*not grammatically correct because it is written to be spoken

Hi everyone my name is Henry Becker. I have been very fortunate to work with the Vector Borne Disease lab this summer studying deer ticks and the pathogens they carry. This is important work, as tick borne illness cases are increasing in Maine and across the US.

It is a commonly held belief that white footed mice and white tailed deer provide the vast majority of blood meals to deer ticks and white footed mice are thought to be the principal reservoir for most tick borne illnesses. These assumptions have not been rigorously tested because until recently, there has not been an accurate and efficient way to determine the previous host of a tick after the tick has molted. Researchers at Tufts university recently developed quantitative PCR assays which can detect remnants of mice and deer blood in tick DNA samples. This allows us to determine the proportion of blood meals and pathogens mice and deer contribute to a given deer tick population.

The assays target genetic sequences called retrotransposons, which are self replicating DNA elements that make up large portions of many mammalian genomes. Why is it so important for these assays to target genetic sequences present in such high concentrations in the mammalian genome? Let's take a look at the flowchart here and I'll explain...

First, an adult female lays eggs, the eggs hatch into larvae, the larvae quest for and attach to a host. In the process of feeding the larvae may acquire whatever pathogens are present in the host's blood. After feeding, a larva will drop off the host and molt into a nymph. The nymph quests again for a second host at which point we collect it by flagging. It is at this point, after the tick has digested most of the blood and molted that we want to determine it's previous host. Because such small amounts of blood remain in the tick at this point its so important for the blood meal analysis assay to target retrotransposons which have many copies of themselves within the deer and mouse genome.

This project marks the very first application of this new blood meal analysis technique to tick research in Maine.

Our results were quite surprising. 110 nymphs were collected and tested. We found that less than 10% of nymphs were positive for mouse or deer blood suggesting over 90% of nymphs fed on animals other than mice and deer. Additionally, of the nymphs carrying pathogens, none tested positive for mouse blood suggesting all infected nymphs acquired pathogens from animals other than mice.

It is possible that some ticks fed on deer or mice but the assay failed to detect the blood remnants. We are sending our samples to Tufts for the developers of the blood meal assay to corroborate our findings. These preliminary results currently show animals other than mice and deer are driving the transmission cycle of tick borne illnesses in the Wells National Estuarine Research Reserve.
This has huge implications for tick management strategies and could help reduce the growing number of tick borne illness cases.

I would like to say a huge thank you to the Twombly family for generously providing the funding for my project and I'd like to thank my mentor Rebecca Robich, and the other members of the vector borne disease lab.

Thank you all for listening and I hope to see you in the poster session!