Analysis of Lymphocyte and Clinical Profile in Nonmonogenic Common Variable Immunodeficiency Patients With and Without Class Switch Recombination Defect

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Common variable immunodeficiency (CVID) is the most common heterogeneous inborn error of immunity (IEI). It is

characterized with reduced class-switched memory B cells (SMBs), hypogammaglobulinemia, respiratory infections, autoimmunity, enteropathy, and lymphoproliferation [1]. Several monogenic defects are associated with the CVID phenotype [2,3], although 50%-80% of patients with no known monogenic IEI [4] develop nonmonogenic CVID. Class switch recombination (CSR) is a DNA rearrangement of the immunoglobulin (Ig) heavy-chain locus that switches the Ig isotype from IgM to IgG, IgA, and IgE, generating SMBs or plasma cells [5]. Defects in genes involved in CSR will cause CSR defect (CSR-D), leading to monogenic CVID, although CSR-D has rarely been observed in nonmonogenic CVID patients [6]. CSR-D is associated with dramatically reduced SMB levels and specific clinical manifestations in CVID patients [7]. We aimed to evaluate alterations in B- and T-lymphocyte subpopulations and clinical manifestations in genetically unresolved cases of CVID with and without CSR-D to identify distinctive immunological and clinical phenotypes for this group.

We included 30 genetically unresolved cases of CVID from the Iranian Immunodeficiency Registry. Using whole-exome sequencing, we excluded known monogenic IEI [8], as previously described [4,9]. Based on clinical diagnosis [10], patients were classified into different groups, namely, infection only, autoimmunity, chronic enteropathy, and lymphoproliferation. We also included 30 age- and sexmatched healthy controls. The study was approved by the ethics committee of Tehran University of Medical Sciences (IR.TUMS.CHMC.REC.1399.003), and patients gave their written informed consent.

Based on serum Ig levels, we classified patients into 2 groups, CSR-D and non–CSR-D. CVID patients with decreased IgG and IgA but normal IgM levels were considered CSR-D. The remaining patients were categorized as non–CSR-D. The laboratory methods have been described elsewhere [11]. In brief, extracellular and intracellular flow cytometry procedures were conducted to detect all B- and T-cell subsets. IBM SPSS Statistics for Windows, Version 24.0 (IBM Corp) was used for the statistical analyses.

Among the CVID patients (Table S1), 16.67% (5 out of 30) had a CSR-D. In the CSR-D group, IgM levels were significantly higher, and delayed diagnosis and pneumonia were significantly more common (Figure S1 and Table S2). Of note, all cases with bronchiectasis belonged to the non– CSR-D group, suggesting the functional role of residual IgM in CSR-D patients. Among CSR-D patients, 80% were infection only and 20% were the noninfectious phenotype (exclusively chronic enteropathy). In the non–CSR-D population, we also found infection only to be the most frequent clinical phenotype (56%) (Table S2).

All gating strategies for lymphocyte subsets have been reported elsewhere [12]. We observed no statistically significant differences in lymphocyte subsets between CSR-D and non-CSR-D (Figure S2). However, in comparison with healthy controls, significant decreases were observed in the non-CSR-D group for the following: total, marginal zone, and IgM-only memory B cells (IgM only MB); SMB; plasmablasts; total, naive, central memory, and regulatory (Treg) CD4⁺ T cells; and naive CD8⁺ T cells. Significant increases were observed in total, effector memory (EM), terminally differentiated effector memory (T_{EMRA}), and activated and cytotoxic CD8⁺ T cells. The same reduction in SMB, IgM only MB, and plasmablasts was observed for CSR-D compared with healthy controls (Table S3). Normalization of B cells and marginal zone B cells was in line with higher levels of IgM and the phenotype of CSR-D. Based on the calculated cut-off values, we observed a higher percentage of patients with decreased SMB, IgM only MB, type 1 helper T cells $(T_{\rm H}1)$, Treg, and naive CD8⁺ T cells, in addition to a higher percentage of patients with increased CD21^{low} and transitional B cells, central memory CD4 $^+$ T cells, and T_{EMRA}T cells among CSR-D than among non-CSR-D (Table S4).

Observation of CSR-D among CVID patients with no known monogenic defects suggests that defects in the other genes involved in CSR may have a potential role in the pathogenesis of CVID rather than the well-known genes. Some of these potential genes have been predicted to cause CVID [6]. Regarding detection of CSR-D among 17% of our nonmonogenic CVID patients, we expected lower SMB levels in the CSR-D group than in the non–CSR-D group. Nevertheless, this reduction was observed among 100% of CSR-D and 96% of non–CSR-D patients, with no statistically significant differences. It seems that CSR-D in nonmonogenic CVID patients is too mild to cause significant alterations in SMB levels or result in other immunological and clinical features.

The cut-off values showed that a defect in CSR had noticeable effects on some lymphocyte subsets, leading to a markedly higher number of CSR-D patients having fewer memory B cells, T_H1 , Treg, and naive CD8⁺ T cells and more CD21^{low} B cells, transitional B cells, CD4⁺ T cells, and T_{EMRA} T cells than non–CSR-D patients. Abnormalities in some of the above-mentioned lymphocyte subsets, irrespective of whether they are CSR-D, have been shown to be associated with particular clinical phenotypes and to play a role in prediction of CVID in children with hypogammaglobulinemia [12,13]. This finding would strongly support the prominent role of abnormalities in CD21^{low} B cells, T_H1 , Treg, and naive and T_{EMRA} T cells in the development of more severe features such as autoimmunity and chronic enteropathy among CSR-D patients later in their lives.

We expected much more severe clinical complications among CSR-D patients [14]. However, to our surprise, despite the higher rate of infection, pneumonia, and delayed diagnosis, all patients with bronchiectasis fell into the non–CSR-D group, indicating the presence of immune dysregulation in the development of bronchiectasis in CVID patients. Having no genetic defects in CVID-related exomes seems to alleviate the adverse impacts of defects in CSR and lead to a milder form of the disease. In summary, we can conclude that observation of CSR-D in genetically unresolved CVID could be a result of defects in predictive genes, epigenetic changes, and environmental or host-intrinsic factors leading to mild modification of B- or T-cell response pathways, which in turn fail to cause severe clinical conditions or considerable alterations.

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Conflicts of Interest

The authors declare that they have no conflicts of interest.

References

- 1. Cunningham-Rundles C. Common variable immune deficiency: Dissection of the variable. Immunol Rev. 2019;287:145-61.
- Fekrvand S, Khanmohammadi S, Abolhassani H, Yazdani R. B- and T-Cell Subset Abnormalities in Monogenic Common Variable Immunodeficiency. Front Immunol. 2022;13:912826.
- Yazdani R, Habibi S, Sharifi L, Azizi G, Abolhassani H, Olbrich P, et al. Common Variable Immunodeficiency: Epidemiology, Pathogenesis, Clinical Manifestations, Diagnosis, Classification, and Management. J Investig Allergol Clin Immunol. 2020;30:14-34.
- Abolhassani H, Hammarström L, Cunningham-Rundles C. Current genetic landscape in common variable immune deficiency. Blood. 2020;135:656-67.
- Roco JA, Mesin L, Binder SC, Nefzger C, Gonzalez-Figueroa P, Canete PF, et al. Class-Switch Recombination Occurs Infrequently in Germinal Centers. Immunity. 2019;51:337-50. e7.
- Amirifar P, Yazdani R, Azizi G, Ranjouri MR, Durandy A, Plebani A, et al. Known and potential molecules associated with altered B cell development leading to predominantly antibody deficiencies. Pediatr Allergy Immunol. 2021;32:1601-15.
- Knight V. The utility of flow cytometry for the diagnosis of primary immunodeficiencies. Int J Lab Hematol. 2019;41 Suppl 1:63-72.
- Tangye SG, Al-Herz W, Bousfiha A, Chatila T, Cunningham-Rundles C, Etzioni A, et al. Human Inborn Errors of Immunity: 2019 Update on the Classification from the International Union of Immunological Societies Expert Committee. J Clin Immunol. 2020;40:24-64.
- Abolhassani H, Aghamohammadi A, Fang M, Rezaei N, Jiang C, Liu X, et al. Clinical implications of systematic phenotyping and exome sequencing in patients with primary antibody deficiency. Genet Med. 2019;21:243-51.
- European Society for Immunodeficiencies. ESID Registry -Working definitions for clinical diagnosis of PID [Available from: https://esid.org/Working-Parties/Registry-Working-Party/Diagnosis-criteria].

- 11. Tofighi Zavareh F, Bagheri Y, Keshtkar AA. Evaluation of B Cell and T Cell Phenotypes in CVID Patients and Its Correlation with the Clinical Phenotypes: Study Protocol. Immunol Genet J. 2020;3:228-35.
- Tofighi Zavareh F, Mirshafiey A, Yazdani R, Keshtkar AA, Abolhassani H, Bagheri Y, et al. Lymphocytes subsets in correlation with clinical profile in CVID patients without monogenic defects. Expert Rev Clin Immunol. 2021;17:1041-51.
- Tofighi Zavareh F, Mirshafiey A, Yazdani R, Keshtkar AA, Abolhassani H, Mahdaviani SA, et al. Immunophenotypic and functional analysis of lymphocyte subsets in common variable immunodeficiency patients without monogenic defects. Scand J Immunol. 2022;96:e13164.
- 14. Abolhassani H, Amirkashani D, Parvaneh N, Mohammadinejad P, Gharib B, Shahinpour S, et al. Autoimmune phenotype in patients with common variable immunodeficiency. J Investig Allergol Clin Immunol. 2013;23:323-9.

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