

AUTHOR CORRECTION

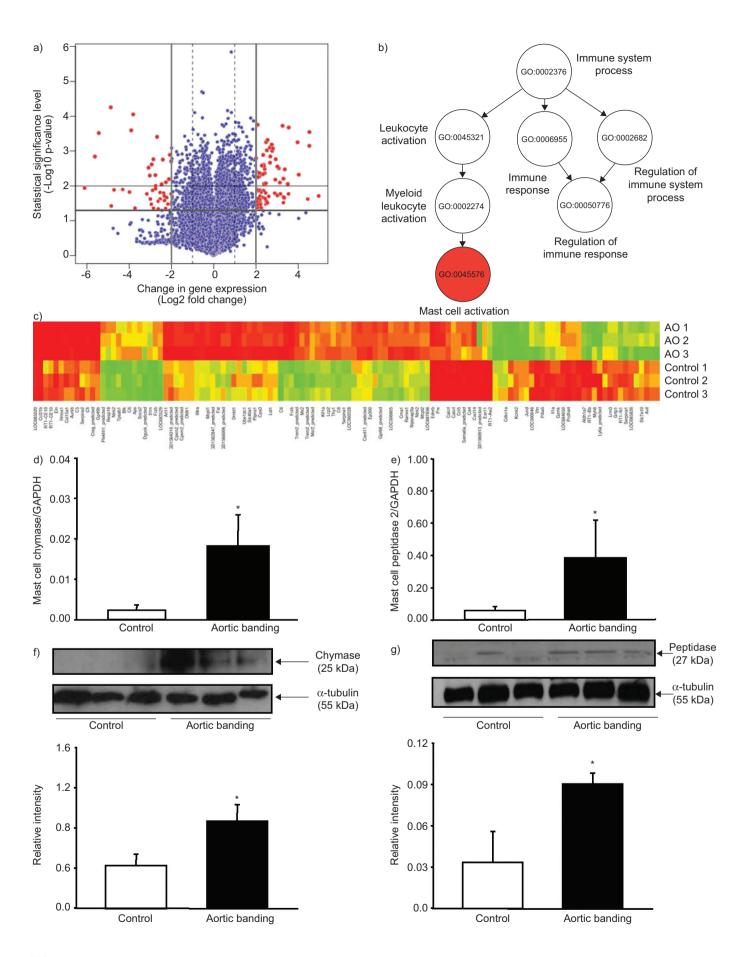
"Mast cells promote lung vascular remodelling in pulmonary hypertension." J. Hoffmann, J. Yin, M. Kukucka, N. Yin, I. Saarikko, A. Sterner-Kock, H. Fujii, H. Leong-Poi, H. Kuppe, R.T. Schermuly and W.M. Kuebler. *Eur Respir J* 2011; 37: 1400–1410.

Unfortunately, some elements of figures 1 and 2 of the above manuscript were published incorrectly.

In the Volcano plot of figure 1a, the lines illustrating the boundaries for four-fold upregulated (Log2 >2) or downregulated (Log2 < -2) genes were incorrectly placed at +1.6 and -1.6 on the abscissa, rather than at +2 and -2. The error relates only to the pictorial representation of the Volcano plot and the quantitative data itself and its interpretation are not affected. The figure caption and the corrected figure are reprinted below and on the following page.

The representative echocardiographic images of figure 2d and f were not drawn from the correct study. However, the incorrect images were inserted during drafting of the original manuscript; the data analyses presented in the manuscript were performed using the correct echocardiographic images and thus remain valid. Figure 2 is reprinted two pages hence.

FIGURE 1. Lung mast cell accumulation in rats with supracoronary aortic banding. a) Volcano plot from whole rat genome microarray analyses (28,000 genes in total) shows differential gene expression in lung homogenates of rats with aortic banding compared with controls (n=3 each). Red spots depict 120 genes that are significantly (p<0.05; -Log10 >1.3) and more than four-fold upregulated (Log2 >2) or downregulated (Log2 < -2) in banded compared with control rats. Conversely, blue dots depict the residual 27,880 genes which were not significantly and/or less than four-fold upregulated or downregulated. b) Dendrogram of the gene ontology (GO) cluster "immune system process" with respective GO terms and accession numbers. Within the entire microarray, differential regulation was most pronounced in the GO class "mast cell activation". c) Heat map depicts expression pattern of the 120 differentially regulated genes from three lungs of rats with aortic banding (AO) and three control lungs. The colour code (red: upregulation; green: downregulation) shows individual gene expression relative to mean gene expression of the whole array. Annotation according to National Center for Biotechnology Information gene symbols. Bar graphs show upregulation of d) mast cell chymase and e) mast cell peptidase 2 in aortic banding compared with control rats. Data from real time RT-PCR of lung homogenates were quantified in comparison to standard curves produced under the same cycling conditions and normalised to glyceraldehyde-3-phosphate dehyrogenase (GAPDH) expression from the same experiment. Bar graphs and representative Western blots from lung homogenate show increased protein expression of f) mast cell chymase and g) mast cell peptidase 2 in lungs from aortic banding rats compared with controls (α-tubulin serves as loading control). Data from n=3 each. *: p<0.05 versus control.



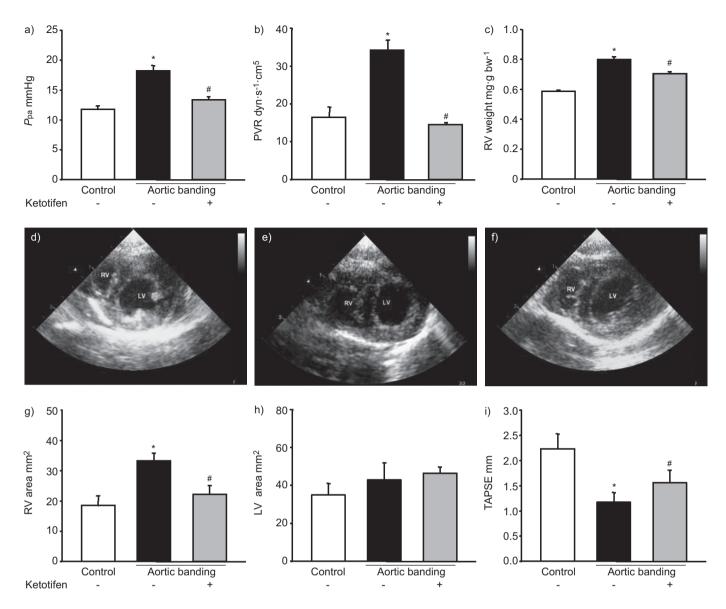


FIGURE 2. Effect of the mast cell stabiliser ketotifen on haemodynamics and right ventricular dysfunction in pulmonary hypertension owing to left heart disease. a) Pulmonary arterial pressure (P_{pa}), b) pulmonary vascular resistance (PVR) and c) right ventricular (RV) weight relative to bodyweight (bw) in controls, banded rats and ketotifen-treated banded rats. Data from n=6 each. d–f) Representative echocardiographic two-dimensional images show left ventricle (LV) and right ventricle (RV) in end-diastole in d) control, e) banded and f) ketotifen-treated banded rats. Note marked dilation of the RV in banded rats, which is attenuated by ketotifen. Replicated in n=10 each. g) RV and h) LV end-diastolic area and i) tricuspid annular plane systolic excursion (TAPSE) in control, banded and ketotifen-treated banded rats. Data from n=10 each; *: p<0.05 versus control; *: p<0.05 versus aortic banding.

DOI: 10.1183/09031936.50043310