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Cellular response to Spike antigens in seronegative kidney transplant recipients after SARS-CoV-2 vaccination

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INTRODUCTION

The quality of immune response has been found to be a crucial factor in infection control. Antigen-specific polyfunctional T-cells (e.g., secreting multiple cytokines simultaneously) have been shown to be associated with lower viral loads in chronic infections. Polyfunctional T-cells are also commonly used to assess vaccine-induced immunogenicity. In addition to neutralizing antibodies, protective immunity to SARS-CoV-2 depends on virus-specific T-cells as they are important actors to help in the generation of high-affinity antibodies and in the elimination of virus-infected cells, therefore globally limiting viral replication.

Immunocompromised individuals are especially vulnerable to COVID-19, with a higher risk of developing severe forms and have therefore been considered as the priorities for immunization against SARS-CoV-2. However, there is increasing evidence that vaccine efficacy is lower in immunosuppression clinical settings. Kidney transplant recipients (KTR) are an example of such a context as they are chronically treated with immunosuppressants in order to prevent the acute transplant rejection. Previous reports show that after COVID-19 vaccination, KTR develop a less robust (or even absent, non-responders) antibody response compared to healthy immunocompetent individuals. COVID-19 vaccination of healthy individuals stimulates both humoral and cell-mediated immunity.

MATERIALS AND METHODS

All participants were recruited at University Hospital of Nancy (France). Thirty-five seronegative non-responders KTR vaccinated with 2 doses of Cominarty® were included. Sixteen healthy subjects (HD) vaccinated either with 2 doses of Cominarty® ("Pfiz") or 1 dose of Vaxzevria® followed by 1 dose of of Cominarty® ("Oxf+Pfiz") were also evaluated. Spike-specific memory CD4 and CD8 T-cells were evaluated by a standard intracellular cytokine staining assay in flow cytometry 3 to 6 weeks after the second vaccination shot. Fresh PBMC were separated by density gradient and washed, 1x10⁶ cells were resuspended in 200µL of AIM-V medium and stimulated overnight (14-16 hours) with peptide pools of overlapping 15-mer peptides spanning the Spike SARS-CoV-2 protein (divided in two pools of peptides: "SK1" and "SK2") (1.25 µg/mL of each peptide). All samples were also co-stimulated with antibodies to CD28 and CD49d (1 µg/mL, BD Biosciences). Brefeldin A (Sigma-Aldrich) was added to each well to block cytokine secretion. Unstimulated PBMCs (medium + 0.5% DMSO, vehicle of the peptide pools) were used as negative controls. As positive controls of global TH1-immunocompetence, PBMC were also stimulated in parallel with PMA (50 ng/mL, Sigma-Aldrich) and Ionomycin (500 ng/mL, Sigma-Aldrich). All peptide pools were from JPT Peptides (Berlin, Germany). After stimulation, cells were collected and washed before an incubation with BD Horizon[™] Fixable Viability Stain 450 (FVS 450) and a cell surface antibody mix of anti-CD3 PerCP-Cy5.5, anti-CD4 FITC and anti-CD8 APC-H7. Cells were then fixed, washed and permeabilized by using the IntraStain® kit (Dako). Next, the cells were incubated with an intracellular antibody mix of anti-IL-2 PE, anti-TNF- α PE-Cy7 and anti-IFN- γ APC. All conjugated antibodies were from BD Biosciences. After 2 washes, cells were resuspended in PBS and immediately proceeded to flow cytometry data acquisition. Data were acquired using a BD FACSLyric[™] ® flow cytometer (Becton Dickinson). SARS-CoV-2 -specific T-cells were identified using Kaluza® software v2.1 (Beckman Coulter) as by a specific gating strategy and a response was considered positive if greater than 0.01% of CD4+ or CD8+ T-cells were cytokine positive over background controls (Winstone et al., Eur J Immunol. 2009). To quantify the polyfunctionality of SARS-CoV-2 specific Tcells, we calculated the Special Polyfunctionality index for each stimulation condition for CD4 and CD8 T-cells as described (Larsen et al., PLoS One. 2012), using a higher ponderation for increasing polyfunctionality as determined by analysis correlating T-cell polyfunctionality and efficacy (Boyd et al., PLoS One. 2015).

Few data are currently available on the concomitant evaluation of humoral and cellular immune responses after COVID-19 vaccination in KTR, compared to immunocompetent subjects. Specially, most of the literature data on cellular responses are based on interferon-gamma releasing assays (IGRA) or activation-induced methods only, with no information available on polyfunctional anti-SARS-CoV-2 T-cells.

Vaccinated non-responders KTR are candidates to prophylactically receive neutralizing monoclonal antibodies directed against the Spike protein. Although not yet reaching a national consensus, a possible clinical strategy is to administer these antibodies only on non-responders KTR in which no concomitant cellular responses to vaccine antigen is detected. By using multiparametric flow cytometry, we then evaluated and characterized Spike-specific CD4 and CD8 T-cells after vaccination in non-responders KTR and compared such cellular responses with those from vaccinated immunocompetent subjects.

RESULTS

No KTR (15 female, 20 male) nor HD (12 female, 4 male) individual had a previous diagnosis of Covid-19. The median age of KTR was 57 years (interquartile range, 50.2 to 65.7) and 47.5 in HD group (interquartile range, 41 to 56) (p < 0.005, t-test). Serological status after vaccination were not systematically determined for HD individuals. Among the 35 seronegative KTR included, 16 had detectable Spike-specific T-cells (45.7%). This was significantly lower compared to HD group, were all tested individuals had detectable Spike-specific T-cells (100%) (p < 0.001, Chi-square test).





Figure 1. Gating strategy for identification of SK-1 and SK-2 memory specific T cells.

Singlet cell population was identified by applying an FSC-Int *vs.* FSC-Peak gate. Next, live T-cells were identified by a gate on CD3+ and low viability Fixable Dye staining. Small viable T-cells were then identified as low SSC CD3+ cells and a CD4 vs CD8 gate was applied. A quadrant gate was set using the negative controls (not shown) for the baseline expression of each cytokine on CD4 and CD8 T-cells, defined as a percentage of IL-2+, $TNF-\alpha+$ or IFN- $\gamma+$ cells. The same gating strategy was then used for SK1 and SK2 - stimulated cells. Mono, bi and trifunctional T cells were identified by Boolean gates using Kaluza® software. Seven populations can be then identified. Shown here are examples of cytokine-positive CD3 T-cells after SK1 stimulation and the resulting bifunctional responses.

Figure 2. Global CD4 and CD8 Spike-specific T-cells.

No significant differences were found between "Pfiz" and "Oxf+Pfiz" vaccination schedules in immunocompetent subjects. They were therefore pooled as HD group. KTR had significantly lower CD4 and CD8 T-cells specific to Spike-1 and Spike-2 peptide pools as compared to HD. The global response (adding all 7 subpopulations of cytokine-positive cells) is shown. Median and the 25th and 75th percentiles, whiskers represent the 10th and 90th percentiles. Black dots represent individual data. *p < 0.05



Figure 3. Proportions of mono and polyfunctional Spike-specific CD4 and CD8 T-cells.

We looked for polyfunctional T cell responses as they are associated with a higher anti-viral efficacy. Overall, there was lower polyfunctional CD8+ T-cell responses in both groups. Compared to HD group, KTR had significantly lower proportions of trifunctional IL-2+, TNF- α + and IFN- γ + CD4 and CD8 T-cells. Bifunctional CD4 and CD8 T-cells were also lower in KTR, reaching statistical significancy in most subpopulations. **p*<0.05

