Bone SPECT Protocol

Version History, Similar Studies & Variations

- 1.0 - 11/29/04 – initial writing
- Whole Body Bone

Indications

- SPECT images are acquired to rule out or visualize bone abnormalities in greater resolution or in hard to visualize areas such as the spine.
- They may be used for any indication appropriate for a whole body bone scan.
- As SPECT studies are done in conjunction with a whole body bone scan, refer to that protocol for administration specifics.

Contraindications

- No barium studies for 48 hours prior to imaging.

Equipment & Supplies

- Camera with a LEHR or LEUF collimator with SPECT capabilities
- 18 - 35 mCiTc-99m-methylene diphosphonate (MDP)
- Angiocath (if performing a three-phase study)

Preparation

- As per Whole Body Bone protocol.

Administration

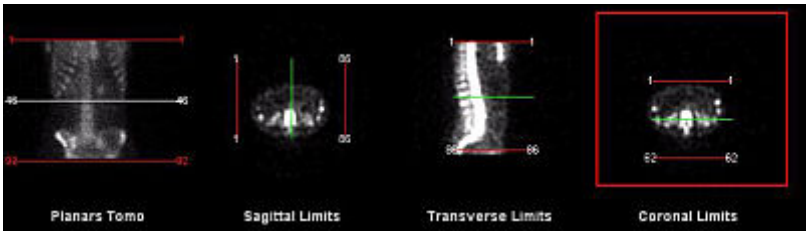
- As per Whole Body Bone protocol.

Acquisition

- At a minimum, anterior and posterior static images of 300 sec, 1000 kcounts, 256x256x16 should be acquired of the area of interest prior to SPECT acquisition
- SPECT acquisition should be 360 degrees total rotation, 64 steps, 40 sec/step, 128x128x16. Dual head cameras may report this as 180 degrees & 32 steps *per head*. Verify that you have the correct settings.
- Specific patient positioning depends entirely upon the area of interest.

Required History

- As per Whole Body Bone protocol.



Processing

- Perform **Patient Rename** on the study to ensure that an Accession# has been assigned to the study.
- Select the Tomo or SPECT study and click on **Bone SPECT** (All Applications -> Bone).
- Adjust the limits (red lines) and centerline (green line) in all projections. Ensure that you do not clip off any of the acquired study or portion of the body.
- Click on the **Review** Tab

- Using the combobox, select **Transversal**. Use the **Scroll** tool or slider to move to the beginning of the slices. Create a screencapture. Move the slices to bring the rest of the transverse slices into view. Perform another screencapture. Repeat again if necessary.
- Using the combobox, repeat the above step with **Coronal** and **Sagittal**.
- Click on File -> **Save & Exit**.
- Select the **Tomo** and the **Result Series** and click on **3D Rendering** (All Applications -> Miscellaneous)
- Click on **Render MIP**. Click on **Proceed**. (See the screenshot at the bottom of this page) Click on the **X** to save and exit.

Hand in Study

- Send the **Tomo** raw data and **SPECT Results** to the Inbox using **Bone SPECT**.
- Send the **3D Results** to the Inbox using **Load to New**.
- Send the screen captures to PACS