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研究課題名(和文) Studying the role of clonal hematopoiesis in mouse solid tumors using a native-tissue relevant context model

研究課題名(英文) Studying the role of clonal hematopoiesis in mouse solid tumors using a native-tissue relevant context model

研究代表者

NGUYEN BICH・TRAN (NGUYEN, BICH TRAN)

筑波大学・医学医療系・研究員

研究者番号：10812901

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研究成果の概要(和文)：クローン性造血(CH)は、固形癌の25%以上で予後と関連していることが確認されている。大腸癌(CR)におけるクローン性造血の役割を明らかにするために、CRオルガノイド細胞をTet2(CHの共通変異遺伝子)KOマウスに多数注入した。VAVCre(全細胞KO)およびCD4(T細胞)マウスでは、CRの肝転移腫瘍負荷(TB)およびTexが減少した。つまり、Tet2欠損T細胞はCRの発生を抑制した。

研究成果の学術的意義や社会的意義

We clarified the roles of clonal hematopoiesis in a colorectal cancer (CRC) liver metastasis model which is native-relevant. Our findings may bring attention about CH in the prognosis and treatment of CRC in the era of precision medicine.

研究成果の概要(英文)：Immune cells with somatic mutations (IMsm) are infiltrated into tumor tissues in cancer patients with clonal hematopoiesis (CH). To examine the roles of IMsm in colorectal liver metastasis (CLM), colon cancer organoid cells (CCOC) were transplanted into spleens of various Tet2 conditional knockout mice: VAVCre (Tet2 deletion in all blood cells), LysMCre (myeloid), CD19Cre (B), and CD4Cre (T). We found that CLM tumor burden of VAVCre and CD4Cre were lower than those of control. Differentially expressed gene analysis for WTA and immunofluorescence staining showed that PDCD1, TIM3, TIGIT, and LAG3, encoding inhibitory receptors were repressed in CD8+ cells sorted from VAVCre and CD4Cre livers comparing to control. In conclusion, deficiency of Tet2 in hematopoietic cells led to decrease of exhausted CD8+ T cells and suppressed CLM.

研究分野：Cancer immunity

キーワード：Clonal hematopoiesis Colorectal cancer TET2

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様式 C-19、F-19-1、Z-19 (共通)

1. 研究開始当初の背景

Clonal hematopoiesis (CH) has been observed in over 20% of patients diagnosed with solid cancers, and it has been associated with a poor prognosis in most cases, with the exception of colorectal cancer (CRC) patients who tend to have a favorable prognosis. Among the various gene mutations detected in CH, *TET2* mutations are particularly prevalent. Previous research has demonstrated that the impact of *TET2*-mutated CH immune cells depends on the specific types of cancer tissues involved. Specifically, studies have shown that Tet2-KO myeloid cells can inhibit the progression of melanoma, while promoting the growth of hepatoma and lung cancers.

2. 研究の目的

We clarified the roles of *TET2*-mutated CH immune cells on CRC progression.

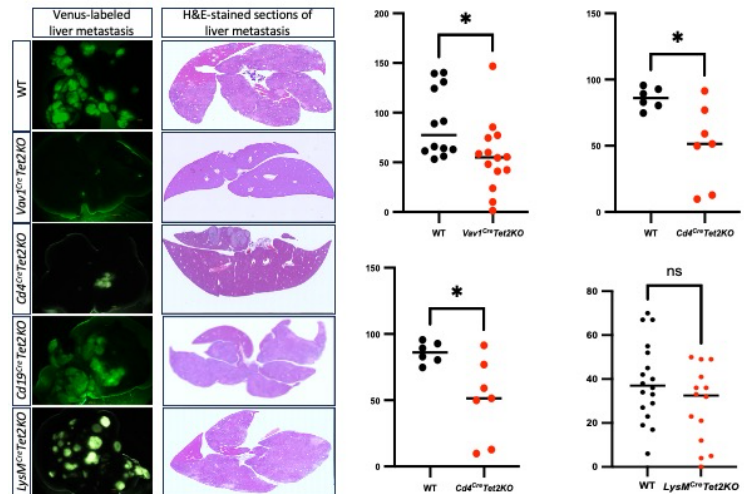
3. 研究の方法

We transplanted CRC organoid cells into the spleens of different types of *Tet2* conditional knockout mice: *Vav1Cre* (with *Tet2* gene deletion in all hematopoietic cells), *LysMCre* (myeloid cells), *Cd19Cre* (B lymphocytes), and *Cd4Cre* (T lymphocytes). After a period of 30 days, we collected livers for analysis. The extent of liver metastasis tumor burden (LMTB) was determined by counting the number of tumor foci on 10 hematoxylin-stained slides, with an interval of 80 μm between each slide. We utilized immunohistochemistry (IHC) and flow cytometry (FC) to analyze immune cells. The number of positive cells was automatically counted in 10 fields at 20x magnification. Furthermore, we performed whole transcriptome analysis (WTA) on sorted CD4+, CD8+, CD11b+, and CD19+ cells, respectively. We also perform scRNA sequencing of CD3 cells to identify the significant cell cluster and target molecules.

4. 研究成果

LMTB was significantly lower in *Vav1Cre* and *Cd4Cre* mice compared to the control mice (*Vav1Cre* vs. control: 55.65 ± 35.62 vs. 89.93 ± 34.57 foci/1000 mm^2 , $p < 0.05$; *Cd4Cre* vs. control: 50.19 ± 30.39 vs. 85.98 ± 7.92 foci/1000 mm^2 , $p < 0.05$). However, the LMTB of *Cd19Cre* and *LysMCre* mice was comparable to that of control mice (Figure 1).

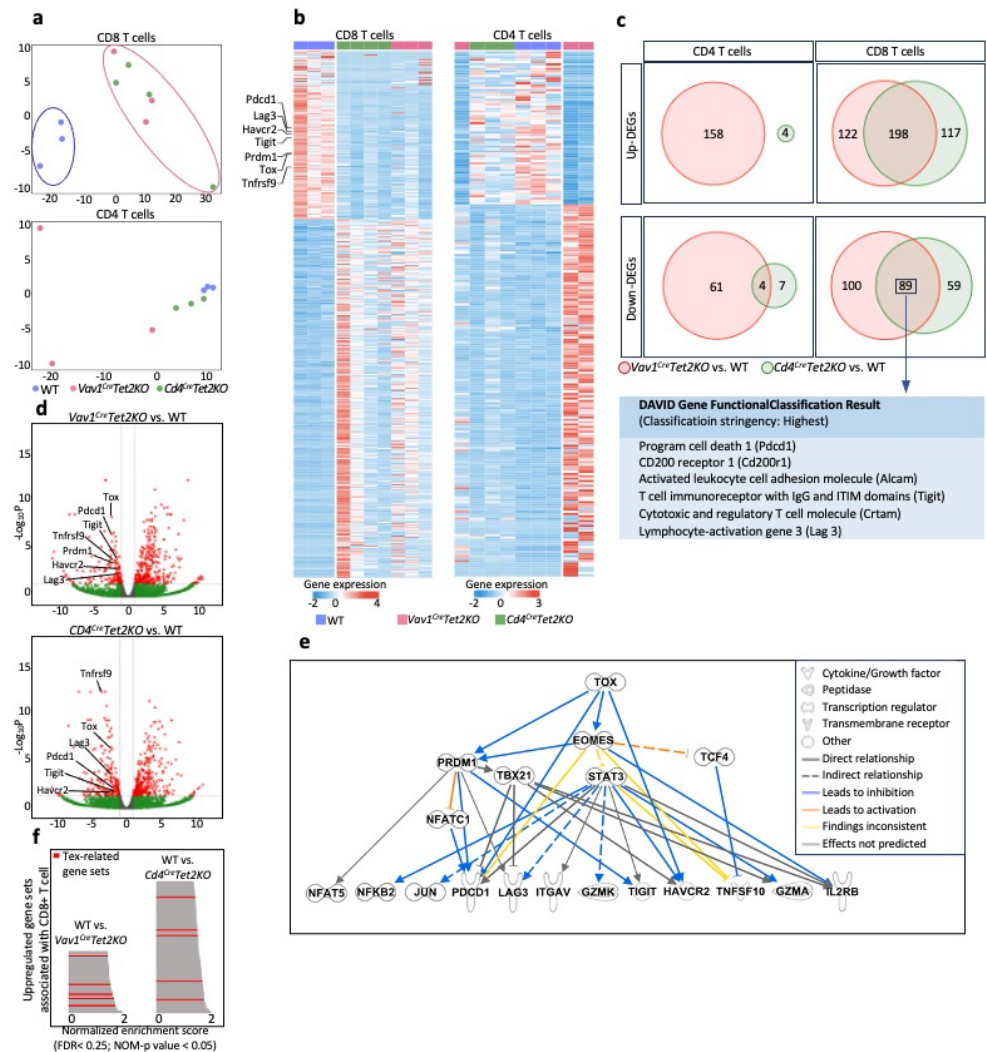
Figure 1: Colorectal liver metastasis tumor burden



The differential gene expression of WTA of CD4+ showed no difference while those of CD8+ cells revealed that 198 genes up-regulated, while 89 genes down-regulated in both of *Vav1Cre* and *Cd4Cre* mice compared the control mice (Figure 2a, b). Among the down-regulated genes, a gene group consisting of *Pdcd1*, *Tigit*, *Lag3*, and *Havcr2*, which encode inhibitory molecules associated with exhausted T cells exhibited enrichment (Enrichment score = 3.77) based on the analysis using DAVID (Figure 2c, d). Ingenuity Pathway Analysis further indicated that these molecules were downregulated by the

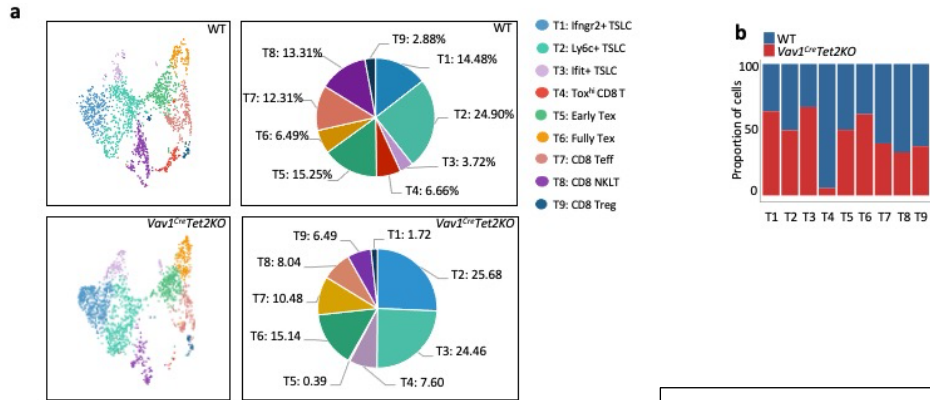
upstream regulator TOX (Figure 2e). Furthermore, T cell exhaustion signaling pathway were downregulated in both *Vav1Cre* and *Cd4Cre* mice by using gene set enrichment analysis (Figure 2f).

Figure 2: Whole transcript analysis of tumor- infiltrating CD4 and CD8 cells



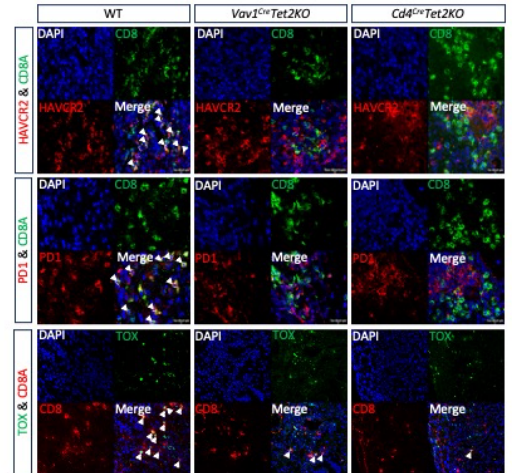
Tumor-infiltrating CD8 T cells (WT, n=1803; *Vav1Cre*, n=2184) were clustered and identified as nine T cell clusters, including *Ifngr2*⁺ stem-like CD8 T cells (*Ifngr2*⁺ TSCL), *Ly6c*⁺ stem-like CD8 T cells (*Ly6c*⁺ TSCL), *Ifit*⁺ stem-like CD8 T cells (*Ifit*⁺ TSCL), highly expressed *Tox* CD8 T cells (*Tox*^{hi} CD8 T), early exhausted T cells (Early Tex), fully exhausted T cells (fully Tex), CD8 effector T cells (CD8 Teff), CD8 NK-like T cells (CD8 NKLT), and *Foxp3*⁺*Cd25*⁺ CD8 regulatory T cells (CD8 Treg) (Figure 3 a). Stack bar plot showed that highly expressed *Tox* CD8 cells were higher in WT compare with those of *Vav1Cre* (Figure 3 b).

Figure 3: ScRNA sequencing analysis of tumor-infiltrating CD8 cells



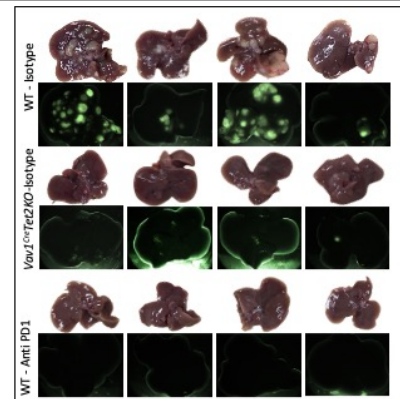
The immunofluorescence results demonstrated that the number of CD8-T cells expressing PDCD1 and HAVCR2 was decreased in *Vav1Cre* mice and *Cd4Cre* compared to the control mice (*Vav1Cre* and *Cd4Cre* vs control; 5.91 ± 2.50 and 12.86 ± 5.3 vs. 35.15 ± 8.21 cells/100 CD8-T cells, $p < 0.01$ for PDCD1; 4.51 ± 4.06 and 13.65 ± 7.84 vs. 24.51 ± 9.94 cells/100 CD8-T cells, $p < 0.01$ for HAVCR2). Moreover, the number of CD8-T cells expressing TOX was also significantly decreased in *Vav1Cre* mice and *Cd4Cre* compared to the control mice (*Vav1Cre* and *Cd4Cre* vs control; 5.19 ± 7.48 and 11.31 ± 14.43 vs. 35.15 ± 16.50 cells/100 CD8-T cells; $p < 0.01$) (Figure 4).

Figure 4: IF staining of exhausted markers



To demonstrate the role of exhausted T cells in CRC liver metastasis, we used anti PD1 antibody to treat the WT mice. We found that both PD1-treated and *Vav1Cre* mice had lower TLMB than isotype-treated mice (Figure 5).

Figure 4: anti-PD1 antibody treatment results



The depletion of *Tet2* gene in hematopoietic cells resulted in a reduction of exhausted CD8+ T cells and suppressed the liver metastasis of CRC organoid cells. These findings provide insights into the favorable prognosis observed in CRC patients with CH. Considering the high prevalence of CH in cancer patients, our results suggest that studying the roles of CH-immune cells could shed new light on understanding the cancer microenvironment from a novel perspective.

5. 主な発表論文等

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〔図書〕 計0件

〔産業財産権〕

〔その他〕

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6. 研究組織

	氏名 (ローマ字氏名) (研究者番号)	所属研究機関・部局・職 (機関番号)	備考
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7. 科研費を使用して開催した国際研究集会

〔国際研究集会〕 計0件

8. 本研究に関連して実施した国際共同研究の実施状況

共同研究相手国	相手方研究機関
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