Characterization of $\gamma\delta$ T-cells via flow cytometry

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Stervbo et al. report on the influences of ageing on a variety of peripheral innate and adaptive immune populations in two publications in the October issue of this journal (Stervbo et al. 2015a; Stervbo et al. 2015b). These articles surveyed peripheral blood mononuclear cell phenotypes from donors recruited in the cross-sectional Protective Immunity in Ageing (PRIMAGE) study. The focus of that study was the investigation of fundamental immunologic questions of the natural ageing process using seasonal influenza vaccination as a model (PRIMAGE 2015). Both papers also nicely combined phenotypic and functional assessment of age-related differences in major compartments of the cellular immune system in peripheral blood. Unlike many earlier studies, Stervbo et al.

also focused on the underinvestigated $\gamma\delta$ T cell compartment (Stervbo et al. 2015a). This is valuable because there are very few data on the impact of age on this conserved minor T cell subset. It is therefore especially important to be certain of the exactitude of the published results. However, we would like to sound a note of caution in this regard due to the use of the pan- $\gamma\delta$ antibody clone B1, which may not be able to identify every $\gamma\delta$ T cell when used in complex antibody panels applied in polychromatic flow cytometry. These issues were addressed by us in a carefully reviewed and validated antibody panel recently published in the journal *Cytometry Part A*'s "OMIP" series of standardized antibody panels (Wistuba-Hamprecht et al. 2014). A possible explanation could be steric hindrance effects because the epitopes recognized by anti-CD3 antibodies and the B1-clone might be in close proximity, which is not the case for the 11F2-clone that for example reliably detects the $\gamma\delta$ T-cell compartment. In parallel to publication of these findings, we informed the manufacturers and one of the largest companies immediately revised their technical data sheet in accordance with these results (Becton Dickinson 2015). It might therefore be problematic to perform subset analysis on the basis of a B1-positive cell population. We felt that readers of Stervbo et al. 2015a, 2015b should be aware of these potential limitations.

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