Appendix A: Land Use, Population, and Load Projections

The Medina River Below Medina Diversion Lake watershed is undergoing rapid changes in land use and land cover due to growth of San Antonio, Bexar County, and the Texas Hill Country regionally.

Potential sources of E. coli identified in the WPP that are directly associated with land uses or habitat include livestock, deer, and feral hogs. Those sources more closely associated with human population include pet waste, on-site sewage facilities (OSSF), and wastewater treatment facilities (WWTF). As population-driven changes in land uses, habitat and grazeable land distribution, and land development occur, the number and distribution of these sources are expected to change accordingly.

Based on stakeholders' local knowledge and guidance, present-day potential bacteria loads were calculated and projected into the future based on trends in land development and population growth rates. These projections allow informed decision making on management strategies to reduce bacteria loading now and into the future, and provide a strong basis for adaptive management of WPP implementation strategies and priorities.

Land Use Projection

Changes in land use and land cover (LULC) were projected for a 10-year period ending in 2036. Changes in coverage of LULC categories were predicted by combining current and historical NLCD data (2001 - 2021) with land development information using GIS tools. Information on county-approved subdivision plats, provided by Medina and Bexar counties, was used as a proxy for land development and provide the basis for projecting watershed-scale land use trends for specific LULC categories.

Bexar County subdivision records were obtained, including subdivision name, spatial information, and date of plat approval records. Medina County records included spatial information and subdivision name (Figure A-1). Approval dates for Medina County records were acquired through the Medina County Clerk website. Where no plat record was listed, the earliest warranty deed or deed of trust date for the subdivision was used. The Microsoft excel function FORECAST.LINEAR was used to project cumulative subdivision areas for 2026, 2031, and 2036 (Figure A 1). Trends developed based on combined Medina and Bexar county data were extrapolated to the entire watershed.



Figure A-1. Approved and proposed subdivisions, 1928 - 2024.

Year	2001	2004	2006	2008	2011	2013	2016	2019	2021
Cumulative Acreage	25,728	27,658	30,605	32,177	33,856	35,437	37,834	42,974	46,611

Table A 1. Cumulative combined acreage for Medina and Bexar County subdivisions during each year NLCD Land Use and Land Cover data were available.



Figure A 1. Cumulative subdivision area for Medina and Bexar Counties from 2011 through 2021, with projected area values for 2026, 2031, and 2036.

GIS was used to determine the total acreage of each LULC category within approved subdivisions and remove them from the areas of grazeable land for cattle and habitat for deer and feral hogs, as discussed below. While some areas within subdivision plats may still be used for grazing or wildlife, trends indicate the vast majority of subdivisions in the watershed are converted to some level of urban uses. The remaining areas were used to predict potential future E. coli loadings for livestock, deer, and feral hogs based on projected land use changes.

Livestock Load Projection

Livestock bacteria loadings were calculated by multiplying an animal density by the total grazeable land (see Appendix C). Grazeable land use includes mixed-deciduous forest, rangeland, grassland, and hay/pasture. Using GIS, grazeable lands located in a subdivision were removed from the total grazeable acreage for each year of the National Land Cover Database (NLCD) LULC from 2001 to 2021 (Figure A 2; USGS 2022). Once acreage totals for grazeable land were adjusted for subdivisions, the subdivision cumulative acreage for each NLCD LULC year from 2001-2021 were graphed with grazeable land. As expected, grazeable land area reductions mirror cumulative

subdivision area for each year but does not match it exactly (Figure A 2). Cumulative subdivision area was then graphed against grazeable land to determine the nature of the relationship. This relationship was used to project grazeable land coverage into the future (Figure A 3).



Figure A 2. Comparison of adjusted grazeable land based on cumulative subdivision area for the Medina River Below Medina Diversion Lake watershed.



Figure A 3. Analysis of the relationship between cumulative subdivision area and grazeable land for the Medina River Below Medina Diversion Lake watershed.

In this example, for every acre increase in subdivision area, grazeable land was reduced by 0.8789 acres (see trendline equation on Figure A 3). This is not a one-to-one relationship as subdivisions overlay other LULC types besides grazeable land. The yintercept of this equation, 174,300, was not used as it represents grazeable land when there was no subdivision area recorded in the late 1920s and 1930s. The y-intercept was manually calculated for projection of LULC in 2021 using known grazeable land of 120,982 acres and known cumulative subdivision acreage of 46,611 acres (Formula A-1). The relationship was then applied to the projected cumulative subdivision acreage for 2026, 2031, and 2036 (Table A 2).

Formula A-1:

$Grazeable \ LULC = -0.8789 * Cumulative \ Subdivison \ Acreage + \ 161,948$

Table A 2. Projected cumulative subdivision acreage for Medina and Bexar Counties within the Medina River Below Medina Diversion Lake watershed and the calculated suitable grazeable land for livestock.

	2026	2031	2036
Projected Cumulative Subdivision Area (Acre)	52,046	58,397	64,749
Projected Grazeable Land (Acre)	116,205	110,623	105,040
Total Projected Livestock Load (CFU/day)	1.51E+14	1.43E+14	1.36E+14

To obtain a projected bacteria loading for livestock in 2026, 2031, and 2036, grazeable land area was multiplied by the total load per acre in 2021 (Formula A-2). The load per acre was used for the projection instead of other strategies used for 2021 loading calculation (see Appendix C) as there wasn't a way to project stocking rates into the future. Projected livestock bacteria loading shows a downward trend as areas within the watershed continue to develop and introduce new subdivisions (Figure A 4; Table A 2).

Formula A-2:

$$Total \ Projected \ Livestock \ Load \ = \left(\frac{Total \ Livestock \ Load \ in \ 2021}{Grazable \ Land \ Area \ in \ 2021}\right) * Projected \ Grazeable \ Land \ Land \ Area \ in \ 2021}$$



Figure A 4. Projected bacteria loading for livestock within the Medina River Below Medina Diversion Lake watershed.

Deer and Feral Hog Load Projection

Bacteria loadings for deer and feral hogs were calculated by multiplying each respective animal density by the suitable habitat for wildlife (see Appendix C). For both feral hogs and deer, suitable habitat includes the LULC categories of mixed-deciduous forest, evergreen forest, rangeland, grassland, hay/pasture, cultivated crops, and wetlands. Similar to the previous projection method for livestock, all suitable habitat for feral hogs or deer within the watershed overlain by subdivisions were removed from the total suitable habitat area for each year of the National Land Cover Database (NLCD) LULC from 2001 to 2021. Once acreage totals for suitable habitat were adjusted, subdivision cumulative acreage for each NLCD LULC year from 2001-2021 were graphed with suitable habitat (Figure A 5). Similarly to livestock projections, the suitable wildlife habitat area mirrors cumulative subdivision area for NLCD LULC years from 2001 – 2021 but is not an exact reflection. To further characterize the relationship between cumulative subdivision area and suitable habitat for each year of the NLCD LULC the variables were graphed against each other (Figure A 6). The relationship was confirmed as a linear relationship using the R-squared value.



Figure A 5. Comparison of adjusted suitable wildlife LULC based on cumulative subdivision area for the Medina River Below Medina Diversion Lake watershed.



Figure A 6. Analysis of the relationship between cumulative subdivision area and suitable wildlife LULC for the Medina River Below Medina Diversion Lake watershed.

In this example, for every acre increase in subdivision area, suitable habitat is reduced by 0.8668 acres (see trendline equation on Figure A 6). Similar to the previous projection method with grazeable land, this is not a one-to-one relationship as subdivisions overlay other LULC types. The y-intercept of this equation, 258,006, was not used as it represents suitable wildlife LULC when there were no subdivisions recorded in the late 1920s and 1930s. The y-intercept was manually calculated for projection of LULC in 2021 using known suitable wildlife habitat of 192,025 acres and known cumulative subdivision acreage of 46,611 acres (Formula A-3). From there, the relationship was applied to the projected cumulative subdivision acreage for 2026, 2031, and 2036 (Table A 3).

Formula A-3:

Suitable Wildlife Habitat = -0.8668 * Cumulative Subdivison Acreage + 232,426

Table A 3. Projected cumulative subdivision acreage for Medina and Bexar Counties within the Medina River Below
Medina Diversion Lake watershed and the calculated suitable wildlife LULC.

Year	2026	2031	2036
Projected Cumulative Subdivision Area (Acre)	52,046	58,397	64,749
Projected Suitable Wildlife LULC (Acre)	116,205	110,623	105,040
Projected Feral Hog Load (CFU/day)	5.58E+11	5.41E+11	5.25E+11
Projected Deer Load (CFU/day)	1.7840E+13	1.73E+13	1.68E+13

Projected bacteria loading for feral hogs in 2026, 2031, and 2036 was calculated through the same process as 2021 bacteria loadings, but using the projected suitable habitat area instead (see Appendix C). Multiplying feral hog density and population (Wagner & Moench, 2009), habitat area, *E. coli* conversion rate (Wagner & Moench, 2009), fecal coliform production rate (Wagner & Moench, 2009), and an animal unit conversion factor results in an estimated projected bacteria loading for feral hogs (Formula A-4). Projected feral hog loads display a downward trend as development continues within the watershed (Figure A 7; Table A 3).

Formula A-4:

Projected Feral Hog Load = 0.03 * *Projected Wildlife Habitat* * 0.63 * 1.21*E* + 09 * 0.125



Figure A 7. Projected bacteria loading for feral hogs within the Medina River Below Medina Diversion Lake watershed.

Projected bacteria loading for deer in 2026, 2031, and 2036 was calculated through the same process as feral hogs, however, a deer density per acre was manually calculated based on 2021 deer head per suitable habitat area. Multiplying deer density, projected wildlife habitat area, *E. coli* conversion rate (Wagner & Moench, 2009), fecal coliform production rate (Wagner & Moench, 2009), and an animal unit conversion factor resulted in a project bacteria loading for deer within the watershed (Formula A-5). Projected deer loads display a downward trend. (Figure A 8; Table A 3).

Formula A-5:

 $\begin{array}{r} Projected \ Deer \ Load \ = \\ \left(\frac{Livestock \ Load \ in \ 2021}{Suitable \ Wildlife \ Habitat \ Area \ in \ 2021} \right) * \ Projected \ Wildlife \ Habitat \ * \ 0.63 \ * \ 1.50E \ + \ 09 \ * \ 0.112 \end{array}$



Figure A 8. Projected bacteria loading for deer within the Medina River Below Medina Diversion Lake watershed.

Population Growth Rate Projection

Changes in watershed population were predicted for a 10-year period ending in 2035 by combining reported and projected student enrollment estimates with current census data. Stakeholders felt that local analyses conducted by the Medina Valley Independent School District (MVISD) are accurately representing growth in the watershed rather than regional or statewide population projections by the Texas Demographic Center.

The MVISD school district covers large swaths of the watershed (Figure A 9) and was suggested by stakeholders as a local data source. This projection was done for 2025, 2030, and 2035. Note that this differs from the previous land use projection methods as population projections were based on census data for 2020, whereas land use projections were based on NLCD LULC up to 2021.



Figure A 9. Medina Valley Independent School District (MVISD) boundaries.

MVISD reported enrollment from 2016 – 2024 and projected enrollment for 2025 – 2034 were acquired from school district quarterly reports (MVISD 2023). Projected enrollment was estimated for 2035 using the 10 years of MVISD projected enrollment and a LINEAR.FORECAST in Microsoft Excel. The yearly dataset from 2020 through 2035 is used to calculate the projected watershed population.

Total MVISD enrolled students per school year were converted to a total number of households containing students in the district by multiplying total students by the census statistic for Medina County, "households with one or more people under 18 *years*" (USCB, 2020). Note that there is some error in the estimate as children under the age of 5 years old have not started school yet and wouldn't be included in actual enrollment for MVISD. For this analysis, the total households in the watershed for 2020 was derived using GIS tools, and may be slightly different than the number of households used in other analyses. Once the number of households with students in the district was determined, a ratio was calculated between the number of households with the MVISD district and the total households within the watershed during the 2020 census to scale up MVISD numbers (USCB, 2020). This ratio of 2.57% MVISD student households to the overall watershed households was then used to calculate the total household in the watershed for each subsequent year. Finally, total households within the watershed were multiplied by 2.65 average persons per household within the watershed based on the 2022 American Communities Survey (Table A 4; USCB, 2022). The projected population growth approved by stakeholders shows a substantial increase in the overall watershed population (Figure A 10).

	2020	2025	2030	2035
MVISD Total Students	5,852	9,484	14,302	20,020
MVISD Total Households with Students	1,990	3,225	4,863	6,807
Total Households in Watershed	77,375	125,443	189,169	264,806
Estimated Watershed Population	205,118	332,423	501,298	701,737
Population Growth Rate	-	62.06%	47.63%	39.98%

Table A 4. Sample of population growth projection statistics for Medina River Below N	Medina Diversion Lake
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Figure A 10. Watershed population projection, 2020 – 2035..

Domestic Pet Load Projection

Projected domestic dog population was calculated using projected households in the watershed for 2025, 2030, and 2035 (Table A 4), dog ownership rate of 0.4460, and the estimated number of dogs per household of 1.46 (AVMA 2022) (Table A-5).

A projected bacteria loading for dogs in 2025, 2030, and 2035 were calculated using the same process as 2020 bacteria loadings, but using the projected households in the watershed for each respective year instead (see Appendix C). Multiplying dog population, *E. coli* conversion rate (Wagner & Moench, 2009), and fecal coliform production rate for dogs (Wagner & Moench, 2009) produces an estimated projected bacteria loading for dogs (Formula A-6). The resulting projected dog bacteria loadings show a significant increase over time (Figure A 11).

Formula A-6:

 $Projected \ Dog \ Load \ = Total \ Dogs \ in \ Watershed \ * \ 0.63 \ * \ 5.00E \ + \ 09$

Table A 5. Projected dog population and bacteria loading for the Medina River Below Medina Diversion Lake watershed.

	2020	2025	2030	2035
Total Dogs in Watershed	50,512	81,654	120,543	168,740
Total Projected Dog Load (CFU/day)	1.59E+14	2.57E+14	3.80E+14	5.32E+14



Figure A 11. Projected bacteria loading for dogs within the Medina River Below Medina Diversion Lake watershed.

OSSF Load Projection

Estimated potential future bacteria loadings were calculated for OSSFs using projected populations of the watershed for 2025, 2030, and 2035. The percent change between subwatershed populations for five-year periods between 2020 and 2035 were calculated and multiplied by the total watershed households and populations (Table A 4). Then, each subwatershed population was divided by the number of households to calculate an average person per household by subwatershed. Next, the estimated number of OSSFs in each county within each subwatershed was multiplied by the percent change (see Appendix C for more details on OSSF enumeration and failure rates).

Potential bacteria loadings from OSSFs were calculated for each county within each subwatershed by multiplying the OSSF count by the failure rate, the default wastewater per person, average person per household (Borel et al. 2015), *E. coli* conversion rate (Wagner & Moench, 2009), the fecal coliform production rate for OSSFs (USEPA 2001), a constant for unit conversions, then dividing by 100 (Formula A-7; Table A 6; Figure A 12).

Formula A-7:

Projected OSSF Load = (OSSF Count * 70 * Average Person Per Household * 0.63 * 1.00E + 07 * 3758.2)/100

Table A 6. Total projected bacteria load from OSSFs within the Medina River Below Medina Diversion Lake watershed.

	2020	2025	2030	2035
Total Projected OSSF Load (CFU/day)	6.47E+13	1.05E+14	1.58E+14	2.21E+14



Figure A 12. The total OSSF bacteria loading for the Medina River Below Diverison Lake watershed.

WWTF Load Projection

Similar to previous estimation methods, future bacteria loadings were calculated for WWTFs using projected populations of the watershed for 2025, 2030, and 2035. Current permitted discharge limits were used as the baseline discharge volume, except for phased permits where the maximum permitted flow for each permit was used. The percent change between watershed populations from 2020 to 2025 and each subsequent five-year period was calculated (Table A 4). Population growth rate was applied to each respective year's reported WWTF flow to estimate potential future discharge (Formula A-8; Table A 7).

By 2025 an additional WWTF is expected to come online within the watershed, the Forest Glen WRRF3 WWTF (PUC 2022). Combining bacteria loading from WWTF plants across the watershed and plotting across the next fifteen years shows a steady increase in pollutants (Figure A 13).

Formula A-8:

Projected WWTF Load = Reported Flow
$$*\frac{126}{100}*1.00E+06*3758.2$$

Year	WWTF	Population Growth Rate	Reported Flow (MGD)	
2020	Portranco Ranch Subdivision WWTF	-	0.079	
2025	Portranco Ranch Subdivision WWTF	62.06%	0.1280	
2030	Portranco Ranch Subdivision WWTF	50.80%	0.1931	
2035	Portranco Ranch Subdivision WWTF	39.98%	0.2703	

Table A 7. Example calculation of parameters used to calculate bacteria loading for each WWTF in the Medina River Below Medina Diversion Lake watershed.



Figure A 13. Combined bacteria loading from all WWTF within the Medina River Below Medina Diversion Lake watershed.

Appendix A References

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Appendix B: Load Duration Curves

Load Duration Curves (LDC) are a widely accepted method to characterize water quality data across different flow regimes. Due to inherent variability in monitoring locations across watersheds, streamflow and water quality data must come from the same site to ensure accuracy. Based on Flow Duration Curves (FDC), this type of analysis can allow stakeholders and technical specialists to estimate pollutant load reductions needed to meet water quality standards.

Flow Duration Curve

The precursor to an LDC, FDCs are constructed to analyze flow volume and frequency of that flow (also known as exceedance), creating a 'fingerprint' for the watershed. This plot will contain exceedance probability on the x-axis and streamflow on the y-axis.

FDCs are developed by aggregating historical flow data for the stream. For many WPPs, the USGS streamflow gages can be used for flow data. There are several USGS stream gages located in the watershed, however, finding USGS gages with continuous streamflow data in conjunction with nearby water monitoring sites and adequate water quality data was a challenge. During these events, instantaneous streamflows are paired with bacteria counts. Due to inherent variability in monitoring locations across watersheds, streamflow and water quality data must come from similar monitoring sites within the same stream assessment unit. For this analysis only water quality monitoring data from the most recent state water quality assessment was used (TCEQ, 2022).

To construct an FDC, flow data for a specific sampling location are sorted in order of highest to lowest and then ranked. From here, a streamflow exceedance probability can be calculated and the resulting graph of streamflow volume versus exceedance is created (Formula B-1).

Formula B-1:

$$p = \frac{i}{(n+1)*100}$$

Where:

p = exceedance probability
i = rank of a given streamflow
n = number of observations

The visualization is then analyzed and flow regimes are categorized for the watershed at certain frequencies. These flow regimes are typically identified as areas of the FDC where slope of the graph changes. For example, on Medina River assessment unit 1903_03, three flow regimes were chosen based on major changes in the relationship

between streamflow (Figure B 1). Based on this FDC, flows exceeded 100 cubic feet per second (cfs) for 21 percent of the time.



Medina River Below Diversion Lake; Dec. 1, 2015 - Nov. 30, 2022

This process was also applied to data from assessment unit 12912_01 on Medio Creek (Table B 1). Data was collected during the most recent 2024 *Texas Integrated Report* assessment period to better understand current instream flow conditions and bacteria loadings.

Table B 1. FDCs and LDCs were created for these AUs using data from the 2024 Texas Integrated Report timeperiod.

Waterbody	Assessment Unit	SWQM Station	Water Quality Data Points Used	Time Period Collected
Medina River	1903_03	12814	37	December 1 st , 2015 –
Medio Creek	1912_01	12916	41	November 30 th , 2022

Load Duration Curve

Once the FDC has been constructed, the curve can be multiplied by the state water quality criterion for bacteria (126 MPN/100 mL) to produce an LDC. This is known as the pollutant "allowable load," and is indicated by the solid line in the LDC graph (Figure B 2). Bacteria data from water quality samples are also multiplied by their respective flow values and are superimposed on the graph, which is demonstrated by the

Figure B 1. Example FDC for the Medina River Below Medina Diversion Lake at assessment unit 1903_03.

blue circles. This shows the prevalence and magnitude of bacteria values in each flow category.

Additional analysis of bacteria data can be conducted using a regression analysis. For this strategy, RStudio was used to perform a linear regression resulting in a "line of best fit" for the monitored samples, referred to as the "existing load" and is indicated by the dashed line in the LDC graph. Where the dashed line is below the solid black line, bacteria loading is likely in compliance with the water quality criterion. When the dashed line is above the solid black line, monitoring data indicates that the bacteria loading is exceeding the water quality standards. This helps visualize which flow categories require the greatest reduction in bacteria loads.

In addition to the regression analysis, a geometric mean of the discrete data point loads within each flow category was calculated, indicated by the squares in the LDC graph. This helps quantify the total bacteria load for each flow category and aids in establishing a numeric target of reductions needed to achieve water quality standards.



Figure B 1. LDC for Medina River Below Medina Diversion Lake at AU 1903_03.

Appendix B References

TCEQ (Texas Commission on Environmental Quality). 2022. 2022 Texas Integrated Report of Surface Water Quality for the Clean Water Act Sections 305(b) and 303(d). Austin, TX: Texas Commission on Environmental Quality. https://www.tceq.texas.gov/waterquality/assessment/22twqi/22txir

Appendix C: Potential Loads and Load Reduction Calculations

The Spatially Explicit Load Enrichment Calculation Tool (SELECT) was developed by Teague et al. (2009) in the Biological and Agricultural Engineering Department at Texas A&M University. SELECT is used to characterize and estimate potential bacteria loads based on unique sources across the watershed so that critical source areas of pollution can be prioritized. This model is also used to analyze changes in potential bacteria loading for various best management practices.

The SELECT method relies on Geographic Information Systems (GIS) software to divide the larger watershed into smaller subwatersheds and estimate total potential bacteria loading for each individual subwatershed based primarily on both land use and land cover classifications and known point sources. Depending on the source, the loading estimates are further refined by considering literature estimates and relying on stakeholder feedback.

Estimates for potential loads are based on the best available data (e.g., local, state, and federal databases, scientific research) and local stakeholder input (e.g., local livestock stocking practices, wildlife densities). Potential loading rates assume a worst-case scenario and are primarily used to calculate where management measures should be implemented first to maximize effectiveness in potential load reductions.

The watershed was divided into 11 hydrologically similar subwatersheds using 12-digit Hydrologic Unit Codes (HUC) watershed boundaries from the National Hydrography Dataset (NHD) from United States Geological Survey (USGS) (USGS, 2023). For required land cover/land use classification information, the 2021 National Land Cover Database (NLCD) for the contiguous United States was obtained (USGS, 2022). As previously stated, the watershed is undergoing a significant amount of development, therefore all land use and land cover for potential load calculations had areas where subdivisions are proposed and/or completed removed from total land use and land cover area.

Livestock

Calculating potential bacteria loads from livestock requires an estimate of total animal population for each subwatershed. USDA Farm Service Agency provides recommended livestock stocking rates by county based on livestock census data (C. Koenig, personal communication, March 15, 2024). Additionally, USDA provides a Census of Agriculture that provides county-wide population estimates (USDA NASS, 2022). These two sources helped provide stakeholders with estimates of livestock population as a basis to present to stakeholders in the watersheds. Stakeholder feedback on these initial population

estimates was that the population based on stocking rates was too low and the population based on the NASS census was too high, however, all other livestock estimates with the NASS census were accurate. To remedy this, the two cattle population estimates were averaged together for each subwatershed. Actual animal numbers fluctuate annually based on local conditions; however, these approaches provide a baseline to estimate potential loadings. Given that animal numbers fluctuate annually and actual stocking rates are difficult to determine, reliance on local stakeholders was critical to properly estimating cattle populations.

Cattle

Cattle are the dominant livestock species in the watersheds and were assessed separately from other livestock. As stated previously, cattle estimates using Farm Service Agency stocking rates were compared to NASS population estimates for watershed counties (Table C 1). The estimates produced by these two methods differed by 6,193 animal units, with a cattle population estimate of 13,028 using the NASS method, and 6,835 using the FSA stocking rate. Stakeholders felt that both methods were inaccurate, and a more appropriate estimate lay somewhere in between the two extremes. Therefore, the calculated cattle population within the watershed is 9,505, an average of the two methods within GIS analysis.

Table C 1. 0.5. Department of Agriculture-recommended cattle stocking rates for Medina County.									
	Pasture/ Hay	Grassland	Rangeland	Deciduous-Mixed Forest					
Cattle Stocking Rates									

15

25.50

Table C 1. U.S. Department of Agriculture-recommended cattle stocking rates for Medina County

6

Using the cattle population estimates generated, potential *E. coli* loading across the watersheds and for individual subbasins was estimated using land use and land cover within GIS. The annual load from cattle was calculated (Formula C-1). The estimated potential annual loading across all subbasins due to cattle is 1.87 x 10¹⁶ cfu *E. coli*/year.

Formula C-1:

(ac/AnU)

$$PALcattle = AnU * FCcattle * Conversion * \frac{365 \ days}{1 \ year}$$

Where:

 $PAL_{cattle} = Potential annual E. coli loading attributed to cattle$

AnU = Animal units of cattle (~1,000 lbs of cattle)

 FC_{cattle} = Fecal coliform loading rate of cattle; 8.55×10⁹ cfu fecal coliform/AnU/day (Wagner and Moench 2009)

Conversion = Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009)

28

Other Livestock

To estimate stocking for goats, sheep, and horses, the numbers reported by NASS were scaled down to the combined watershed area in appropriate landcovers using GIS. Potential *E. coli* loading for individual subbasins were calculated using these estimates. The annual load from other livestock was calculated (Formula C-2).

Formula C-2:

 $PALOL = [(AnU * FCgoat) + (AnU * FChorse) + (AnU * FCsheep)] * Conversion * \frac{365 \text{ days}}{1 \text{ year}}$

Where:

 $\begin{aligned} PAL_{OL} &= \text{Potential annual E. coli loading attributed to other livestock} \\ AnU &= \text{Animal units (~1,000 lbs of live animal weight)} \\ FC_{goat} &= \text{Fecal coliform loading rate of cattle; } 4.32 \times 10^9 \text{ cfu fecal coliform/AnU/day (Wagner and Moench 2009)} \\ FC_{berse} &= \text{Fecal coliform loading rate of cattle; } 3.64 \times 10^8 \text{ cfu fecal coliform/AnU/day (Wagner and Moench 2009)} \\ FC_{sheep} &= \text{Fecal coliform loading rate of cattle; } 5.8 \times 10^{10} \text{ cfu fecal coliform/AnU/day (Wagner and Moench 2009)} \\ FC_{sheep} &= \text{Fecal coliform loading rate of cattle; } 5.8 \times 10^{10} \text{ cfu fecal coliform/AnU/day (Wagner and Moench 2009)} \\ Conversion &= \text{Estimated fecal coliform to E. coli conversion rate; } 126/200 = 0.63 (Wagner and Moench 2009) \end{aligned}$

Bacteria Load Reductions from Livestock Management

To estimate expected *E. coli* reductions, stakeholder recommended efficacy value of 75% was used. The potential load reduction achieved by implementing conservation practices depends on the specific BMPs implemented by each individual landowner, the number of animals in each operation, existing practices, and existing land condition. With an estimate of 24 annual conservation plans over the course of 10 years totaling 240 conservation plans (Formula C-3). Using above-described inputs, estimated annual *E. coli* reductions from livestock management total 1.43x10¹⁵ cfu, or approximately 2.72% of annual bacteria loading from livestock in the watershed.

Formula C-3:

$$LR = Nplans * FCanimal * Conversion * \frac{365 \, days}{1 \, year} * BMP Efficacy$$

Where:

LR = Potential annual load reduction of E. coli through management efforts Nplans = Number of WQMPs and CPs, 240 are proposed by this plan AnU/Plan = Animal Units of cattle, sheep/lambs, goats, and horses per management plan $FC_{animal} = Fecal coliform loading rate in cfu fecal coliform/AnU/day (Wagner and Moench 2009);$ $Cattle = 8.55 \times 10^{9},$ $Sheep/Lambs = 2.90 \times 10^{11},$ $Goats = 2.54 \times 10^{10},$ $Horse = 1.21 \times 10^{9}$ Conversion = Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009) Efficacy = Median BMP efficacy value; 0.75

Feral Hogs

Feral hog populations were estimated using a population density of 32 ac per hog of suitable habitat (Wagner and Moench 2009). Suitable habitat includes mixed-deciduous forest, evergreen forest, rangeland, grassland, cultivated crops, and wetland land use and land cover. GIS analysis was used to estimate watershed-wide and subbasins feral hog populations. Based on this analysis, an estimated 6,001 feral hogs exist within the watershed. Like other population estimates, these numbers provide general estimates that change based on conditions within the watershed. Furthermore, feral hogs roam across large areas that might be larger than individual subbasins; however, these estimates provide guidance on where to focus control efforts based on suitable habitats. Using the feral hog population estimates, the potential *E. coli* loading across the watersheds and for individual subbasins was estimated. The annual load from feral hogs was calculated (Formula C-4). The estimated potential annual loading across all subbasins due to feral hogs is 2.09 x 10¹⁴ cfu *E. coli*/year.

Formula C-4:

$$PAL_{fh} = N_{fh} * AnUC * FC_{fh} * Conversion * \frac{365 \ days}{1 \ year}$$

Where:

PALfh = Potential annual E. coli loading attributed to feral hogs
Nfh = Number of feral hogs
AnUC = Animal unit conversion; 0.125 AnU/feral hog (Wagner and Moench 2009)
FCfh = Fecal coliform loading rate of feral hogs; 1.21×109 cfu fecal coliform/AnU/day (Wagner and Moench 2009)
Conversion = Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009)

Bacteria Load Reductions from Feral Hog Management

Loading reductions for feral hogs assume that existing feral hog populations can be reduced and maintained by a certain amount on an annual basis. Therefore, the total potential load reduction is calculated from the population reduction in feral hogs achieved in the watersheds (Formula C-5). The established goal is to reduce and maintain the overall population by 8%, which translates to approximately 50 feral hogs per year. The estimated annual potential loading reduction from feral hog management totals 1.74x10¹³ cfu or approximately 8.33% of annual bacteria loading from feral hogs in the watershed.

Formula C-5:

 $LRfh = Nfh * FCfh * Conversion * \frac{365 \ days}{1 \ year}$

Where:

 LR_{h} = Potential annual E. coli load reduction attributed to feral hog removal N_{h} = Number of feral hogs removed FC_{h} = Fecal coliform loading rate of feral hogs; 1.21×10⁹ cfu fecal coliform/AnU/day (Wagner and Moench 2009)

Conversion = Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009)

Deer

White-tailed deer populations were estimated using a calculated population density obtained from averaged the last 5 years of densities per deer management unit (DMU) from Texas Parks and Wildlife Deer Management Unit Survey (TPWD staff, personal communication, January 29, 2024) Table C 2). It's important to note that this document only pertained to white-tailed deer. Suitable habitat includes mixed-deciduous forest, evergreen forest, rangeland, grassland, cultivated crops, and wetland land use and land cover. Portions of four DMUs are located within the watershed, however, no deer density was recorded for Urban San Antonio DMU. While there is likely some number of deer living within this DMU, without a density no reasonable estimate can be made. GIS analysis was used to estimate watershed-wide deer populations using land use and land cover per each DMU per each subwatershed.

08 West	Deer/1000 acres	08 East	Deer/1000 acres	07 North	Deer/1000 acres	Urban San Antonio	Deer/1000 acres
2021	34.14	2022	34.7	2021	168.11	NA	NA
2019	40.27	2020	24.3	2019	174.97	NA	NA
2017	37.06	2018	15.58	2017	125.18	NA	NA
2016	22.03	2016	19.6	2016	155.11	NA	NA
2015	19.04	2015	33.98	2015	159.79	NA	NA
Average	30.508	Average	25.632	Average	156.632	NA	NA

Table C.2	Deer densities ner	1000 acres based	on the TPWD	Deer Management	Linit Survey
	Deel densities per			Deel Management	Onit Survey.

Based on this analysis, an estimated 17,280 deer exist within the watershed. Like other population estimates, these numbers provide general estimates that change based on conditions within the watershed. Using the deer population estimates, the potential *E. coli* loading across the watersheds and for individual subbasins was estimated. The annual load from deer was calculated (Formula C-6). The estimated potential annual loading across all subbasins due to deer is 6.68 x 10¹⁵ cfu *E. coli*/year.

Formula C-6:

$$PAL_{deer} = N_{deer} * AnUC * FC_{deer} * Conversion * \frac{365 \text{ days}}{1 \text{ year}}$$

Where:

$$\begin{split} PAL_{deer} &= \text{Potential annual E. coli loading attributed to deer} \\ N_{deer} &= \text{Number of deer} \\ AnUC &= \text{Animal unit conversion; 0.112 AnU/deer (Wagner and Moench 2009)} \\ FC_{deer} &= \text{Fecal coliform loading rate of deer; 1.50 \times 10^{10} cfu fecal coliform/AnU/day (Wagner and Moench 2009)} \\ Conversion &= \text{Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009)} \end{split}$$

Bacteria Load Reductions from Deer Management

No management measures were identified for reducing bacteria loads from white-tailed deer, therefore no load reductions are calculated.

Domestic Pets

Dog population estimates were generated using a total percentage of households owning dogs (44.6%) multiplied by the average number of dogs per pet-owning household applied to 2020 U.S. Census block household data for the watershed (AVMA 2022). Within the watershed, there are an estimated 50,384 dogs. Based on stakeholder input, it was assumed that no significant number of dog owners in the watershed pick up dog waste. Using the resulting dog population estimate, the annual load due to dogs was

estimated (Formula C-7). The estimated potential annual loading attributed to dogs is 5.79×10^{16} cfu *E. coli*/year in the watershed.

Formula C-7:

$$PAL_d = N_d * FC_d * Conversion * 365 \frac{days}{year}$$

Where:

 PAL_d = Potential annual E. coli loading attributed to dogs N_d = Number of dogs that owners do not pick up after FC_d = Fecal coliform loading rate of dogs; 5.00×10⁹ cfu fecal coliform/dog/day (EPA 2001) *Conversion* = Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009)

Bacteria Load Reductions from Dog Management

The watershed contains approximately 50,384 dogs. To reduce bacteria loading for domestic pets, management efforts focus on increasing the number of dog owners who pick up dog waste. Load reduction calculations included goals of increasing the overall number of households managing waste by 15%, and that these households clean up dog waste at least 25% of the time (Formula C-8). The annual estimated potential load reduction attributable to dog waste management is 2.17x10¹⁵ cfu.

Formula C-8:

$$LRd = Mgmt \ Goal \ 1 * Mgmt \ Goal \ 2 * FC_d * Conversion * \ 365 \frac{days}{year}$$

Where:

 LR_d = Potential annual E. coli loading attributed to proper dog waster diposal Management Goal 1 = Number of additional households managing waste; goal is 15% Management Goal 2 = How often owners pick up dog waste; goal is 25% FC_d = Fecal coliform loading rate of dogs; 5.00×10⁹ cfu fecal coliform/dog/day (EPA 2001) Conversion = Estimated fecal coliform to E. coli conversion rate; 126/200 = 0.63 (Wagner and Moench 2009)

OSSFs

Potential *E. coli* loading for individual subbasins was estimated using the watershed OSSF estimates and distribution. Potential bacteria loadings from OSSFs were calculated for each county within each subwatershed by multiplying the OSSF count by the failure rate, the default wastewater per person, average person per household (Borel et al. 2015), *E. coli* conversion rate (Wagner & Moench, 2009), the fecal coliform production rate for OSSFs (USEPA 2001), a constant for unit conversions, then dividing by 100.

Estimated failure rates for aerobic and conventional systems in Medina county were provided by county officials. Failure rates for Atascosa, Bandera, and Bexar counties were derived from (Reed-Stowe & Yanke 2001). Atascosa and Bandera counties are located in Region II, with an average failure rate of 12% across all system types. Bexar county failure rates were estimated to be an average of Regions II and III rates of 12% and 3%, respectively, across all system types. Methods to estimate OSSF locations and numbers are described in Chapter 4 of this WPP. The annual load from OSSFs was calculated (Formula C-9). The estimated potential annual loading across all subbasins due to OSSFs is 2.36×10^{16} cfu *E. coli*/year in the watershed.

Formula C-9:

$$PAL_{ossf} = N_{ossf} * N_{hh} * Production * Failure Rate * FC_s * Conversion * 365 \frac{days}{vear}$$

Where:

 PAL_{ussf} = Potential annual E. coli loading attributed to OSSFs N_{ussf} = Number of OSSFs N_{bb} = Average number of people/household per subwatershed, using the 2020 US Census Production = Assumed sewage discharge rate; 70 gallons/person/day (Borel et al. 2015) Failure Rate = Different for each county, see Table C 3. FC_s = Fecal coliform concentration in sewage; 1.0×106 cfu/100 mL (EPA 2001) Conversion = Conversion rate from fecal coliform to E. coli; 126/200 = 0.63 (Wagner and Moench 2009) and mL to gallon (3785.4 mL/gallon)

Table C 3. Estimated failure rates of OSSFs in the watershed.

County	Aerobic Systems	Conventional Systems
Medina	65%	10%
Bexar	7.5%	7.5%
Atascosa	12%	12%
Bandera	12%	12%

Bacteria Load Reductions from OSSF Management

Load reductions for OSSFs are calculated based on the number of failing OSSFs that are repaired or replaced (Formula C-10).

Formula C-10:

$$LRossf = N_{ossf} * N_{hh} * Production * FC_s * Conversion * 365 \frac{aays}{year}$$

Where:

$$\begin{split} LR_{OSSF} = & \text{Potential annual E. coli loading attributed to OSSFs} \\ N_{assf} = & \text{Number of OSSFs} \\ N_{bb} = & \text{Average number of people per household according to 2020 US Census; 2.8} \\ Production = & \text{Assumed sewage discharge rate; 70 gallons/person/day (Borel et al. 2015)} \\ FC_i = & \text{Fecal coliform concentration in sewage; } 1.0 \times 10^7 \text{ cfu/100 mL (EPA 2001)} \\ Conversion = & \text{Conversion rate from fecal coliform to E. coli; } 126/200 = 0.63 (Wagner and Moench 2009) and mL to gallon (3785.4 mL/gallon) \end{split}$$

For this WPP, the goal is to address 60 failing OSSSFs annually (20 aerobic and 10 conventional in Medina County, 20 conventional in Bandera County and 10 conventional systems in Atascosa and Bandera counties). This results in a potential annual reduction of 1.04x10¹⁵ cfu. This translates to a reduction of approximately 4.4% of bacteria loading from OSSFs annually.

WWTFs

Potential loadings from WWTFs were calculated for all permitted dischargers with a bacteria monitoring requirement. Except for the Medio Creek Water Recycling Center, potential loads were calculated as the sum of the maximum permitted discharges of all WWTFs multiplied by the maximum permitted *E. coli* concentration. For the Medio Creek Water Recycling Center, the reported discharge was used (Formula C- 11).

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Formula C-10:

PAL_{wwtf} = Discharge * Concentration_{max} * Conversion * \frac{365 \ days}{year}
Where:

PAL_{wwf} = Potential \ annual \ E. \ coli \ loading \ due \ to \ WWTF \ discharges
Discharge = Maximum \ permitted \ daily \ discharge
Concentration_{max} = Maximum \ average \ permitted \ concentration \ of \ E. \ coli \ in \ wastewater \ discharge \ (126 \ cfu/100 \ mL)
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Conversion = Unit conversion (3785.4 mL/gallon)

The estimated potential annual loading across all subbasins due to WWTF discharges are 1.88×10^{13} cfu *E. coli*/year to the watershed. This is a very small portion of the combined bacteria loading of all potential sources.

Bacteria Load Reductions from WWTF Management

No management measures selected for WWTF management and therefore no bacteria load reductions were calculated. Stakeholders chose to focus on more effective management measures.

Appendix C References

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