The nutrient-sensing Rag-GTPase complex in B cells controls humoral immunity via TFEB/TFE3-dependent mitochondrial fitness

Xingxing Zhu¹, Yue Wu^{2,3}, Yanfeng Li¹, Xian Zhou¹, Jens O. Watzlawik⁴, Yin Maggie Chen⁵, Ariel L. Raybuck⁶, Daniel D. Billadeau⁵, Virginia Smith Shapiro⁵, Wolfdieter Springer^{4,7}, Jie Sun^{2,3}, Mark R. Boothby⁶, Hu Zeng^{1,5, *}

¹Division of Rheumatology, Department of Medicine, Mayo Clinic Rochester, MN 55905, USA

²Carter Immunology Center, University of Virginia, Charlottesville, VA 22908, USA

³Division of Infectious Diseases and International Health, Department of Medicine, University of Virginia, Charlottesville, VA 22908, USA

⁴Department of Neuroscience, Mayo Clinic, Jacksonville, FL 32224, USA

⁵Department of Immunology, Mayo Clinic Rochester, MN 55905, USA

⁶Department of Pathology, Microbiology & Immunology, Molecular Pathogenesis Division, Vanderbilt University Medical Center and School of Medicine, Nashville, TN 37232, USA

⁷Neuroscience PhD Program, Mayo Clinic Graduate School of Biomedical Sciences, Jacksonville, FL 32224, USA

*Corresponding author: Hu Zeng; E-mail: Zeng.hu1@mayo.edu



Supplementary Fig. 1. RagB deficiency doesn't affect early B cell development in BM and peripheral B cells. Expression of RagA, TFEB, TFE3 (A) and Raptor (B) was examined by immunoblot. (C) Representative flow plots of splenic CD4⁺ T cells and B220⁺ B cells from WT mice (n = 7), $Cre^{ER}Rraga^{M/R}Rragb^{M/R}$ (n = 7), and $Cre^{ER}Rptor^{M/R}$ (n = 5). (D) flow plots of splenic follicular B cells (CD21^{Int}CD23^{Int}) or marginal zone (CD21^{Int}CD23^{Int}) from WT mice (n = 8), $Cre^{ER}Rraga^{M/R}Rragb^{M/R}$ (n = 7), and $Cre^{ER}Rptor^{M/R}$ (n = 7). (E and F) Summaries of p-S6 and p-4EBP1 expressions in the B cells stimulated with LPS/IL-4/BAFF for 72 h and examined by immunoblot. E, WT mice (n = 7), and $Cre^{ER}Rptor^{M/R}$ (n = 8). F, WT mice (n = 9) and $Cre^{ER}Rraga^{M/R}Rragb^{M/R}$ (n = 9). (G) The percentages of Annexin V+7-AAD⁻ and Annexin V+7-AAD⁺ B cells were examined by flow cytometry. WT mice (n = 7) and $Cre^{ER}Rraga^{M/R}Rragb^{M/R}$ (n = 6). (H) Expression of CXCR4 on BM B220^{Int}CD43⁻ B cells. Right, the relative MFI of CXCR4 level on BM B220^{Int}CD43⁻ B cells. WT mice (n = 7), $Cre^{ER}Rraga^{M/R}Rragb^{M/R}$ (n = 7), and $Cre^{ER}Rptor^{M/R}$ (n = 2). (I) Representative flow plots of bone marrow B220 and CD43 expression from WT (n = 9), and Cre^{ER}Rraga^{M/R} (n = 8) mice. (J) Representative flow plots of BP-1 and CD24 expression in BM B220^{Int}CD43⁺ IB cell precursors from WT (n = 9) and Cre^{ER}Rragb^{M/R} (n = 8) mice. (K) Representative flow plots of splenic follicular B cells (CD21^{Int}CD23^{Int}) or marginal zone (CD21^{Int}CD23^{Int}) from WT (n = 9) and Cre^{ER}Rragb^{M/R} (n = 8) mice. (K) Representative flow plots of splenic follicular B cells (CD21^{Int}CD23^{Int}) or marginal zone (CD21^{Int}CD23^{Int}) from WT (n = 9) and Cre^{ER}Rragb^{M/R} (n = 8) mice. (K) Representative flow plots of splenic follicular B cells (CD21^{Int}CD23^{Int}) or marginal zone (CD21^{Int}CD23^{Int}) from WT (n = 9) and Cre^{ER}Rragb^{M/R} (n = 8) mice. (L) Representative flow plots of GL-7 and Fas expr



Supplementary Fig. 2. Rag-GTPases deficiency intrinsically disrupts B cell development. (A-D) Tamoxifen was administered to μ MT:Cre^{ER}*Rraga*^{#/#}*Rragb*^{#/#} (n = 5), and WT (n = 4) chimera mice by oral gavage daily for 4 consecutive days. Mice were analyzed 7 days after the last injection. (A) Representative flow plots of bone marrow B220 and CD43 expression from μ MT:Cre^{ER}*Rraga*^{#/#}*Rragb*^{#/#}, and WT chimera mice. Right, summaries of the percentages and numbers of B220^{lo}CD43⁻, B220^{hi}CD43⁻ and B220⁺CD43⁺ cells. (B) Representative flow plots of BP-1 and CD24 expression in BM B220⁺CD43⁺lgM⁻ B cell precursors from μ MT:Cre^{ER}*Rraga*^{#/#}*Rragb*^{#/#}, and WT chimera mice. Right, summaries of the percentages and numbers of bone marrow fraction A (CD24⁻BP-1⁻), fraction B (CD24⁺BP-1⁻), and fraction C/C'(CD24⁺BP-1⁺) cells. (C) Representative flow plots of splenic follicular B cells (CD21^{int}CD23^{hi}) or marginal zone (CD21^{hi}CD23^{int}) from μ MT:Cre^{ER}*Rraga*^{#/#}*Rragb*^{#/#}, and WT chimera mice. Right, summaries of the percentages of splenic follicular B cells (CD21^{int}CD23^{hi}) or marginal zone (CD21^{hi}CD23^{int}) B cells. (D) Representing flow plots of Fas and GL-7 expression on B cells from the Peyer's patches of μ MT:Cre^{ER}*Rraga*^{#/#}*Rragb*^{#/#}, and WT chimera mice. Right, summaries of GC (GL-7⁺Fas⁺) B cells. Data in graphs represent mean \pm SEM. ns, not significant. *p < 0.05, **p < 0.01, ***p < 0.001, two-tailed Student's t test was used.







Supplementary Fig. 3. Rag-GTPases deficiency reduces GC formation and antibody production independent of mTORC1 in peptide immunization. (A-G)

Tamoxifen was administered to chimera mice by oral gavage daily for 4 consecutive days. Mice were immunized intraperitoneally (100 mg NP-OVA/alum) 7 days after the last injection. (A) Representative flow plots of GL-7 and Fas expression on B cells from the mesenteric lymph node (mLN) of immunized WT (n = 7), μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 9), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 7) chimera mice. (B) Representative flow plots of NP⁺IgG1⁺ GC B cells from the spleen of immunized WT (n = 9), μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 13), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 9) chimera mice. (C) Representative flow plots of NP⁺IgG1⁺ GC B cells from the mLN of immunized WT (n = 4), μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 7), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 3) chimera mice. (D) Cryosections from the spleens of immunized WT, μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 7), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 3) chimera mice. (D) Cryosections from the spleens of immunized WT, μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 9), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 7) chimera mice. (D) Cryosections from the spleens of immunized WT (n = 7), μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 9), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 7) chimera mice. (F) Representative flow plots of CD138 and B220 expression in mLN of WT (n = 7), μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 9), and μ MT:Cre^{ER}*Rptor^{MR}* (n = 7) mice. (G) Active caspase-3 was measured on CD19⁺, GC and CD138⁺ B cells of spleens and mesenteric lymph nodes (mLN) from immunized chimera mice, WT (n = 3) and μ MT:Cre^{ER}*Rraga^{MR}Rragb^{MR}* (n = 5). Data in graphs represent mean \pm SEM. ns, not significant. *p < 0.05, **p < 0.01, ***p < 0.001, and ****p < 0.0001, one-way ANOVA (A-F), two-tailed/unpaired student T-test (G). Source data are provided as a Source Data file.



Supplementary Fig. 4. Rag-GTPases regulate TFEB/TFE3 axis in B cells. (A-B) Rapamycin was added into the culture medium at 24 h after B cells were stimulated with LPS/IL-4/BAFF. TMRM (A) or MTDR (B) staining was examined by flow cytometry after B cells were stimulated for additional 48 h, WT (n = 5) and Cre^{ER}*Rraga^{MI}Rragb^{MI}* (n = 4). The mean fluorescence intensity (MFI) of TMRM and MTDR was normalized to that of WT B cells treated with DMSO (set as "1"). The numbers indicate the fold differences of average TMRM or MTDR MFI between WT and RagA/RagB deficient B cells. Data in graphs represent mean ± SEM. **p < 0.01, ***p < 0.001, two-tailed/unpaired Student's t test (A and B). (C) Bulk RNA sequencing was performed on the B cells activated with LPS/IL-4/BAFF for 72 h, then GSEA was conducted on differentially expressed genes (DEGs), and significantly enriched pathways were plotted according to NES (normalized enrichment score). (D) Volcano plot of the lysosome genes enriched in RagA/RagB deficient B cells. (E-G) GC B cells were sorted from immunized *Aicda^{Cre}Rraga^{MII}Rragb^{MIII}*, and WT mice, and conducted bulk RNA sequencing. (E) *Rraga*, and *Rptor* levels from the bulk RNA sequencing data. (F) PCA plot from the bulk RNA sequencing analysis. (G) Statistics of differently expressed genes from different comparisons. (H) Cytosolic and nuclear proteins were isolated from the B cells activated with LPS/IL-4/BAFF for 72 h. Expression of TFE3 was examined by immunoblot. Lamin B was used as a nuclear control, tubulin was used as a cytosol control. Source data are provided as a Source Data file.



Supplementary Fig. 5. Mitophagy modulates B cell activation. (A and B) B cells were labeled with Celltrace violet (CTV) and stimulated with LPS/IL-4/BAFF in the presence of mitophagy activators CMPA-39 (1 μ M), MF094 (1 μ M) or Urolitin A (1 μ M) for 72 h, IgG1 expression (A) and dilution of CTV (B) were examined by flow cytometry. Right, the percentage of IgG1⁺ B cells (A) or divided CTV (B). (C-F) B cells were labeled with CTV and stimulated with LPS/IL-4/BAFF and mitophagy inhibitors 3-MA (1 mM), IC-87114 (5 μ M) (C and D) or PRT062607 (1 μ M) (E and F) for 3 days, IgG1 expression and CTV dilution were measured by flow cytometry. Data presented in the graphs were collected from 3 independent experiments. Data in graphs represent mean \pm SEM. ns, not significant. *p < 0.05, **p < 0.01, ***p < 0.001, and, one-way ANOVA (A-D), two-tailed/unpaired student T-test (E and F). Source data are provided as a Source Data file.



Supplementary Fig. 6. TFEB plays a critical role in Rag GTPases regulated B cell function. (A) Schematic of the experimental design for making WT TFEB and Ca TFEB plasmids (Created in BioRender. Zhu, X. (2023) https://BioRender.com/w00l228). (B) Representative histogram of GFP expression on the vector, WT TFEB or Ca TFEB transduced B cells. (C) Representative flow plots of CD138⁺ expression on vector, WT TFEB, and Ca TFEB transduced GFP⁺ B cells, n = 4 for each group. (D) Representative flow plots of CTV dilution from vector, WT TFEB, and Ca TFEB transduced GFP⁺ B cells. (E) p-S6 (n = 7 per group) and p-4EBP1(n = 5 per group) levels were measured on GFP⁺ B cells by flow cytometry and the relative MFI was presented. (F) Representative flow plots of IgG1 and CTV expression activated in LPS/IL-4/BAFF with different concentrations of compound C1 for 72 h, n = 4 for each condition. (G) Representative flow plots of CTV dilution from different concentrations of compound C1 treated B cells. (H) Significantly enriched pathways were plotted according to NES. (I) Splenic B cells from Cre^{ER}*Rraga^{MR}Rragb^{MM}* (n = 5), and WT (n = 5), mice were transduced with vector or TFEB TDN, and TFEB downstream target genes were examined on GFP⁺ B cells. (J) Splenic B cells from were transduced with vector or TFEB TDN, IgG1⁺ B cells and MitoSox were measured. For IgG1⁺ B cells, Cre^{ER}*Rraga^{MR}Rragb^{MM}* (n = 4), and WT (n = 5) mice. For MitoSox, Cre^{ER}*Rraga^{MR}Rragb^{MM}* (n = 5), and WT (n = 3). (K) TFEB downstream target genes were measured on the activated B cells. For *Tfeb*, *Rragc* and *Rragb^{MM}Tfeb^{MM}* (n = 6) mice. For *Lamp1*, WT (n = 4), Cre^{ER}*Rraga^{MR}Rragb^{MM}* (n = 6), mice. For *Lamp1*, WT (n = 4), Cre^{ER}*Rraga^{MM}*Rragb^{MM} (n = 5), and Cre^{ER}*Rraga^{MM}*Rragb^{MM} (freb^{MM} (n = 7). (M) p-S6 and p-4EBP1 levels were measured on activated B cells by immunoblot, Cre^{ER}*Rraga^{MM}* (n = 9), and Cre^{ER}*Rraga^{MM} Rragb^{MM} Tfeb^{MM}* (n = 7). Data in graphs represent mean ± SEM. ns, not significa





Supplementary Fig. 7. Abrogating TFEB rescues the deficiency in Rag-GTPases KO mice in context-dependent manner. (A) Representative flow plots of BP-1 and CD24 expression in BM B220⁺CD43⁺IgM⁻ B cell precursors from WT (n = 14), Cre^{ER}Rraga^{1//I}Rragb^{1//I} (n = 10), and Cre^{ER}Rraga^{1//I}Rragb^{1//I} (n = 11) mice. (B) Representative flow plots of B220 and CD43 expression in BM lymphocytes from Cre^{ER}Rraga^{®/#}Rraga^{®/#}(n = 10), Cre^{ER}Rraga^{®/#}Rraga mice. (C) Representative flow plots of GL-7 and Fas expression in lymphocytes from the Peyer's patches of WT (n = 9), Cre^{ER}Rraga^{®/iff} (n = 6), and Cre^{ER}Rraga^{1/1}*Rragb^{1/1}Tfeb^{1/1}* (n = 5) mice. (D-I) Tamoxifen was administered to animals by oral gavage daily for 4 consecutive days. Mice were immunized intraperitoneally (100 mg NP-OVA/alum) 7 days after the last injection. (D) Representative flow plots of GL-7 and Fas expression on splenic B cells from the spleen of WT (n = 7), µMT:Cre^{ER}Rraga^{#/#}Rragb^{#/#} (n = 8), and µMT:Cre^{ER}Rraga^{#/#}Rragb^{#/#}Tfeb^{#/#} (n = 9) immunized chimera mice. (E) Representative flow plots of CD138 and B220 expression in spleens from immunized WT (n = 7), μ MT:Cre^{ER}*Rraga*^{fi/fl} (n = 8), and μ MT:Cre^{ER}*Rraga*^{fi/fl}*Treb*^{fi/fl} (n = 9) chimera mice. (F) Representative flow plots of NP+lgG1+ GC B cells from the spleen of immunized WT (n = 7), µMT:Cre^{ER}Rraga^{fl/fl}Rragb^{fl/fl} (n = 9), and µMT:Cre^{ER}Rraga^{fl/fl}Rragb^{fl/fl} (n = 9) chimera mice. (G) Representative flow plots of splenic CD138⁺IgC1⁺ cells from immunized WT (n = 7), µMT:Cre^{ER}Rraga^{fiff}Rragb^{fiff} (n = 8), and µMT:Cre^{ER}Rraga^{fiff}Rraga^{fiff} (n = 8), and µMT:Cre^{ER}Rraga^{fiff} (n (n = 9) chimera mice. (H) high-affinity NP-specific antibodies of all classes were measured using the sera of immunized WT (n = 6), μMT:Cre^{ER}Rraga^{fl/fl} (n = 8), and µMT:Cre^{ER}Rraga^{1/#}Rragb^{1/#}Tfeb^{1/#} (n = 9) chimera mice. (I) Total NP-specific antibodies of all classes were measured using the sera of immunized WT (n = 6), μMT:Cre^{ER}Rraga^{fifi}Rragb^{fifi} (n = 8), and μMT:Cre^{ER}Rraga^{fifi}Rragb^{fifi} (n = 9) chimera mice. (J) Representative flow plots of splenic CD138⁺ cells from TNP-LPS immunized WT (n = 8), µMT:Cre^{ER}Rraga^{fifi}Rragb^{fifi} (n = 7), and µMT:Cre^{ER}Rraga^{fifi}Rragb^{fifi}Tfeb^{fifi} (n = 8) chimera mice. (K) anti-TNP antibody titers in the sera of immunized WT (n = 8), µMT:Cre^{ER}Rraga^{a/#}Rragb^{a/#} (n = 7), and µMT:Cre^{ER}Rraga^{a/#}Rragb^{a/#}Treb^{a/#} (n = 8) chimera mice. (L) WT mice were immunized with TNP-LPS or NP-OVA/alum, TMRM or MTDR on CD138⁺ cells were measured at day 9 (NP-OVA/alum) or 7 (TNP-LPS) post-immunization. Data in graphs represent mean ± SEM. ns, not significant. *p < 0.05, **p < 0.01, ***p < 0.001, and ****p < 0.0001, one-way ANOVA (B, C, D, E, F, G and J), two-way ANOVA (A, H, I and K), twotailed/unpaired Student's t test (L). Source data are provided as a Source Data file.



Supplementary Fig. 8 Gating strategies for FACS. (A) B cell analysis from the spleen or mLN of immunized mice, which is related to Fig. 3A-3C, Fig. 3H-3L, Fig. 7I-7K, Supplementary Fig. 3A-3C and 3E-3G, Supplementary Fig. 7D-7G, and 7J. (B) Hardy fraction gating strategy of Bone marrow, which is related to Fig. 2A-2D, Fig. 2H-2L, Fig. 7A-7B; Supplementary Fig. 1I-7J; Supplementary Fig. 2A-2B; Supplementary Fig. 7A-7B. (C) Germinal center B cell analysis in the Peyer's patch, which is related to Fig. 2E, Fig. 7C, Supplementary Fig. 1L, Supplementary Fig. 2D, Supplementary Fig. 7C. (D) Follicular and marginal zone B cells were analyzed in the spleen, which is related to Supplementary Fig. 1C-1D and 1K, Supplementary Fig. 2C. (E) Virally transduced B cells were analyzed/sorted by flow cytometery, which is related to Fig. 6B-6K, Supplementary Fig. 6B-6K.

Supplementary table

Gene	Name	Primer sequence
β-actin	β-actin-F	CGTCGACAACGGCTCCGGCATG
	β-actin-R	GGGCCTCGTCACCCACATAGGAG
Flcn	Flcn-F	GATGACAACTTGTGGGCGTGTC
	Flcn-R	CATCTGGACCAGGGTGTCCTCT
Tfeb	Tfeb-F	CCACCCCAGCCATCAACAC
	Tfeb-R	CAGACAGATACTCCCGAACCTT
Rragd	Rragd-F	CTGTTTGACGTGGTCAGTAAGAT
	Rragd-R	GTTGAGTCCTTGTCATACGGG
Lamp1	Lamp1-F	CAGCACTCTTTGAGGTGAAAAAC
	Lamp1-R	ACGATCTGAGAACCATTCGCA
Rragc	Rragc-F	AGATGTCACCCAATGAGACTCT
	Rragc-R	AGTCGTCCTGTGCATCAATGA