**Visual Summary**:

**Facility D** has 3 red (“During”) links and 10 blue links (aka “After”) connecting to blue nodes (OXA-23). **Facility E** has 2 green (“Before”) links, 3 red links, and 10 blue links, connecting to 15 blue nodes. **Facility F** has 2 green links and 13 blue links connecting to 16 blue nodes.

**Facility A** has 7 links connecting to orange, blue, and yellow nodes. Two green (“Before”) links are connected to a yellow (OXA-24) node and the other is connected to a blue (OXA-23) node. Of the 5 red links, only two are connected to orange (OXA-23 & OXA-24) nodes and the rest are connected to yellow (OXA-24) nodes.

**Facility** B has 6 links connecting to yellow and blue nodes. Three green (“Before”) links are connected to 2 yellow (OXA-24) nodes and 1 blue (OXA-23) node. The other three links are red (“During”) connected to yellow (OXA-24) nodes.

**Facility C** has 4 links connected to yellow and blue nodes. The 3 red (“During”) links are connected to yellow (OXA-24) nodes meanwhile a green (“Before”) link is connected to a blue (OXA-23) node.

P1 has the most connections to facilities and the epidemiological data supports the transmission of OXA-24 to P40 before leaving to Facility A.

At the top of the network, some nodes have an initial connection to Facility A, B, or C and a secondary link that also connects to one of these facilities. A similar pattern is observed at the bottom of the network, where some nodes are initially connected to Facility D, E, or F and also have a secondary link to one of these facilities.

**Conclusion**

There appears to be two propagated outbreaks occurring in the network. One of which Facilities A, B, and C are involved regarding the transmission of the OXA-23 gene. The other propagated outbreak involves Facilities D, E, and F regarding the transmission of the OXA-24 gene. The result of this outbreaks has led two individuals in Facility A to acquire both AMR genes.

