Bone Structural Analysis on Different Resolutions in Magnetic Resonance Imaging

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Introduction

It is known that trabecular bone structure gives additional information to bone mineral density (BMD) in the prediction of bone strength in vitro and in the discrimination of patients with without osteoporotic vertebral and femur fractures. The trabecular bone structure has been studied using MR images^{[1][2]}. But for in vitro MR imaging, the resolution of the image is limited by scan time. Thus, we developed bone structural analysis program and investigated the effect of different resolutions of magnetic resonance image on the calculation of trabecular bone parameters

Materials and Methods

MRI: Bone specimens were removed at distal femoral condyle during knee joint replacement procedure. They were cut by a saw (1x1x1 cm³) and then fixed in formalin for storage. In preparation for scanning, the bone specimens were defatted, degassed, and immersed in 0.5% volume-% gadopentetate doped water. Three dimensional trabecular bone images of the bone specimens were obtained on a 4.7T Bruker BioSpec MRI with 40cm bore size. A 2.5cm birdcage coil with quadrature detection was used. Bone marrow susceptibility difference causes blurring at the trabecular bone marrow interface and it is also necessary to reduce scanning time to obtain high resolution 3D trabecular images. Thus, a 3D fast large-angle spin-echo (FLASE) sequence with 140° pulse (TR = 100 ms and TE = 10ms) was used to overcome the above two problems. The resolutions of the three 3D images were 62x62x62 µm³, 125x125x125 µm³, and 250x250x250 µm³ respectively. **Bone structural analysis**: We applied cubic interpolation to increase image resolution. At each image, we extracted 27 VOIs. On each VOI, we segmented bone structure by using Fuzzy-connectedness based algorithm. The Fuzzy-connectedness parameters were calculated from histogram analysis, seed point, mean, variance etc. We applied 3D morphological thinning for extracting centerline points was calculated. Secondly, Hessian classification was performed on every centerline points. We classified each voxel to one of local intensity structures, like blob, line and sheet. Most of voxels on the centerlines have sheet-like shape, and voxels on the joint of two sheet-like structures (TH), fraction of structuring elements (SE) and shape fraction (SF).



Results

For 62µm resolution image, the average values of TH, SE parameters were 226µm, 5.6% respectively. For 125µm, 248µm, 4.9%. For 250µm, 346µm, 3.3%. There were three parameters in SF, blob, line and sheet fraction values. For 62µm resolution image, the average values of three parameters (blob, line and sheet order) were 0.6, 9.5, 82.8% respectively. For 125µm, 0.7, 9.5, 84.3%. For 250µm, 3.3, 13.5, 73.3%.

Discussion & Conclusion

As the voxel size became bigger, SE values tended to be calculated smaller, which means that some elements were eliminated by the partial volume effect. Figure1 showed that 125µm and 250µm images were significantly different from 62µm image (ANOVA p<0.000, tukey HSD post-hoc analysis p<0.000). The fractions of sheet-like and line-like structural elements can be considered good features for bone structural analysis^[1]. Therefore, using

the shape fraction analysis, we evaluated that the characteristic portion of the bone structures in 125µm image was not changed (t-test, p>0.05). Otherwise, three shape fractions in 250µm image were different from those in 62µm and 125µm images. TH values on coarse resolution images were overestimated by the partial volume effect. In conclusion, in the viewpoint of the shape fraction analysis of trabecular structure, the image resolution of the 125µm image was regarded as comparable to that of 62µm image.



References

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