Supplemental Information

Structural Features of Biobased Composite Foams Revealed by X-Ray Tomography

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SEM images of these foams reveal an open cell structure (Figure S1). The control sample has cells with maximum Feret length ranging 200-500 μ m. Cross-sections were prepared by cutting by hand with a razor blade. It should be noted that all SEM samples were cut perpendicular to the rising direction. Therefore, these images only provide one perspective on cell size and shape. The samples containing rice hull particles have similar cell structures. Particles can clearly be seen fully encased within cell walls. It should be noted that the most visible particles are also the largest particles. Smaller particles (<50 μ m) may also be present in the cross section but are more difficult to distinguish from the polymer matrix in these images. Figure S1d shows a representative example of an individual CRH particle which has an anisotropic flake-like shape and its own internal porosity.



Figure S1. SEM images of biofoam samples (a) control, (b) 10CRH, (c) 30CRH, (d) high magnification image of a coarse rice hull particle cross section.

An image analysis workflow was applied to the XCT scans to enable quantitative analysis of foam structural features. Figure S2 outlines the image analysis process for the control sample. Figure S2a shows the virtual 2D slice obtained from XCT. The matrix and pores were separated using a threshold segmentation, based on their difference in gray values. Figure 4b shows the binarized image where all pores (shown in blue color) are foreground pixels, and the rest are the background. It can be seen from Figure 4b that all the pores in these foams are interconnected. Individual pores were further separated using the watershed algorithm (Figure 4c). It can be seen from Figure 4c that the pores located on the boundary do not lie completely within the field of view. These pores were removed before quantification. Figure 4d shows the 3D volume rendering of the pores, where individual pores can be seen to be separated.



Figure S2. Segmentation process for distinguishing individual pores. (a) single scan of control sample with examples of individual pores outlined in yellow, (b) single scan after segmentation process, (c) single scan after watershed algorithm is applied to separate pores, (d) 3D rendering after all single scans have been segmented and all pores along the scanning boundary are removed.

Compressive testing was conducted on foam samples to determine compression modulus both parallel and perpendicular to the foam rising direction. Figure S3 shows representative examples of stress-strain curves from which compression moduli were calculated.



Figure S3. Representative stress vs. strain curves for a) coarse rice hull and b) fine rice hull foam samples with force applied either parallel or perpendicular to the foam rising direction.

Cyclic creep-recovery was conducted as a means of mechanically fatiguing a set of foam samples prior to XCT analysis. Figure S4 shows representative examples of strain data from the first and 20th cycle. Each cycle was a total of three minutes with a creep force applied during the first minute followed by a recovery force (10 mN) for two minutes. Before the start of the first cycle, samples were held at 10 mN for one minute. A maximum strain of approximately $50 \pm 5\%$ was targeted for all samples.



Figure S4. Representative creep-recovery curves for coarse and fine rice hull foam samples over 20 cycles prior to XCT analysis. The x-axis on each cycle shown is a 4-minute period.

Sample	Cell volume (×10 ⁷ μm ³) (average ± standard deviation)	Orientation of cells w.r.t. rising direction (°) (average ± standard deviation)	Aspect ratio of cells (average ± standard deviation)
Control	4.1 ± 5	3 ± 8	1.5 ± 0.1
10FRH	2.7 ± 5	13 ± 17	1.5 ± 0.9
30FRH	1.7 ± 4	17 ± 19	1.5 ± 0.8
10CRH	1.8 ± 4	21 ± 13	1.2 ± 0.2
30CRH	1.2 ± 4	20 ± 20	2.0 ± 1.9

Table S1. Several parameters of cells quantified from the XCT data using an integrated image analysis approach