus (SLE) and IL17A cytokine overproduction, indicating a potential role of PP2A in 26 controlling T_H17 differentiation and inflammation. By generating a mouse strain with ablation of the 27 catalytic subunit α of PP2A in peripheral mature T cells (PP2A cKO), we demonstrate that the PP2A 28 complex is essential for $T_H 17$ differentiation. These PP2A cKO mice had reduced $T_H 17$ cell numbers 29 and less severe disease in an experimental autoimmune encephalomyelitis (EAE) model. PP2A 30 deficiency also ablated C-terminal phosphorylation of SMAD2 but increased C-terminal 31 phosphorylation of SMAD3. By regulating the activity of RORyt via binding, the changes in the 32 phosphorylation status of these R-SMADs reduced *Il17a* gene transcription. Finally, PP2A inhibitors 33 showed similar effects on $T_H 17$ cells as were observed in PP2A cKO mice, i.e., decreased $T_H 17$ 34 differentiation and relative protection of mice from EAE. Taken together, these data demonstrate that 35 phosphatase PP2A is essential for $T_{H}17$ differentiation, and that inhibition of PP2A could be a possible 36 therapeutic approach to controlling $T_{\rm H}17$ -driven autoimmune diseases.

37 Significance statement

38 By using a gene knockout that leads to T-cell specific deletion, we reveal the essential role of Ser/Thr 39 phosphatase PP2A in T_H17 differentiation. We also show that this works through the regulation of 40 SMAD2/3 phosphorylation status, which elucidates molecular pathways by which PP2A modulates the 41 expression of $T_H 17$ phenotypes. This finding extends our understanding of the close relationship 42 between PP2A overexpression and inflammatory disease. PP2A is the first Ser/Thr phosphatase shown 43 to be capable of controlling $T_{\rm H}17$ differentiation via modulating R-SMADs activity. We also 44 demonstrate the translational potential of these findings by showing a therapeutic effect of PP2A inhibitors in controlling autoimmune disease in the EAE model. 45

46 Keywords: $T_H 17$, PP2A, TGF β

48 /body Introduction.

T-helper type 17 (T_H 17) cells, a subset of CD4⁺T cells defined by IL17, IL22 and IL21 production, are essential for control and clearance of extracellular bacterial and fungi (1, 2). However, excessive T_H 17 responses are involved in chronic inflammation and development of many human autoimmune diseases (3). Upon encountering antigen in the context of a local cytokine milieu including transforming growth factor β (TGF β) and IL6, naïve CD4⁺T cells undergo differentiation into effective T_H 17 cells. TGF β is the principal, essential factor promoting the differentiation of T_H 17 cells (4, 5).

Through two related transmembrane Ser/Thr kinase receptors, TGFβ induces Ser/Thr signal cascades in activated T cells. Recent work including work from our lab has revealed the regulatory roles of some other Ser/Thr kinases in this process. For example, both MEKK2/3 and MINK1 suppress T_H17 differentiation through direct phosphorylation of the TGFβ signaling components SMAD2 and SMAD3 (6, 7). Precise regulation of SMAD2/3 Ser/Thr phosphorylation status is thus important in driving T_H17 differentiation (6-8). Dephosphorylation of SMAD2/3 is equally critical in this process but the specific phosphatases that catalyze SMAD2/3 dephosphorylation remain unknown.

62 As one of the major Ser/Thr phosphatases in eukaryotes, phosphatase PP2A is critical for many cellular 63 functions including cell survival, proliferation, activation and differentiation (9). It has been reported 64 that elevated PP2A expression levels are linked to the upregulation of IL17A production by CD4⁺ T 65 cells in human systemic lupus erythematosus patients (10). Studies in the PP2Ac transgenic mouse 66 model also demonstrated the relationship and mechanism linking of PP2A and Ill7-dependent 67 immunopathology (11, 12). PP2A is composed of three polypeptide chains, the structural A, the 68 regulatory B and the catalytic C subunits (13). The heterodimer of the A subunit and the C subunit 69 $(PP2A_A-PP2A_C)$ forms the PP2A core enzyme that associates with one regulatory B subunit, thus 70 determining the substrate specificity of the holoenzyme complex (13).

T1 In TGFβ signaling, two related regulatory B subunits, Bα (*Ppp2r2a*) and Bδ (*Ppp2r2d*), opposingly modulate TGFβ/Activin/Nodal signaling (14), while carboxy terminal phosphorylation of MAD (the SMAD homolog protein in Drosophila) is negatively regulated by the PP2A inhibitor Okadaic Acid (15). By analogy, these observations suggest that PP2A might be a Ser/Thr phosphorylation modulator involved in controlling $T_H 17$ differentiation.

76 Here, we present data showing that $T_H 17$ cell polarization was largely impaired when *Ppp2ca* was

ablated in mature T cells and rendered resistance towards MOG-induced experimental autoimmune encephalomyelitis (EAE). We also show that PP2A knockout leads to altered activation of R-SMADs (specifically decreasing SMAD2 activation and increasing SMAD3 activation). This synergistically inhibited ROR γ t mediated *Il17a* transcription. This work thus reveals specific role of PP2A in regulating the canonical TGF β -R-SMAD-ROR γ t signaling process during T_H17 differentiation and indicates a possible therapeutic approach for controlling T_H17 driven autoimmune diseases *via* inhibition of PP2A.

85 **Results.**

86 Normal T cell development in PP2A cKO mice. To explore the function of PP2A in peripheral T cells, 87 we deleted the dominant PP2A C α isoform of PP2A catalytic subunit (PP2Ac) in T cell by crossing 88 dis-Lck (dLck) Cre with *Ppp2ca*^{fl/fl} mice (in which exons 3-5 of *Ppp2ca* are *loxP* flanked) (16) to 89 generate *Ppp2ca*^{fl/fl} dLck-Cre (termed PP2A cKO mice) and *Ppp2ca*^{fl/+} dLck-Cre or *Ppp2ca*^{+/+} 90 dLck-Cre mice (collectively called PP2A WT mice here) (*SI Appendix*, Fig. S1A and B). The dLck-Cre 91 was driven by the distal promoter of the lymphocyte protein tyrosine kinase (*Lck*) gene, enabling 92 investigation of the *Ppp2ca* deletion after positive selection in T cells (17).

93To assess deletion efficiency, *Ppp2ca* mRNA and protein levels were measured and showed clear94reduction in peripheral T cells in PP2A cKO mice, while remaining normal in thymic subsets and95splenic B cells (*SI Appendix*, Fig. S1C and D). The catalytic subunit of PP2A has two isoforms, Cα and96Cβ (encoded by *Ppp2ca* and *Ppp2cb* respectively). Notably we didn't observe compensatory97overexpression of *Ppp2cb* (*SI Appendix*, Fig. S1C). PP2A activity in cKO CD4⁺ T cells was reduced to98half of that measured in WT controls (*SI Appendix*, Fig. S1E).

Analysis of the numbers and frequencies of different T cell subsets in these mice showed that cKO
mice exhibited normal T cell development in thymus (*SI Appendix*, Fig. S2A-C) as well as in peripheral
lymphoid organs (*SI Appendix*, Fig. S2A, D and E). The proportions of naïve/effective T cells in spleen
and mesenteric lymph nodes (MLN) were also similar between WT and cKO littermates (*SI Appendix*,
Fig. S2F and G). The normal development of peripheral lymphocytes in PP2A cKO mice allowed
further investigation of the role of PP2A in T cell differentiation.

105 T_{H} 17 cell numbers are reduced in PP2A cKO mice. To clarify whether PP2A is involved in T helper 106 cell lineage commitment, we analyzed the populations of T helper subsets *in vivo*. Interestingly, CD4⁺ 107 T cells from PP2A cKO mice only contained half the number of $T_{\rm H}17$ cells comparing to their WT 108 littermates (SI Appendix, Fig. S3A and B), while the numbers of $T_{\rm H}1$ and Treg CD4⁺ T cells were not 109 affected in the peripheral lymphoid organs (SI Appendix, Fig. S3A, C, D and F). The frequency of 110 Foxp3⁺ regulatory T cells in the thymus was also comparable between PP2A WT and cKO mice (SI 111 Appendix, Fig. S3E and F). Similarly, subsets analysis of the lamina propria also showed a consistent 112 reduction of T_H17 cells (SI Appendix, Fig. S3G and I). These data demonstrate that PP2A is involved in 113 maintaining $T_H 17$ cell composition, while other T cell subsets, including Treg and $T_H 1$, appear 114 unaffected.

115 **PP2A deletion impairs T_H 17 differentiation** *in vitro.* To investigate whether reduced levels of $T_H 17$ 116 cells in PP2A cKO mice result from impaired $T_H 17$ differentiation, we sorted naïve CD4⁺ T cells from 117 both WT and cKO cells and polarized them under $T_H 1$, $T_H 2$, $T_H 17$ and iTreg conditions to compare 118 their differentiation efficiencies. The results showed that only the generation of $T_H 17$ cells notably 119 declined with the PP2A deficiency, while other T helper subsets were not affected (Fig. 1*A* and *B* and 120 *SI Appendix*, Fig. S4A and B). The expression levels of *Ppp2ca* mRNA and PP2A C α protein were more 121 abundant in $T_H 17$ cells than in other T helper subsets (*SI Appendix*, Fig. S4G and H).

122 p-PP2Ac (Y307) levels, a negative indicator for PP2A activity, are lower in $T_{\rm H}17$ and $T_{\rm H}1$ than in the 123 other subsets, indicating higher PP2A activity in these two subsets (SI Appendix, Fig. S4I). Cytokine 124 production showed similar results, confirming that PP2A deficiency specifically reduced $T_{\rm H}17$ 125 differentiation (Fig. 1C and SI Appendix, Fig. S4C). We further tested the expression of several key 126 $T_{\rm H}17$ signature genes and found notably decreased II17a and II17f expression and slightly reduced 127 expression of Rora and II21, while the expression of Rorc, II22 and II23r were not significantly 128 affected (Fig. 1D). The alteration of the expression pattern of T_H17 signature genes (including II17a 129 and *II17f*) induced by PP2A deficiency was also confirmed by an RNAseq analysis (SI Appendix, Fig. 130 S5A and B and Dataset 1-3).

131 The proliferation capacity of WT and cKO T cells was measured under T_H17 conditions and were 132 comparable 2 and 5 days after stimulation (SI Appendix, Fig. S4D). Upon PI and Annexin staining, WT 133 and cKO cells showed comparable apoptotic rates (SI Appendix, Fig. S4E). Thus, reduced IL17A⁺ 134 CD4⁺ T cell levels and IL17A production were not due to either impaired proliferation or increased 135 apoptosis in cKO cells. Furthermore, we did not observe an increased portion of IFN γ^+ or Foxp3⁺ CD4⁺ 136 T cells in cKO T cells under $T_{\rm H}17$ conditions, which rules out the likelihood of $T_{\rm H}17$ cells converting to 137 other cell subsets in these circumstances (Fig. 1A and SI Appendix, Fig. S4F). These findings therefore 138 demonstrate a T-cell intrinsic impairment of the $T_{\rm H}17$ polarization program upon PP2A deficiency 139 which is independent of proliferation, apoptosis or subset conversion.

Reduced severity of EAE in mice with PP2A deficiency. Given the required role of PP2A in inducing
 normal T_H17 polarization, the question of whether defective T_H17 PP2A cKO cells also influence
 T_H17-driven autoimmune disease was investigated *in vivo* using an experimental autoimmune
 encephalomyelitis (EAE) model. We therefore immunized PP2A WT and cKO mice with myelin

144 oligodendrocyte glycoprotein peptide of amino acids 35–55 (MOG₃₅₋₅₅) to induce EAE.

145 Clinical scoring showed that PP2A deficiency alleviated symptoms of autoimmunity (Fig. 2A). 146 Histological examination showed significantly less mononuclear cell infiltration and demyelination in 147 the cerebral and spinal cord of the cKO mice (Fig. 2B). Inflammatory cell infiltration into the central 148 nervous system (CNS) was also greatly diminished in the cKO group (Fig. 2C). Although the 149 proportion of CD4⁺ T cells was unchanged in the CNS of cKO mice, the total numbers of infiltrating 150 $CD4^+$ and $CD8^+$ cells were significantly reduced (Fig. 2C). IL17A producing $CD4^+$ T cells were also 151 present in significantly decreased numbers in both the CNS and draining lymph nodes (DLN), whereas 152 the frequencies of IFN γ producing CD4⁺ T cells were unchanged. (Fig. 2D-F). These data indicate that 153 reduced IL17A production upon PP2A cKO results in less severe MOG-induced CNS inflammation. 154 Indeed, in vitro MOG recall analysis also showed reduced IL17A production by PP2A cKO splenocytes, 155 while IFN γ production was unaffected (Fig. 2G). Intriguingly, Foxp3⁺ CD4⁺ T cell proportions were 156 also reduced in the CNS but not in the DLN (Fig. 2D-F). This might be explained by markedly milder 157 inflammation in the CNS which consequently recruited less regulatory cells. PP2A cKO mice are thus 158 resistant to EAE and this is strongly correlated with an observed significant reduction in $T_H 17$ cell 159 induction.

160 Intact TCR and IL6 signaling in PP2A cKO CD4⁺ T cells. We next investigated how PP2A 161 deficiency affected intracellular signaling in controlling $T_{\rm H}17$ cell differentiation. Intact TCR signaling 162 is indispensable for $T_{\rm H}17$ commitment (18). However, our results showed that PP2A deficiency did not 163 affect normal CD69 upregulation (SI Appendix, Fig. S6A), cell proliferation (SI Appendix, Fig. S6B) or 164 production of IL2 or IFNy (SI Appendix, Fig. S6C) following anti-CD3 stimulation. Interestingly, 165 Western Blot analysis showed upregulation of pERK and pP38 in PP2A deficient cells (SI Appendix, 166 Fig. S6D) and these two pathways are known to play opposing roles in $T_{\rm H}17$ differentiation. Inhibition 167 of MEK-ERK signaling enhances T_H17 differentiation while activation of P38 is critical for optimal 168 $T_{\rm H}17$ polarization (19-21). We found that use of an MEK inhibitor (inhibiting ERK, U0126) failed to 169 restore $T_{\rm H}17$ differentiation due to PP2A deficiency (SI Appendix, Fig. S6E). Thus, subtle changes in 170 MAPKs activation are not correlated with decreased $T_{\rm H}17$ differentiation due to PP2A deficiency. 171 PP2A overexpression has been previously reported to upregulate *II17a* gene transcription by enhancing 172 IRF4 activity (11). However, the observed mRNA, protein and IRF4 activity did not support 173 involvement of IRF4 in leading to diminished *Il17a* transcription (*SI Appendix*, Fig. S5C-E).

By using the PP2A inhibitor OA, previous work has suggested a possible regulatory role of PP2A in regulating IL6 signaling, including promoting the stability of IL6 receptor gp130 (CD130) (22) and modulating STAT3 phosphorylation (23). However, our experiments did not show any alterations in either IL6 receptor expression (*SI Appendix*, Fig. S7A and B) or STAT3 phosphorylation (Y705 and S727) after IL6 stimulation in cKO T cells (*SI Appendix*, Fig. S7C) thus excluding the possibility that the inhibition of $T_H 17$ differentiation upon PP2A deletion is due to TCR or IL6 signaling changes.

180 Differential modulation of SMAD2/3 activity by PP2A deficiency restrains T_H17 differentiation.

181 In TGF β pathway, TGF β RI and RII, which are reported to be opposingly regulated by two different 182 PP2A B subunits (14), were similarly expressed in PP2A cKO T cells (Fig. 3A and B). Meanwhile, we 183 found that pSMAD2 (Ser465/467) level was decreased but pSMAD3 (Ser423/425) level was increased 184 after TGF_β stimulation in PP2A cKO cells (Fig. 3C). In accordance, SMAD2 hyper-phosphorylation 185 and SMAD3 under-phosphorylation was observed in PP2A Ca overexpressed 293FT cells after TGFB 186 stimulation (SI Appendix, Fig. S8A and B). We next performed the Co-IP assay in Jurkat cells to 187 explore the binding of R-SMADs to PP2Ac. We found that PP2Ac can form stable complex with 188 SMAD2 and SMAD3, which does not depend on either TCR or TGFβ stimulation (SI Appendix, Fig. 189 S8C and D).

190 In addition, in vitro dephosphorylation assay showed that PP2A can directly dephosphorylate pSMAD3 191 (SI Appendix, Fig. S8E-G). Studies on SMAD2 and SMAD3 conditional knockout mice have revealed 192 the opposite functions of these two molecules in inducing $T_H 17$ cells (24-27). We thus suspected that 193 the altered activation of SMAD2/3 in PP2A cKO cells might serve as the major contributor towards 194 decreased *II17a* transcription. Indeed, when we expressed different activation forms of SMAD2/3 (WT, 195 dominant negative form 2SA, constitutive active mutants 2SD) in naïve CD4⁺ T cells and analyzed cell 196 differentiation in $T_H 17$ condition, the results clearly showed that insufficient activation of SMAD2 197 caused defective $T_{\rm H}17$ differentiation, while constitutively activated SMAD2 promoted optimal $T_{\rm H}17$ 198 priming (Fig. 3D and E). On the contrary, ectopic expression of SMAD3 dramatically repressed $T_{\rm H}17$ 199 polarization. Interestingly, a SMAD3-2SA mutant also showed inhibitory activity to $T_{\rm H}17$ polarization 200 although to a lesser degree (Fig. 3F and G), indicating that suppression of $T_{\rm H}17$ differentiation by 201 SMAD3 depends on both SMAD3 activation and on its overall expression level. To rule out alterations

in iTreg cell skewing condition in the previous experiments, we also used a series of TGFβ doses for
suboptimal iTreg priming but observed no difference between the PP2A cKO and WT groups (*SI Appendix*, Fig. S7D).

205 Changes in SMAD2/3 activity synergistically downregulate II17a transcription via reducing 206 RORyt activity. We next asked how the shift of SMAD2/3 phosphorylation status affected *1117a* 207 transcription. We found that the protein expression levels of ROR γ t and ROR α were not different in 208 PP2A WT and cKO T_H17 cells (Fig. 4A and B). More importantly, retrovirus-mediated ectopic 209 expression of RORyt could not completely restore $T_{\rm H}17$ potentiation in cKO T cells (Fig. 4C and D). 210 These data supported the hypothesis that PP2A controlled $T_{\rm H}17$ differentiation is independent of RORyt 211 protein expression. To address whether overactivation of SMAD3 and insufficient activation of 212 SMAD2 could work cooperatively to suppress RORyt activity, ChIP analysis of RORyt occupancy of 213 1117a gene region was carried out. The result confirmed our hypothesis that with equal RORyt 214 expression, its activity was largely reduced due to PP2A deficiency (Fig. 4E). Phosphorylation changes 215 of SMAD2/3 affected their binding ability with ROR γt . In cKO T_H17 cells, ROR γt binded more 216 SMAD3 and less SMAD2 than observed in WT $T_{\rm H}17$ cells (Fig. 4*F*).

217 Different activation forms of SMAD2/3 were then co-transfected with RORyt in the 293FT cell line. 218 These experiments showed that the constitutively active SMAD2/3 preferentially interacts with RORyt 219 over the inactive forms, and that SMAD3 is more accessible to bind RORyt than SMAD2 (Fig. 4G). 220 These results suggest that phosphorylation changes in SMAD2/3 may inhibit RORyt activity by 221 affecting the capacity of SMAD2/3 to form complexes with RORyt. Based on this hypothesis, we 222 performed rescue experiments with SMAD2-2SD transfection or SMAD3 knockdown. Both 223 approaches significantly improved T_H17 polarization in cKO naïve CD4⁺ T cells (Fig. 4*H*-*K*). SMAD3 224 knockdown efficiency by siRNA was verified by Western Blot and RT-PCR (SI Appendix, Fig. S9A and 225 B).

226 PP2A inhibitors phenocopy phosphorylation changes of SMAD2/3 and restrain T_H17 polarization

in vitro. We observed that administration of PP2A inhibitors in 293FT cells phenocopied the SMAD2/3 activation changes in a dose dependent manner (Fig. 5*A*). Further, the PP2A inhibitor Cantharidin (CAN) restrained ROR γ t mediated *Il17a* promoter activation (Fig. 5*B*). More importantly, when administrating PP2A inhibitor Cantharidin in T_H17 culture medium, we also observed a dose dependent inhibitory role at a concentration that had no effect on cell proliferation (Fig. 5C-E). Another two PP2A
inhibitors OA and Fostriecin (FOS) also showed similar effects upon T_H17 differentiation (*SI Appendix*,
Fig. S10A-E). In addition, PP2A cKO T cells did not display suppression effects by PP2A inhibitors,

ruling out the off-target effects might result in $T_H 17$ depression (Fig. 5F and SI Appendix, Fig. S10F).

235 A PP2A inhibitor protects mice from EAE. We examined whether Cantharidin can block $T_H 17$ cell 236 mediated inflammation in EAE. A significant reduction of disease severity was observed in Cantharidin 237 treated PP2A WT mice compared to PBS treated WT mice (Fig. 6A). Histological examination also 238 showed significantly less mononuclear cells infiltration and demyelination in the spinal cord of the 239 Cantharidin treated WT mice (Fig. 6B). Meanwhile, there was no observable aggravation of clinical 240 symptoms by applying Cantharidin in PP2A cKO mice, suggesting that Cantharidin dose was within a 241 safe range (Fig. 6A). Fewer mononuclear lymphocytes and CD4⁺ T cells infiltrated into the CNS of 242 Cantharidin treated WT mice than of the PBS WT group at the onset or peak of EAE, while the CD8⁺ 243 and myeloid population was not significantly changed (Fig. 6C-D). Additionally, the ratio of $T_{\rm H}17$ cells 244 was lower in Cantharidin treated WT mice than in PBS treated WT mice (p=0.08) (Fig. 6E). The 245 number of infiltrated $T_H 17$ cells was also significantly lower in the CNS. Treg cells and IFN γ 246 producing cells were slightly decreased (Fig. 6F). Furthermore, Cantharidin treatment in PP2A cKO 247 groups did not alter the number of inflammatory lymphocytes infiltrated into CNS (Fig. 6G-H). 248 Cantharidin treated cKO groups showed no effects to EAE symptoms, suggesting the specific targeting 249 of Cantharidin to PP2A in T cells in this experimental setting. However, whether Cantharidin can also 250 act on other cells and contribute to the therapeutic effects is unclear. Collectively, data above showed 251 that PP2A inhibitor Cantharidin can limit EAE development principally by reducing $T_{\rm H}17$ 252 differentiation.

254 Discussion.

By using peripheral T cell specific KO mice, we have established the positive regulatory role of PP2A in $T_H 17$ differentiation as well as in inflammatory autoimmune diseases. We have also proved that underactivated SMAD2 and overactivated SMAD3 downstream of TGF β signaling collectively reduced ROR γ t mediated *II17a* transcription in PP2A cKO mice. PP2A inhibitors also reduced $T_H 17$ polarization, indicating a promising therapeutic avenue for treating $T_H 17$ cell mediated autoimmune diseases.

PP2A is one of the most abundant phosphatases and crucial for many key cellular events. A total knockout of the PP2A catalytic subunit a in mice is lethal (16). To our surprise, PP2A deficiency did not lead to fundamental changes in basic processes such as cell survival and proliferation. This is either because of the residual PP2A expression in our cKO mice or the stage and cell specific functions of PP2A.

As shown by RNAseq and RT-PCR analysis, the transcriptional changes of $T_H 17$ signature genes induced in PP2A cKO were limited. Obvious changes were observed in *II17a* and *II17f*, but not in *Rorc*. Expression of ROR γ t was intact, which exclude the possibility that PP2A is involved in the pathways leading to ROR γ t induction. Therefore, intracellular signaling events downstream of ROR γ t and closely related to *II17a* transcription might be the candidate targets of PP2A mediated inhibition of $T_H 17$ differentiation.

SMAD2, SMAD3 and SMAD4 are all critical for TGF β signaling and participate in T_H17 or iTreg cell 272 273 priming to induce balanced expression of Foxp3 and RORyt (24-26, 28-30). It is intriguing that 274 SMAD2 knockout mice show reduced $T_H 17$ cell differentiation and ameliorated EAE, while a 275 deficiency in SMAD3 has the opposite effects (24, 26-28). Furthermore, overexpression of SMAD2 276 and ROR γ t augments the differentiation of T_H17 cells. However, SMAD3 binds to ROR γ t in Co-IP 277 experiments and decreases its transcriptional activity (26). Moreover, R-SMAD activation is mainly via 278 the phosphorylation of the C-terminal SSXS motif, which is critical for R-SMAD function. The active 279 form of SMAD3 might enhance its binding affinity with RORyt and it is known that SMAD3 can 280 compete with SMAD2 for binding with RORyt (27). These results suggest that active SMAD2 plays a 281 positive role and active SMAD3 plays a negative role in $T_{\rm H}17$ cell differentiation likely via dynamic 282 interaction with RORyt (26, 27).

283 Our study confirmed that altered SMAD2/3 activation by PP2A affects $T_H 17$ differentiation, resulting

in decreased *II17a* transcription *via* forming complex with ROR γ t and reducing its activity and thus affecting T_H17 differentiation. Importantly, this is the first study to identify PP2A as the critical phosphatase responsible for Ser/The dephosphorylation on R-SMADs and necessary for efficient T_H17 differentiation.

It is important to know the precise dephosphorylation site on R-SMAD and the responsible kinases. 288 289 Our previous work has elucidated the importance of threonine residue T324 in the α -helix 1 region of 290 SMAD2 for regulation during $T_{\rm H}17$ differentiation (6). It is thus likely that PP2A upregulates SMAD2 291 C-terminal phosphorylation via modulating MINK1 activity. However, the function of PP2A appears to 292 be broader and more dominant than this single phosphorylation event, since we also observed increased 293 SMAD3 phosphorylation in cKO CD4⁺ T cells, which also contributes to deceased T_H17 differentiation. 294 This observation is in accordance with a previous finding that the PP2A structural subunit PR65 could 295 interact with SMAD3 (31).

It is also likely that PP2A directly regulates the phosphorylation status of ROR γ t. Recent study showed that two functional phosphorylation sites identified on ROR γ t played opposite roles in T_H17 polarization. IKK α was discovered as upper stream regulator for the phosphorylation change (32). Whether PP2A participates in the interaction with IKK α or ROR γ t in regulating ROR γ t activity remains to be elucidated.

301 The classical TGFβ pathway is also critical for iTreg differentiation (33). SMAD2 and SMAD3 double 302 knockout mice showed dramatic loss of Foxp3 induction (28). Then why is iTreg differentiation not 303 affected by PP2A deficiency? It is most likely because of the redundant roles of SMAD2 and SMAD3 304 in TGFB induced iTreg plasticity (28). Overactivated SMAD3 may compensate for insufficient 305 activation of SMAD2 in Foxp3 induction. In a recent study, PP2A was reported to be indispensable for 306 the maintenance of the suppressive function of Treg cells via regulating the activity of the mTORC1 307 complex. Specific ablation of PP2A in Treg cells by Foxp3-YFP-Cre leads to autoimmunity with 308 similar clinical features of scurfy mice (34). We also observed the same Treg phenotype in dLck-driven 309 PP2A cKO mice, but the overall outcome of PP2A defect in peripheral T cells is dominated by $T_{\rm H}17$ 310 differentiation impairment, which is demonstrated by their reduced susceptibility to autoimmune 311 diseases induction.

312 Finally, in addition of finding the importance of PP2A to $T_{\rm H}17$ differentiation, we demonstrated the

- 313 translational potential of this pathway by showing the therapeutic effect of PP2A inhibitor in
- 314 controlling autoimmune diseases in the EAE model.

316 Materials and Methods.

Mice. *Ppp2ca* flowed mice were provided by X. Gao, Model Animal Research Center of Nanjing University. Mice with
 Cre recombinase driven by the distal promoter of the gene encoding the kinase Lck were bought from the Jackson Laboratory.
 The experimental protocols were approved by the Review Committee of Zhejiang University School of Medicine and followed

- 320 institutional guidelines.
- 321 EAE Induction. EAE was induced as described previously (35). Briefly, mice aged 6-8 weeks were immunized with 200 mg
- 322 MOG₃₅₋₅₅ (Sangon, MEVGWYRSPFSRVVHLYRNGK) in an equal amount of Complete Freund's Adjuvant (Chondrex, Inc.) and
- 323 received 200 ng pertussis toxin (List Biochemicals) intravenously on days 0 and 2 post-induction. Clinical evaluation was
- 324 assigned daily using a 5-point scale: 1, flaccid tail; 2, impaired righting reflex and hindlimb weakness; 3, hindlimb paralysis; 4,
- 325 hindlimb and forelimb paralysis; 5, moribund. Detailed materials and methods are presented fully in SI Appendix, SI Materials
- 326 and Methods.
- 327 Statistical Analysis. Statistical analysis was performed using GraphPad Prism. The data were analyzed by Student's t-test. All P
- 328 value less than 0.05 was considered significant (P < 0.05 = *; P < 0.01 = **; P < 0.001 = ***).
- 329

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451 **Figure legends**

452 Fig 1. PP2A deficiency specifically limits T_H17 differentiation *in vitro*.

453 (A, B) Flow cytometry (A) and quantification (B) of IL17A staining in naïve CD4⁺ T cells from PP2A 454 WT and cKO mice differentiated under T_H17 polarizing condition for 5 days. (C) Enzyme-linked 455 immunosorbent assay (ELISA) of IL17A in the culture medium of each polarizing condition (n=3 456 technical replicates). (D) RT-PCR analysis of T_H17 signature genes (n=3 technical replicates). Each 457 symbol represents an individual mouse (n=8), error bars show mean ± SEM. Data are representative of 458 at least three independent experiments with similar results.

459 Fig 2. Loss of PP2A protects mice from EAE by repressing IL17A production.

460 (A) Mean clinical scores for EAE from each group. (B) Representative histology of the brain and spinal 461 cord (hematoxylin and eosin (H&E) on the left and luxol fast blue (LFB) on the right) of mice after 462 EAE induction (day 19). Arrowheads indicate inflammatory infiltration (left) and demyelination (right). 463 Scale bars represent 100 µm. (C) Number and frequency of mononuclear cells or CD4⁺ or CD8⁺ T cells 464 infiltrated into central nervous system. (D) Flow cytometry of IL17A, IFNy and Foxp3 staining from 465 CNS (left panel) or DLN (right panel) CD4⁺ T cells. (E, F) Quantification of IL17A⁺, IFN γ^+ and Foxp3⁺ CD4⁺ T cells in CNS (E) or DLN (F). (G) Splenocytes were rechallenged with MOG peptide 466 467 (5µg/ml) or control vehicle for 3 days, and cytokine production was measured by ELISA. Each symbol 468 represents an individual mouse (n=4-6); error bars show mean \pm SEM. Data are representative of three 469 independent experiments with similar results.

470 Fig 3. Insufficient SMAD2 activation and overactivated SMAD3 under TGFβ pathway restrains

471 T_H17 differentiation.

472 (A, B) Histograms (A) and mean fluorescence intensity (MFI) quantification (B) of TGF^β receptor I 473 and II staining on CD4 gated cells from splenocytes of PP2A WT and cKO mice. (C) Enriched CD4⁺ T 474 cells from PP2A WT and cKO were stimulated with 10 ng/ml TGF\beta as indicated, whole cell lysates 475 were probed with the indicated antibodies in the immunoblots. (D, E) Flow cytometry (D) and 476 quantification (E) of $T_{\rm H}17$ polarization with ectopic expression of Vector, WT, 2SA and 2SD of 477 SMAD2 in WT naïve CD4⁺ T cells. GFP expressing cells were gated for analysis on day 3. (F, G) Flow 478 cytometry (F) and quantification (G) of $T_H 17$ polarization with ectopic expression of Vector, WT, 2SA 479 and 2SD of SMAD3 in WT naïve CD4⁺ T cells. GFP expressing cells were gated for analysis on day 3. 480 Each symbol represents an individual mouse (n=4). Error bars show mean \pm SEM. Data are 481 representative of three independent experiments (C) or two independent experiments with two 482 replicates (D, F).

483 Fig 4. Differential modulation of SMAD2/3 inhibits RORyt mediated Il17a transcription by

484 forming complex with RORγt.

485 (A) Flow cytometry of ROR γ t staining from naïve CD4⁺ T cells primed under T_H17 polarizing 486 condition for 2 days. (B) ROR α was immunoblotted with whole cell lysate of T_H17 cells. (C-D) Flow 487 cytometry (C) and quantification (D) of T_H17 polarization with ectopic expression of Vector or ROR γ t 488 in PP2A WT and cKO naïve CD4⁺ T cells. GFP expressing cells were gated for analysis on day 3. (E) 489 RORyt binding to the sites of the II17a gene promoter was analyzed by using chromatin 490 immunoprecipitation (ChIP) assay with RT-PCR. (F) Co-IP analysis of binding ability with RORyt 491 among SMAD2/3 in WT and cKO T_H17 cells. (G) Co-IP analysis of binding ability with ROR γ t among 492 WT, 2SA and 2SD mutant of SMAD2/3 in 293FT cells. (H) Flow cytometry of $T_{\rm H}17$ polarization with 493 ectopic expression of Vector or SMAD2-2SD in PP2A WT and cKO naïve CD4⁺ T cells. (I) Ratio of 494 IL17A frequency comparing VEC-cKO or SMAD2-2SD-cKO to VEC-WT. (J) Flow cytometry of $T_{\rm H}17$ 495 polarization after suppressing SMAD3 expression by siRNA in naïve CD4⁺ T cells. (K) The ratio of 496 IL17A frequency in cKO cells transfected with siRNA-SMAD3 or control to the frequency of WT cells 497 transfected with control. Error bars show mean \pm SEM. Data are representative of three (A, B, G, H, J) 498 or two (C, D, E, F) independent experiments.

499 Fig 5. PP2A inhibitors lead the same change of SMAD2/3 activation under TGFβ pathway and

500 limit $T_H 17$ priming *in vitro*.

501 (A) SMAD2/3 was overexpressed in the 293FT cells and PP2A inhibitors were added in serum free 502 medium for 2 hours followed by TGF β (3 ng/ml) stimulation for 3 hours. Western Blot analysis using 503 phospho-specific SMAD2/3 (p-SMAD2/3) and FLAG-tag (total-SMAD2/3) antibodies. (B) Il17a 504 promoter and SMAD2/3 with or without RORyt was transfected into 293FT cells and then treated with 505 PP2A inhibitors and TGF β as Figure (A). Luciferase activity was measured and normalized based on 506 Renilla luciferase gene. (C) Sorted naïve $CD4^+$ T cells were polarized under T_H17 priming condition 507 with the indicated concentration of Cantharidin for 3 days and IL17A⁺ population was analyzed using 508 flow cytometry on day 5. (D) The concentration of IL17A in the culture supernatant was measured by 509 ELISA. (E) Histogram of CFSE fluorescence staining of cells in Figure (C). (F) WT naïve CD4⁺ T cells 510 cultured with Cantharidin (5 μ M) for the first 3 days in T_H17 priming condition and analyzed IL17A⁺ 511 population by flow cytometry on day 5. Error bars show mean \pm SEM. Data are representative of two 512 independent experiments with similar results.

513 Fig 6. A PP2A inhibitor suppresses EAE development.

514 (A) PP2A WT and cKO mice were immunized with $MOG_{(35-55)}$ peptide. PP2A inhibitor Cantharidin 515 $(0.6 \ \mu g/g)$ was administered intraperitoneally daily from day 10 to day 12 and then was given once 516 every two days. Mean clinical scores for EAE from each group. (B) Representative histology of the 517 spinal cord (H&E left and LFB right) of mice after EAE induction (day 19). Arrowheads indicate 518 inflammatory infiltration (left) and demyelination (right). Scale bars represent 100 µm. (C) 519 Quantification of total mononuclear cells, CD4⁺ T cells, CD8⁺ T cells and myeloid cells that infiltrated 520 into the CNS of WT mice at peak of the disease. (D) Ratio of CD4⁺ and CD8⁺ T cells (gated at CD45^{hi} 521 CD11b) in the CNS of WT groups. (E, F) Ratio (E) and number (F) of IL17A⁺ or Foxp3⁺ or IFN γ^+ 522 CD4⁺ cells in the CNS of the WT groups at disease peak. (G) Quantification of total mononuclear cells, 523 CD4⁺ T cells, CD8⁺ T cells and myeloid cells that infiltrated into the CNS of the cKO groups. (H) Ratio 524 of CD4⁺ and CD8⁺ T cells (gated at CD45^{hi} CD11b⁻) that infiltrated into the CNS of the cKO groups. 525 Each symbol represents an individual mouse (n=5-7 per genotype); error bars show mean \pm SEM. Data 526 are representative of two independent experiments with similar results.











