Reflections on septic discharges

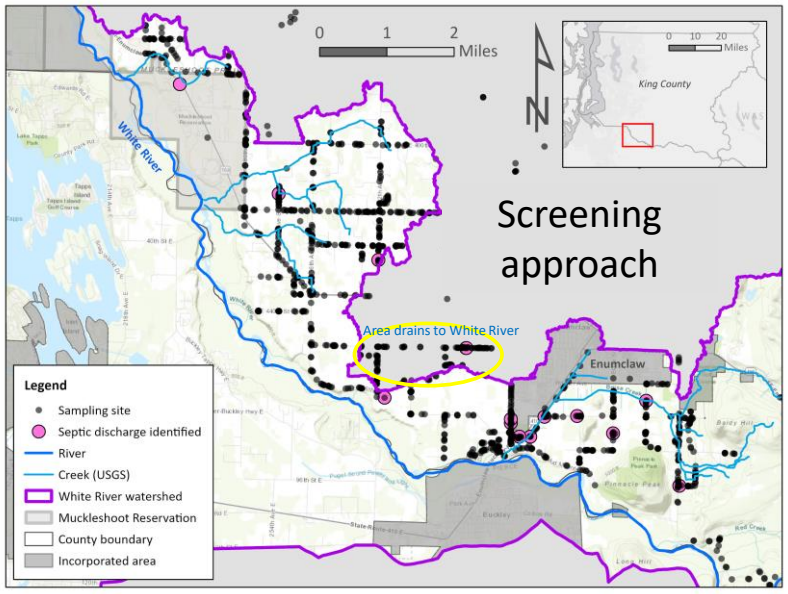
and other sources of fecal bacteria pollution in White River tributaries

King County Stormwater Services

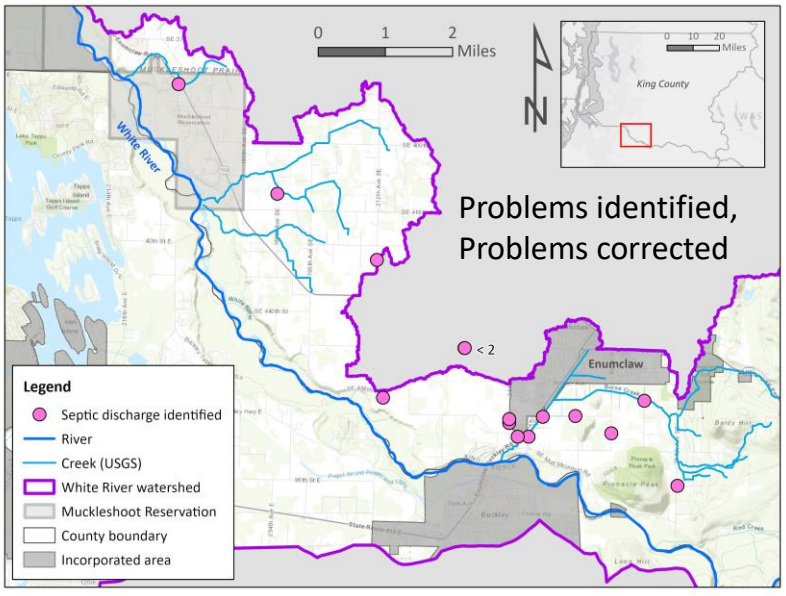
January 21, 2025

Context

- High bacteria levels in White River led to TMDL for fecal bacteria
- Boise Creek main focus, along with principal seasonal tributaries – Pussyfoot, Second, Jones Creeks
- Two main anthropogenic sources suspected:
  - On-site septic systems
  - Domestic animals
  - Wildlife?



King County has taken samples at hundreds of locations in the area, mostly in the stormwater system, but also in streams. Most of the stormwater system in this area is comprised of roadside ditches, but there are some areas where the drainage is underground ("pipe and catch basin"). Essentially all the samples are taken from public property. Our stormwater system is dry in the summer; there is basically no water leaving it in the dry season. So, we generally do more sampling in the wet season. Dilution downstream can make it hard to find these sources unless you are close to them. Therefore, we cut to the chase and have systematically sampled every known private pipe and ditch entering our stormwater system, as well as at nodes and closely-spaced intervals throughout the system.



Fifteen septic discharges have been identified to date; almost all have been eliminated, thanks to the work of our Public Health department. Most are in the Boise Creek basin. However, this elimination of these sources has not been enough to bring the creeks into compliance.

Rare:

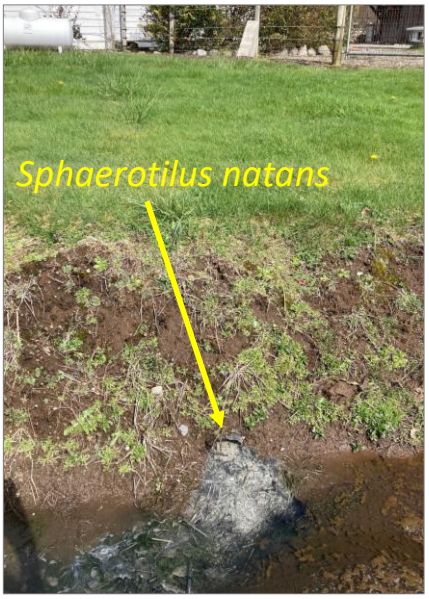
Drainfield failure;
sewage surfacing

The following slides include photos of septic issues we have discovered through our screening. This photo shows a wholesale failure of a septic drainfield – the septage is surfacing over an area of a square foot or two, along the edge of a roadside ditch. Most of the problems we have found are not of this nature.

In this example, a homeowner has plumbed his septage to the County's stormwater system. There is a storm drain buried under the planter in the foreground. The homeowner sent the septage into a gravel filled, L-shaped trench with a perforated pipe running through it. From the storm drain, the water goes under the road into an open County ditch. Over the course of a year, our sampling results in the vicinity had led us to suspect a problem in this area, but it wasn't until we did some recon in September that we saw this green L shape in the lawn. The pipe daylighting in the County ditch had been completely filled in, buried under rocks. Jeanne is here uncovering it. This property needed a new mound system, due to high groundwater in the vicinity. Again, most of the problems we have discovered are not of this nature.

Common: Roof downspout or field drain in proximity to OSS drainfield

Most of the problems we have found are where a small pipe, either perforated or cracked, either a field drain or a roof downspout leader, passes through or near a septic drainfield. Partially treated septage mixed with clean groundwater or rainwater enters the pipe and flows to a ditch or storm drain. Water leaves the pipe at a low rate. In some of these cases, the problem can be resolved by removing the pipe, and an expensive repair or replacement of the septic system is not needed.


Sphaerotilus natans


Septic discharges:
partially treated septage;
low flow rates

How does a typical septic problem impact bacteria levels?

- Most septic problems we find are a combination of clean groundwater and partially treated septage
- Flow rate = ~1.0 gallon per minute (or, 1/449 ft^3/s)
- Concentration = 12000 CFU/100mL
- In a clean stream running at **1 ft^3/s**, discharge would be diluted
  - Increase in *E. coli* concentration in this small stream would be 12000/449 = **27 CFU/100ml** (i.e., below State standard)

Flow rate: Typically a steady rate – if the rate increases during a storm (downspouts), concentration decreases

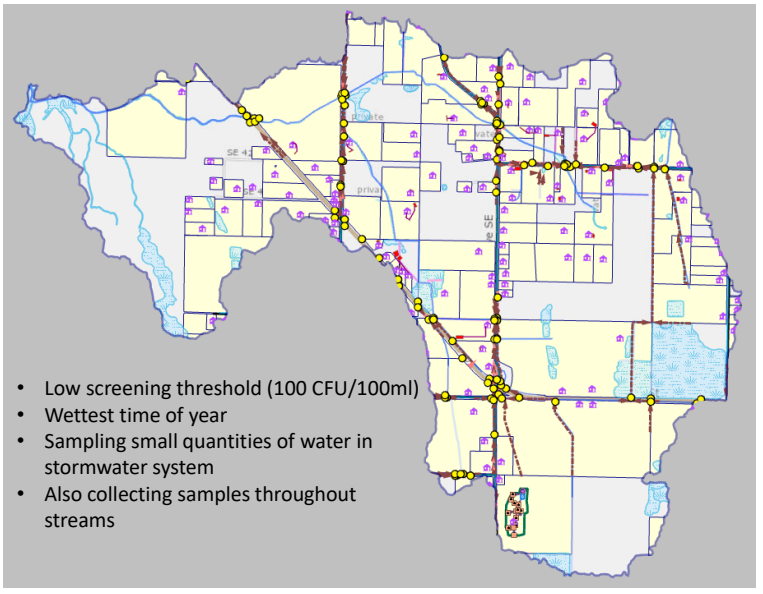
Bacteria loadings (concentration x volume)

- Boise Creek on 12/18/24
  - *E. coli* = 520 CFU/100ml
  - Flow rate = 110 ft^3/s
  - Assume 10 septic discharges in basin at 2 gpm and 10000 CFU/100ml
  - The load from these would only account for 0.77% of E. coli present

We don't think there are actually 10 septic discharges entering Boise Creek. This calculation is merely to illustrate that, even if we assume there are a bunch out there, they don't seem to represent a significant fraction of the E. coli bacteria present.

Are we missing problems?

It's unlikely – and if we are, it probably isn't many



This map shows the Second Creek basin. Most properties in each creek subbasin are not located directly on the creek itself. Only a small subset of the properties are located on the creeks themselves. For most properties, the closest surface water drainage feature is actually a smaller ditch, whether a private ditch, or a roadside ditch belonging to the County, and not the stream. Thus, if sewage is to leave the property, whether on the surface or as shallow groundwater, the surface drainage feature that will intercept it is a ditch or the stormwater system, and not the creek itself. Thus, a close examination of the stormwater system should be able to find most of the septic problems located in the basin. Sampling in the stormwater system, where flow rates are relatively low, means that dilution is less of a confounding factor.

We set our screening threshold at the WQ standard for the geomean E. coli level. We visit all these sites in the winter when the groundwater level is high. Water in the stormwater system is generally very clean between storms. If septic systems were impacting the ditches, we would notice that. And this is how we have found problems but also, generally, ruled out the possibility that there are many others out there.

As a side note, Most properties in this basin, and on most of the White River side of the plateau outside of the Boise Creek basin, are served by private wells. There is incentive

to keep septic systems high and dry. If high groundwater in the winter impacted wells it would be a major issue. Setbacks from wells and from surface water are usually the same -- 100 ft. Studies show that even if drainfields come in contact with groundwater, bacteria levels drop to near-zero after passing through 100 feet of soil.

Microbial Source Tracing - qPCR

- Microbial Source Tracking (MST) – any method that is intended to differentiate between sources of fecal contamination

E. Coli bacteria are not specific to humans – they are found in the gut of any warm-blooded animal. In order to differentiate between animal sources, we need to do a different type of test.

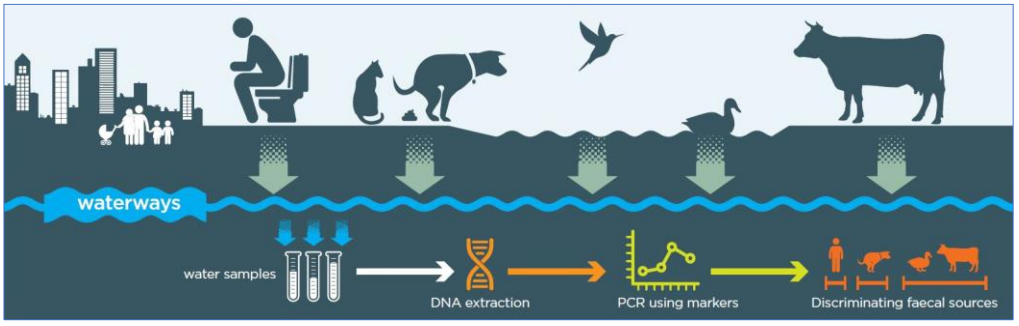
Microbial Source Tracing - qPCR

- Microbial Source Tracking (MST) – any method that is intended to differentiate between sources of fecal contamination

- quantitative Polymerase Chain Reaction
  - Technique to copy/multiply a "target" DNA segment so that it can be detected by instrument
  - "Target" is genetic material of certain bacteria species that is specific to intestines of a particular animal type (human, ruminant, cow, etc.)
  - Genetic material degrades quickly in environment; detection suggest recent contamination event

Thermal Cycler

Microbial Source Tracking



Two types of samples submitted for Microbial Source Tracking analysis:

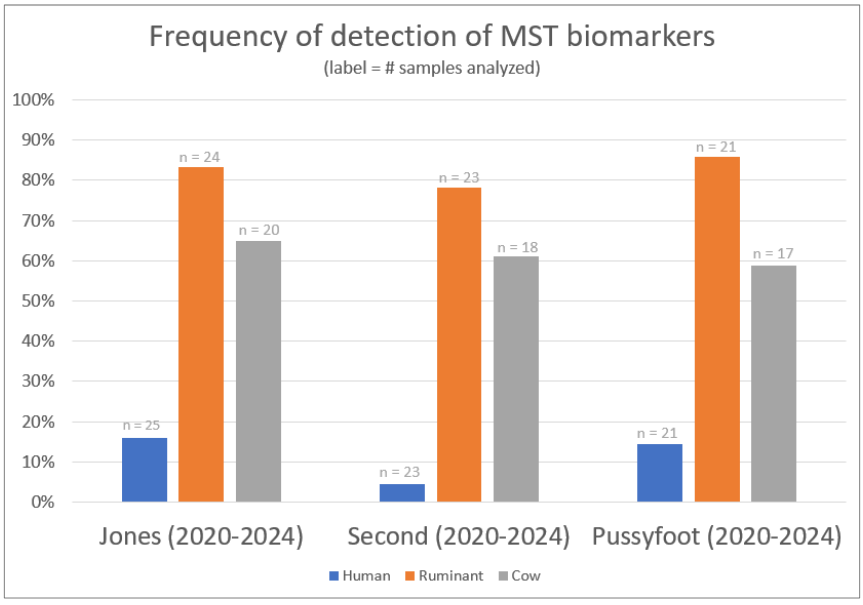
1. From stormwater system, where there are repeated, high levels of *E. coli*
2. From streams, as another method of detecting problems,
   and also to see in general which markers are detected more frequently

How does dilution impact qPCR detections?

- Influent to KC WWTP analyzed in 2017
  - *E. coli* = 50000-70000 CFU/100ml
  - Hu-2 = 6,000,000+ gene copies/ml
    - Consistently detected at 1000x dilution
    - Sometimes detected at 10000x dilution
    - Never detected at 100000x dilution

If septage is diluted such that the human biomarker is indetectable, it is likely having a small impact on *E. coli* levels

Let's talk a little bit about dilution of sewage and how this might make it difficult to find a problem simply by taking samples from a stream. Tests were done on influent to the County's wastewater treatment plant. The sewage was diluted at 10x, 100x, 1000x, and by increasing factors of 10, up to a hundred million times. E. coli levels seemed to scale with the level of dilution – in other words, at a dilution of 10000x, the E. coli result was in the neighborhood of 5-7 CFU/100ml. In the case of the human genetic marker – that target strand of DNA referenced earlier -- there was a non-linear response. Although raw sewage showed around 6 million gene copies or more per milliliter, the human marker could not be detected at a dilution of 100000. This is because the result produced (6000000) is the result of repetitive cloning, or doubling, of what is found in the solution, and while a high result it might give an indication of the amount of human waste present, that relationship isn't perfect, because of the many cycles of cloning that occur. A high result is better thought of as giving us high confidence that there was SOME genetic material present. Whereas a well-mixed sample which is then diluted could be expected to have E. coli present throughout, there might be only a small amount of the genetic material in the sample which does not find its way through the dilution process, and therefore it can not be found by the instrument for the purposes of cloning.



This graph illustrates the frequency of detection of the human, ruminant and cow markers over the last five years in four of the main seasonal tributaries to the White River. Boise Creek is not included because dilution might make the analysis more difficult; also, over the last five years our focus has been on tributaries besides Boise. We can see that the human marker is detected infrequently relative to the ruminant and cow markers. In Jones Creek, we have not found any human waste sources; we also haven't had a hit on the human marker in over three years. We have found two septic issues in the Pussyfoot basin. We haven't found any in Second Creek, where we had only one detection in 5 years, and it was at a low level. Not represented here is how high or low the detections were, which is also important, but in the interest of brevity I am only showing here the frequency of detection.

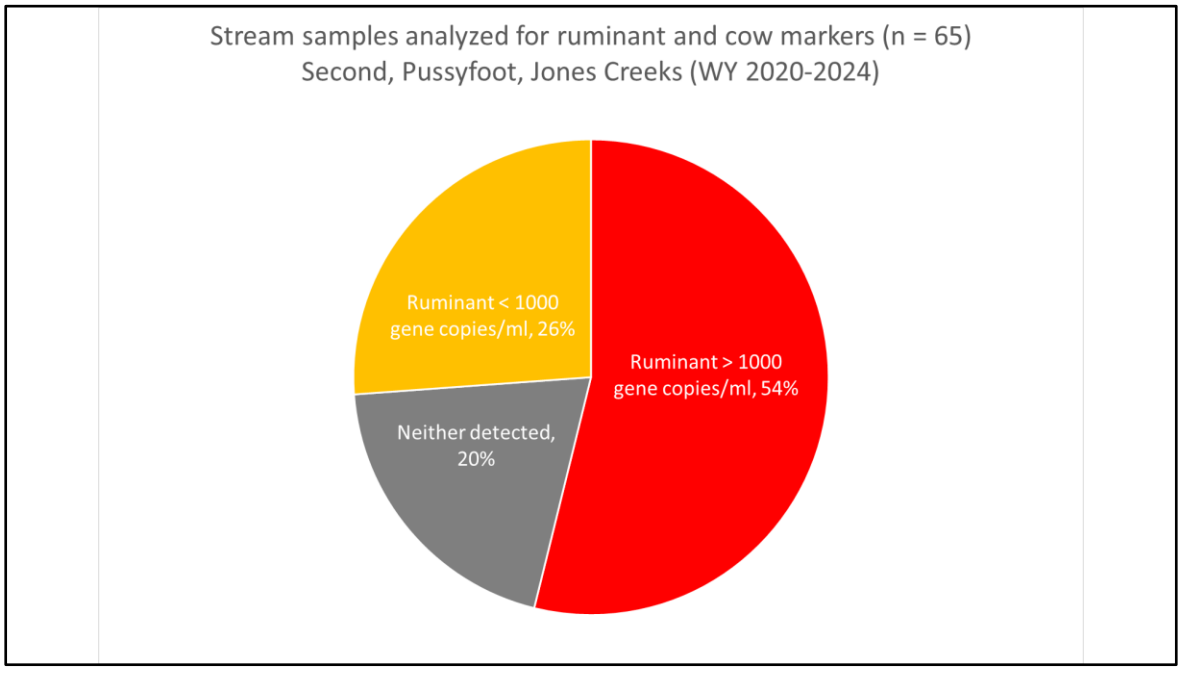
Note on ruminant and cow markers

- Two types of genetic material we might seek in cow poop:
  - One bacterium is specific to intestines of ruminants in general – not just cows, but deer, elk, goats, etc. – the "ruminant marker"
  - Another bacterium is specific to only cows, and not other ruminants – the "cow marker"

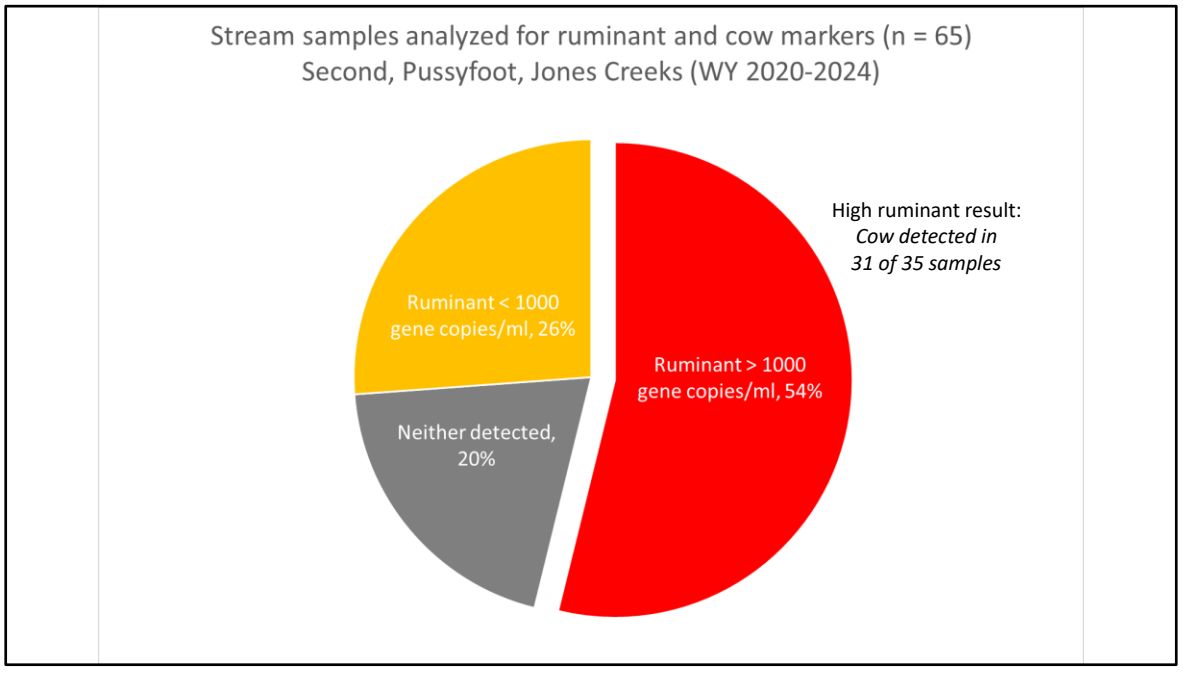
Note on abundance of target bacteria

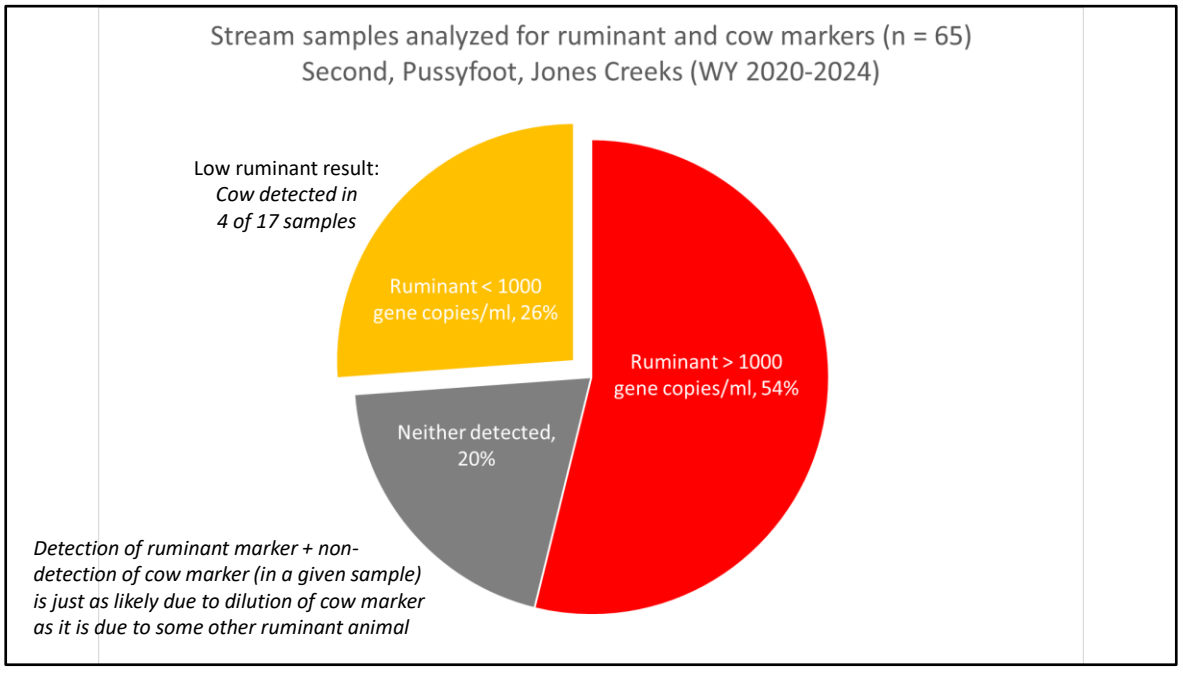
- KCEL 2019 study (small *n*)
- In one gram of cow feces, there are roughly:
  - 150000-800000 gene copies of the ruminant marker
  - 250-800 gene copies of the cow marker
    - In cow poop, there are ~1000x more copies of ruminant marker than cow marker
    - Appears that cow marker is "diluted out" more easily than ruminant marker

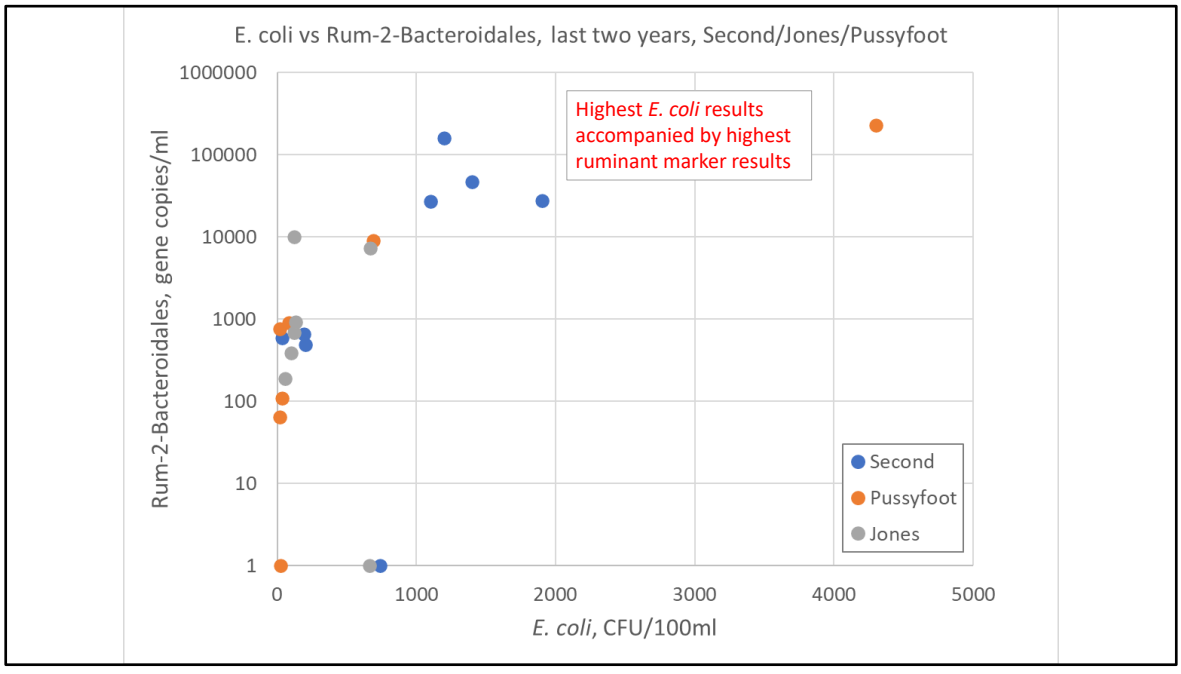
Another matter worth discussing is the fact that the target genetic material (from the intestinal bacteria) used to identify different species' waste varies in quantity from species to species, and also among individuals within those species. It is also possible that amount of target bacteria in the feces from a specific individual might vary over time…we just don't know much about this. However, it does seem that the marker used to identify ruminants is much more prevalent in cow poop than the more specific marker used to identify cows. Cows are ruminant, and some of their gut bacteria are similar to other ruminants, but some is more specific to cows. Incidentally, the limited info we have suggests that the abundance of target genetic material per gram of feces is roughly the same when comparing humans to ruminants. [DOG: 1000-100000 gene copies of the dog marker per gram feces]



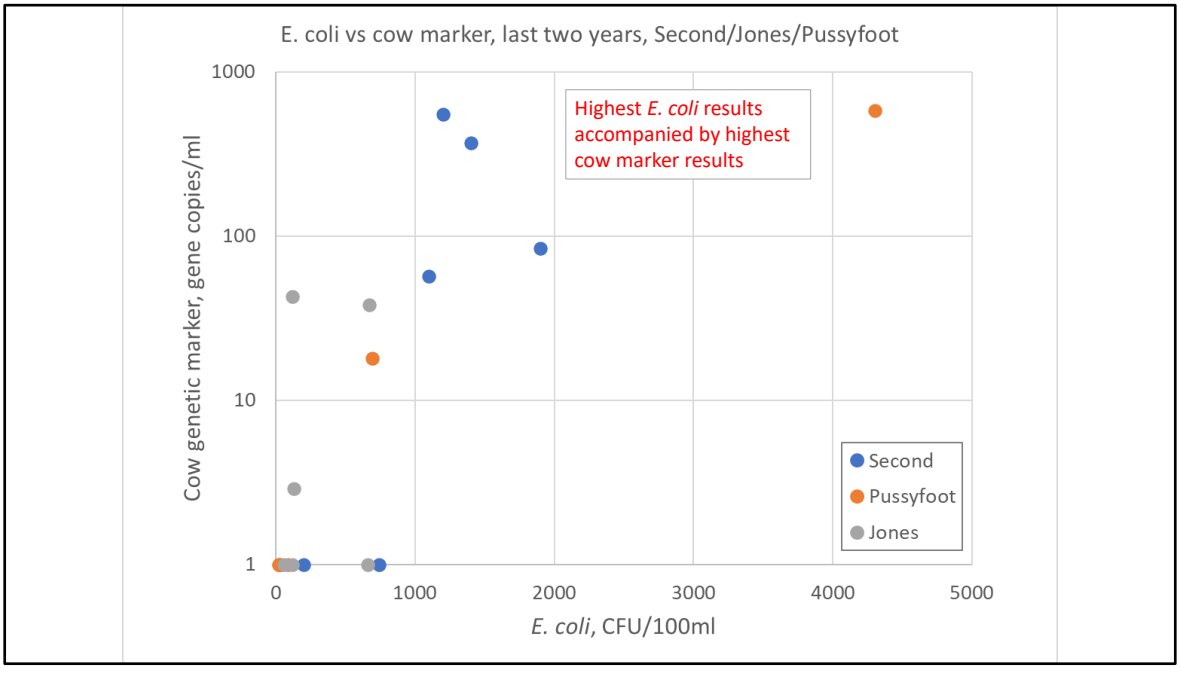
As seen in the previous graph, the ruminant marker was detected more frequently than the cow marker, which makes sense, especially given that there are other ruminants besides cows (goats, deer, elk, etc), and also because there is more of the ruminant marker in a gram of feces than the cow marker, as discussed above. To that point, whether or not the cow marker is detected appears to depend heavily on how high the ruminant result is. This might suggest again that the cow marker is being diluted beyond detection more easily than the ruminant marker. A detection of the ruminant marker without a cow detection does not necessarily mean that some other ruminant is responsible…but it could.


Stream samples analyzed for ruminant and cow markers (n = 65)
Second, Pussyfoot, Jones Creeks (WY 2020-2024)
Ruminant < 1000 gene copies/ml, 26%
Ruminant > 1000 gene copies/ml, 54%
Neither detected, 20%
High ruminant result:
Cow detected in
31 of 35 samples


Stream samples analyzed for ruminant and cow markers (n = 65)
Second, Pussyfoot, Jones Creeks (WY 2020-2024)
Low ruminant result:
Cow detected in
4 of 17 samples
Ruminant < 1000
gene copies/ml, 26%
Ruminant > 1000
gene copies/ml, 54%
Neither detected,
20%
Detection of ruminant marker + non-
detection of cow marker (in a given sample)
is just as likely due to dilution of cow marker
as it is due to some other ruminant animal



In the last two years, looking at the three seasonal tribs of interest, the highest E. coli results have been accompanied by the highest results for the ruminant and cow markers.



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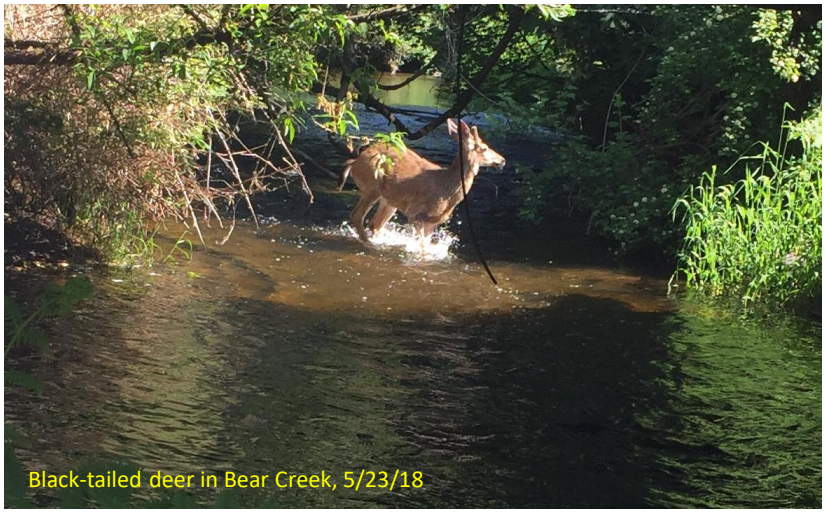
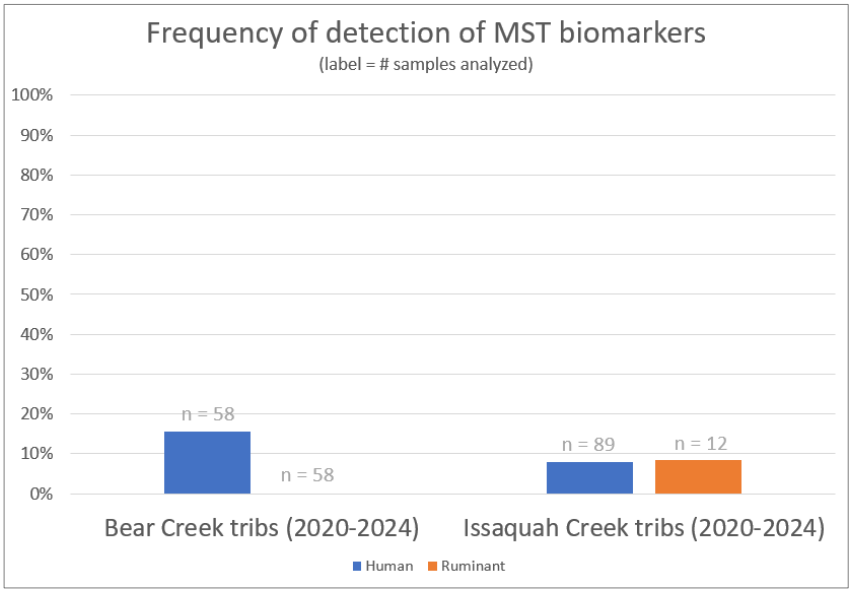
What about other parts of the County?

Comparisons with other stream basins

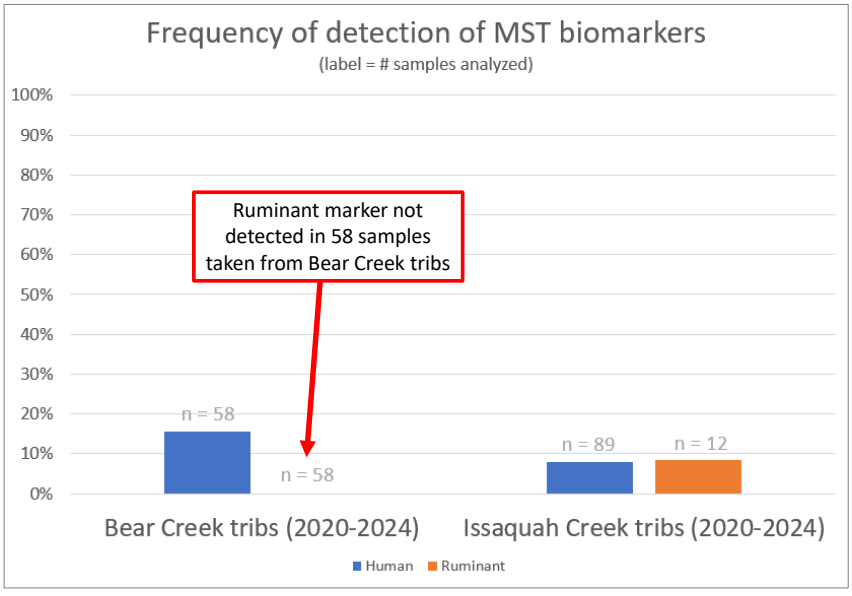


Black-tailed deer in Bear Creek, 5/23/18

The White River area is not the only part of the County where we use these biomarkers. We also do work in the Bear Creek and Issaquah Creek basins. I am personally much more familiar with the Bear Creek basin. Deer are prevalent there. I feel like I see groups of deer about every other time that I am in the basin. Studies show that deer are found at higher densities in suburban areas than in open forest where there are no humans. They like the foliage better. Lots of shrubs, gardens. I don't see many deer on the Enumclaw plateau (we'll get to elk in a moment) – the plateau is very open; there are small patches of forest with large gaps between them. The Bear Creek basin, while highly developed in a surburban sense, has retained much of its tree cover due to the County's development regs. Hard to get numbers, but there are likely many hundreds of deer in the basin, possibly more than 1000.



This graph illustrates the frequency of detection of the human and ruminant markers in the principal tributaries to Bear and Issaquah Creek (not in the mainstems, where there would be much more dilution). In Bear Creek, the ruminant marker has not been detected in 58 samples analyzed. In Issaquah Creek tribs, it was only detected in 1 of 12 samples. The human marker is detected at about the same frequency as in the White River tributaries.



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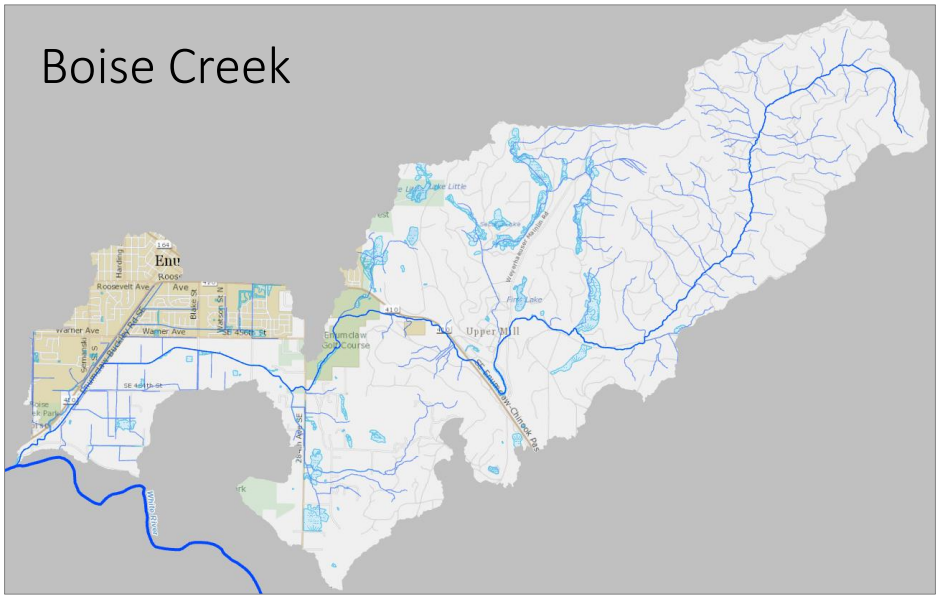
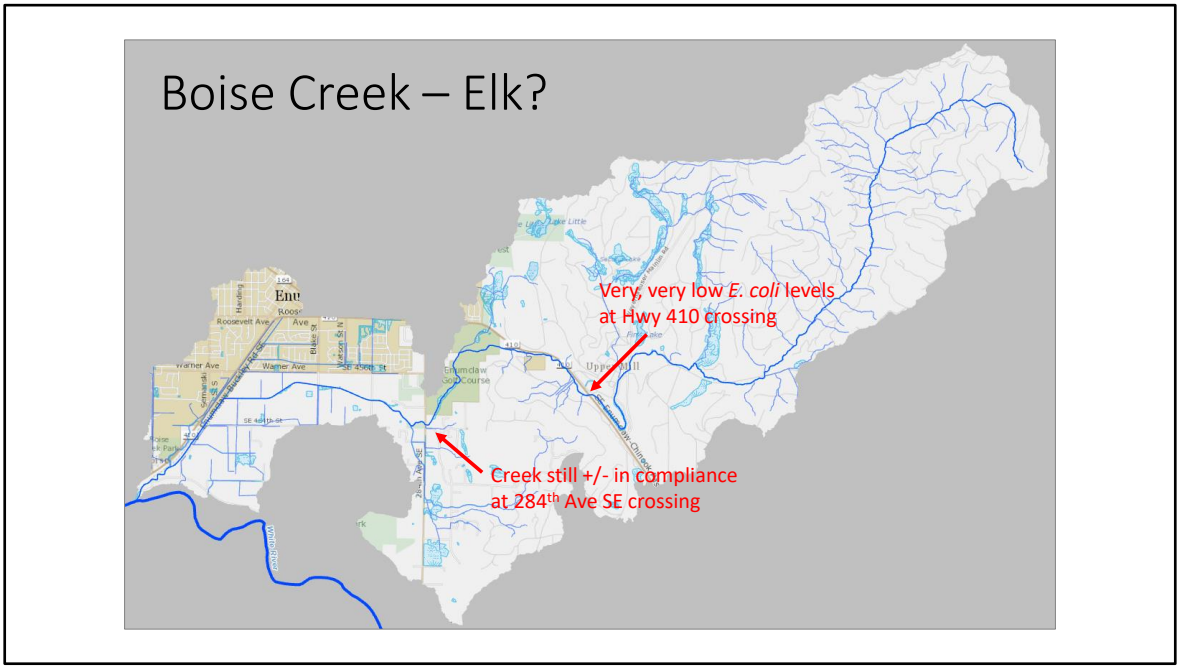
Elk

A not-infrequently-heard refrain is that elk are responsible for WQ impairments in the white river tributaries. They come in large groups and poop everywhere. They are also the bane of farmers, occasionally knocking down fences, and acting as potential vectors of disease. While I don't live on the plateau, I only have seen elk once or twice in hundreds of visits.

Some effort has been made to test the theory that elk are contributing to fecal pollution. A former colleague here at the County, ten years ago, collected samples of fresh elk feces and sent them to a lab in Florida. The lab created an "elk biomarker" from this material. We then sent a total of 15 samples to the lab for elk analysis. We collected these samples from our stormwater system in the Boise Creek basin during storms on 11/1/2015 and 12/8/2015.

Boise Creek

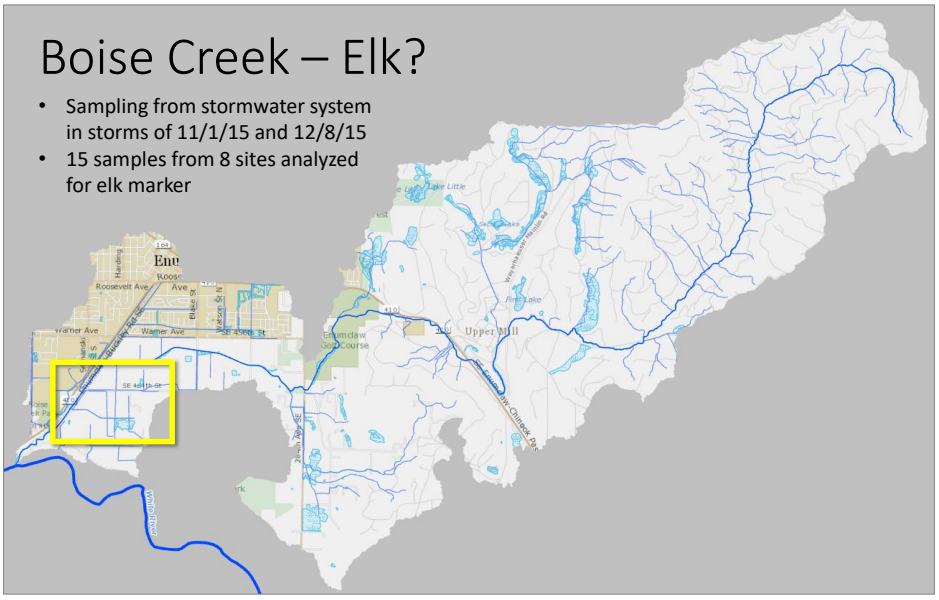

Roosevelt Ave
Warner Ave
Warner Ave
SE 45th St
Drumclaw Golf Course
Upper Mill
Boise River

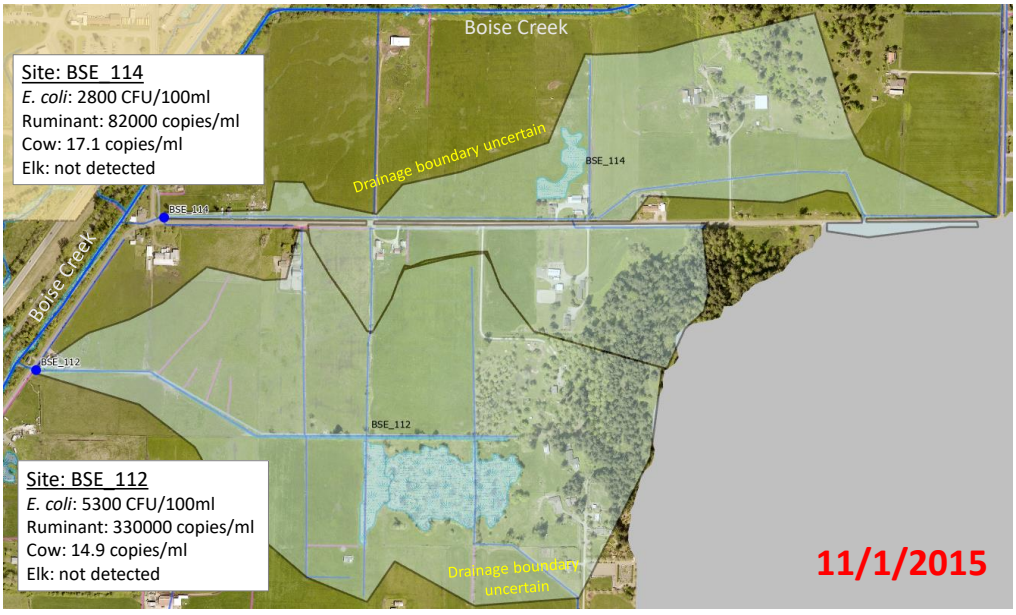


Presumably there are elk in the upper portion of the basin, and not just in the fields on the plateau. Yet, this does not cause bacteria impairments.

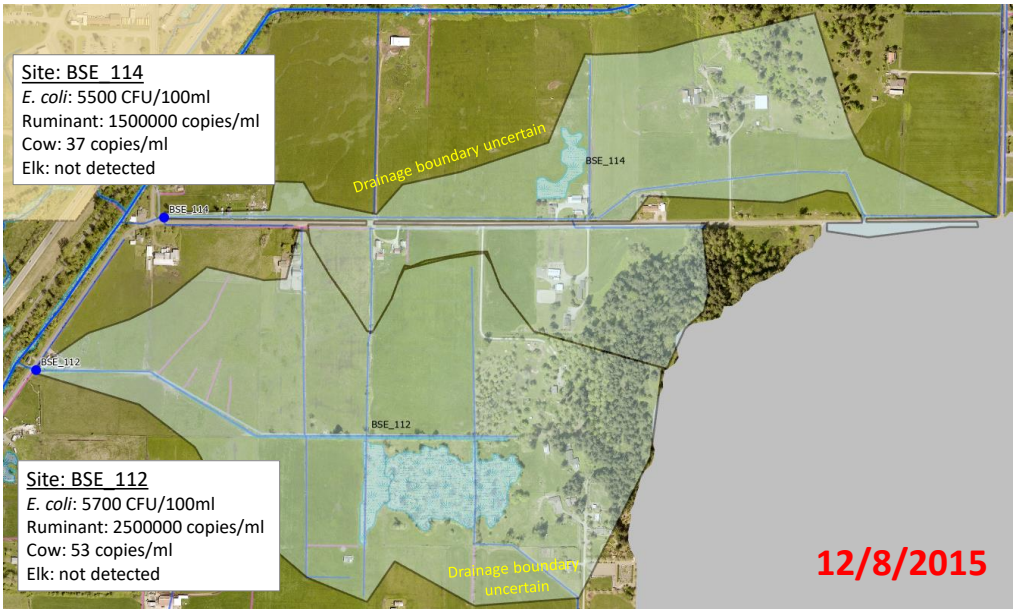
Boise Creek – Elk?

- Sampling from stormwater system in storms of 11/1/15 and 12/8/15
- 15 samples from 8 sites analyzed for elk marker





In the interest of brevity and simplicity, I'm only going to share info from two sites. However, the results at these sites were similar to those from other sites. Looking at the 15 samples analyzed for elk: they all had high EC results and high hits for the ruminant marker. All but one tested positive for cow. At the one negative for cow, there were goats in the contributing area. The elk marker was not detected in any of the samples.



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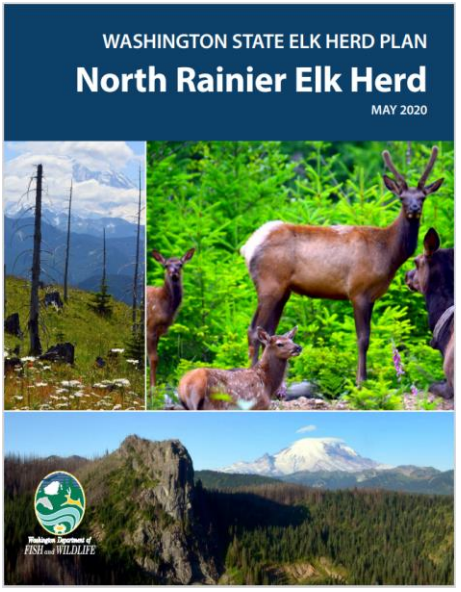
WDFW estimates there are a total of 100 individual elk that visit the Enumclaw plateau.

This number will likely decrease due to management practices.



Notify your elk friends.

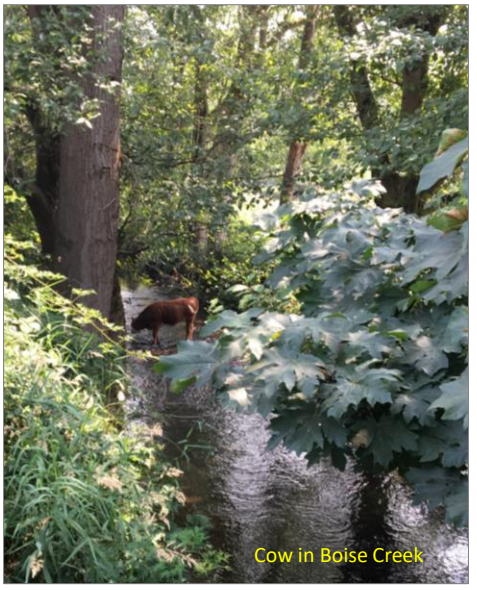
Summary

- Elimination of various septic discharges has not brought creeks into compliance with WQ standards
- Unlikely that there are many remaining septic discharges, and if there are, they likely account for a small fraction of bacteria loads

New septic system installation, Boise Creek basin

Summary

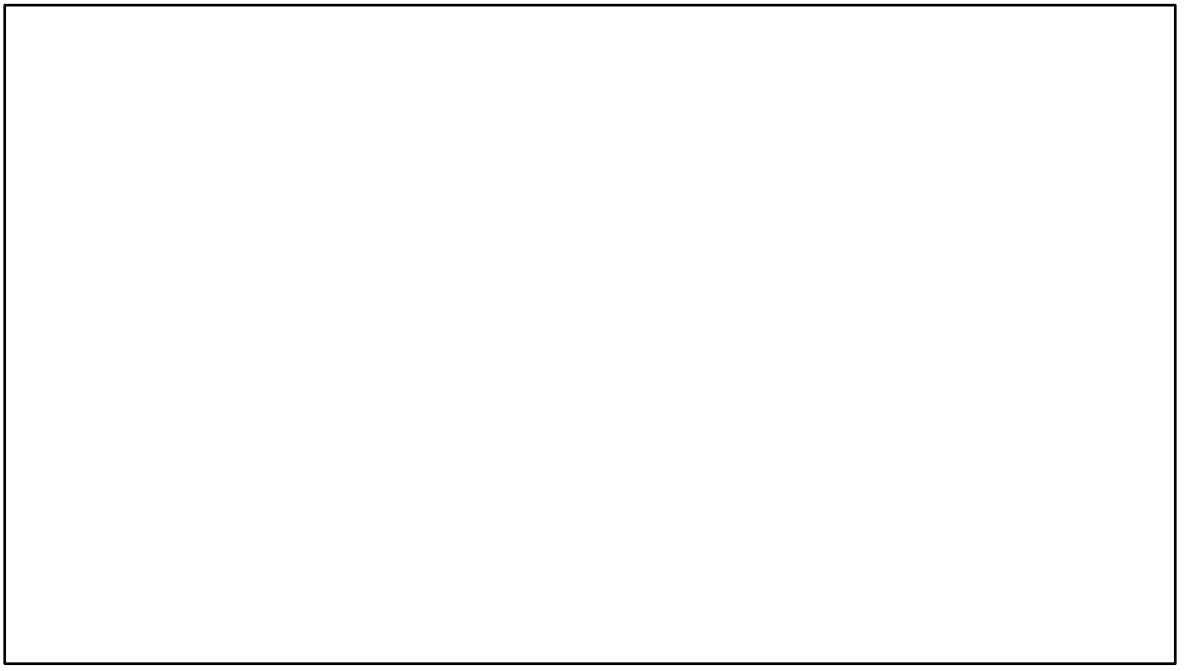
- MST suggests that ruminants/cows are more important contributor than humans
- Ruminant/cow marker found much more frequently on plateau than in other drainage basins
- Available info suggests elk waste can not explain impairments



Cow in Boise Creek

It seems there is a relation with ruminants, cows, and E. coli in these streams, but we don't have information about other animals. We don't have a viable horse marker. We have an avian marker that just came on line, and we plan to start using this. But it is not possible, with the tools currently available to us, to say that X% of the E. coli in a water sample are due to one animal, X% are due to another animal, etc. Nonetheless, if we are looking to reduce


Thank you



Extra/rejected slides below

How much *E. coli*?

- *E. coli* levels are LOW
  during dry periods in the winter when groundwater levels are high
  → true of streams and the stormwater system
- *E. coli* levels GO UP
  during storms in the winter
  → true of streams and the stormwater system
- *E. coli* levels GO UP
  in the summer when there less dilution; there is no water flowing in the stormwater system – we don't find septic issues during this period, only in the wet season

Impairments largely are due to conditions in the DRY SEASON.

Dilution, *E. coli*, qPCR

- Influent to KC WWTP analyzed in 2017
  - *E. coli* = 50000-70000 CFU/100ml
    - Concentration scales with dilution more or less linearly
  - Hu-2 = 6,000,000+ gene copies/ml
    - Consistently detected at 1000x dilution
    - Rarely detected at 10000x dilution
    - Never detected at 100000x dilution
  - (Ruminant, cow markers not detected in raw sewage)
  - (Dog marker detected in sewage at 10x dilution, but not at 100x dilution)

Let's talk a little bit about dilution of sewage and how this might make it difficult to find a problem simply by taking samples from a stream. Tests were done on influent to the County's wastewater treatment plant. The sewage was diluted at 10x, 100x, 1000x, and by increasing factors of 10, up to a hundred million times. E. coli levels seemed to scale with the level of dilution – in other words, at a dilution of 10000x, the E. coli result was in the neighborhood of 5-7 CFU/100ml. In the case of the human genetic marker – that target strand of DNA referenced earlier -- there was a non-linear response. Although raw sewage showed around 6 million gene copies or more per milliliter, the human marker could not be detected at a dilution of 100000. This is because the result produced (6000000) is the result of repetitive cloning, or doubling, of what is found in the solution, and while a high result it might give an indication of the amount of human waste present, that relationship isn't perfect, because of the many cycles of cloning that occur. A high result is better thought of as giving us high confidence that there was SOME genetic material present. Whereas a well-mixed sample which is then diluted could be expected to have E. coli present throughout, there might be only a small amount of the genetic material in the sample which does not find its way through the dilution process, and therefore it can not be found by the instrument for the purposes of cloning.