



Identification of leukocyte subpopulations as potential biomarkers of long-term survival with normal allograft function after lung transplantation

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Introduction	Patients & Methods
Long-term survival after lung transplantation (LT) is limited by the development of	Sixty-two double lung transplant recipients were included in this multicenter cross-

chronic lung allograph dysfunction (CLAD). Despite this fact, a small number of lung transplant recipients are long-term survivors with a good allograft function (LTS).

A study of this particular population could be a first step to search for transplant tolerance biomarkers that can lead to the reduction of immunosuppressive drugs in treatment plans and improve personalized medicine. The objective of this study was to identify leukocyte subpopulations as potential biomarkers of LTS after lung transplantation.

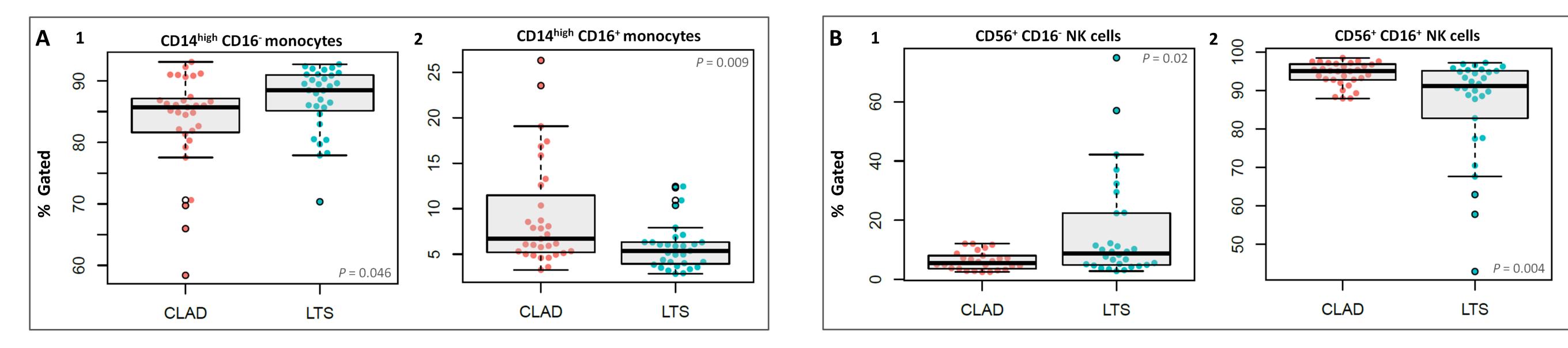
sectional study: 31 patients with CLAD and 31 patients with stable lung allograft function after 10 years from LT (LTS).

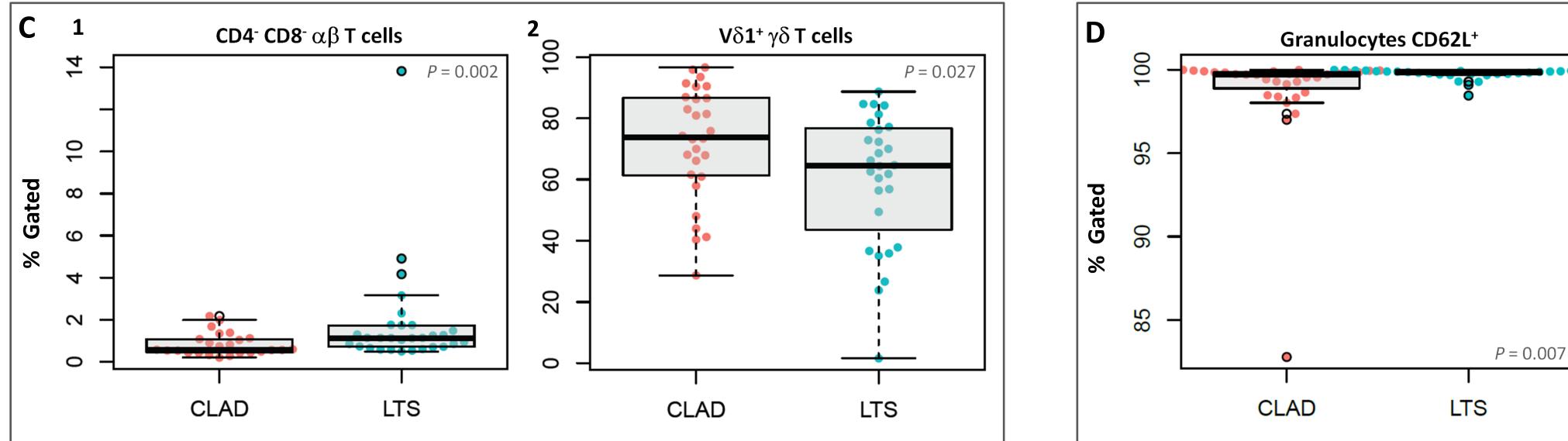
Six leukocyte profiling panels computing 4 to 10 markers were used for whole blood leukocyte subset profiling by flow cytometry. The percentages of the different leukocyte subpopulations were compared between both groups.

Results

Leukocyte subsets that significantly differ between LTS and CLAD groups are summarized in Table 1.

		Leukocyte Subsets (%)		p value	Table 1. Leukocyte subpopulations with significant differences between LTS (cases)
		LTS v	rs. CLAD		and CLAD (controls) groups.
Monocytes	CD14 ^{high} CD16 ⁻	86.9	83.5	0.046	
	CD14 ^{high} CD16 ⁺	5.8	9.3	0.009	 LTS: Long-term survivors;
NK cells	CD56 ⁺ CD16 ⁻	15.6	6.2	0.02	CLAD: Chronic lung allograph dysfunction;
	CD56+CD16+	86.3	94.2	0.004	NK: Natural killer.
T cells	CD4-CD8-αβ	1.8	0.8	0.002	
	$V\delta 1^+\gamma\delta$	59.9	71.9	0.027	15
Granulocytes	CD62L ⁺	99.8	98.8	0.007	





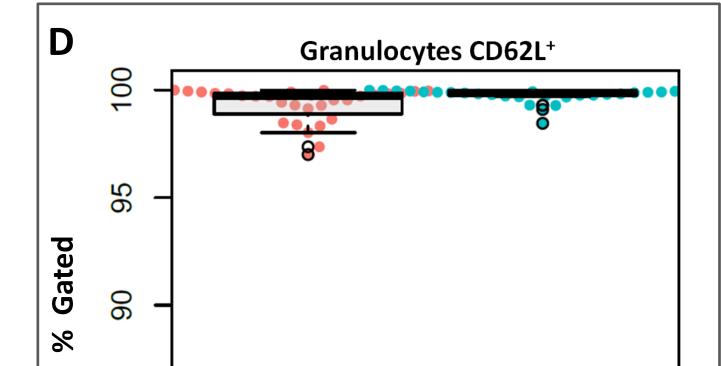


Figure 1. Quantitative differences of leukocyte subpopulations between LTS and CLAD groups. (A) Monocytes, expressed as the percent of CD14^h CD16⁻ (1) and CD14^h CD16⁺ (2) of the total monocytes. (B) Natural killer cells, expressed as the percent of CD56⁺ CD16⁺ (1) and CD56⁺ CD16⁺ (2) of the total NK cells. (C) CD4⁻ CD8⁻ $\alpha\beta$ T cells (1) shown as the percent of the total $\alpha\beta$ T cells and V δ 1⁺ T cells (2) shown as the percent of the total γδ T cells. (D) Granulocytes CD62L⁺ expressed as the percent of the total granulocytes. Boxes depict median and IQR; whiskers denote 1.5 x IQR. Two-sided P values for Mann-Whitney *U* test comparisons between groups are shown (P<0.05).

Conclusions	Acknowledgements
These results suggest that CD14 ^{high} CD16 ^{-/+} monocytes, CD56 ⁺ CD16 ^{-/+} NK cells,	This study has been funded by Instituto de Salud Carlos III through the project
CD4 ⁻ CD8 ⁻ $\alpha\beta$ and V δ 1 ⁺ $\gamma\delta$ T cell subpopulations could be potential biomarkers of long	"PI13/01076" (Co-funded by European Regional Development Fund/European Social
term allograft survival in lung transplant patients.	Fund) "Investing in your future"), FUCAP, Astellas, Novartis and Chiesi.

No relationships to disclosure