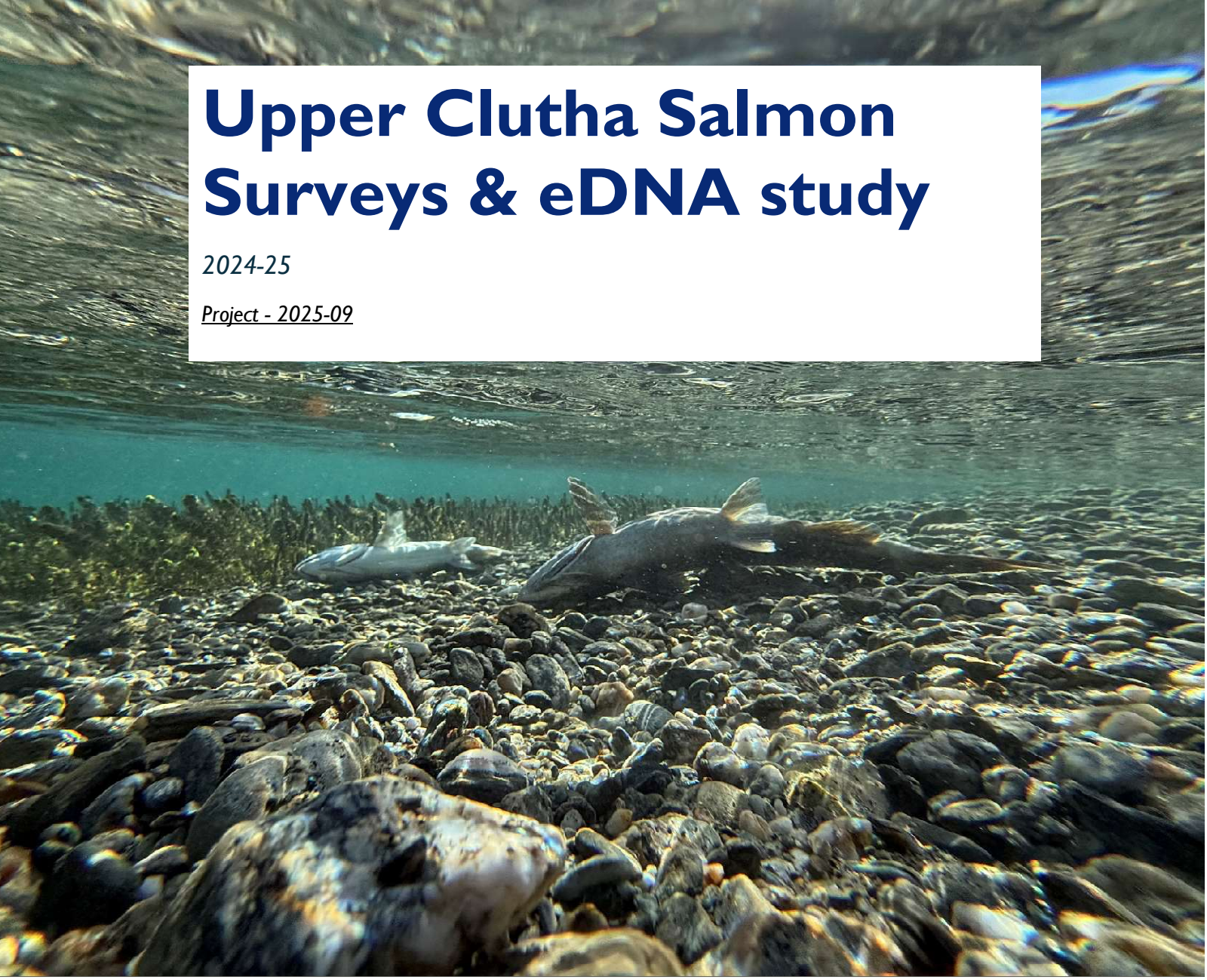

Upper Clutha Salmon Surveys & eDNA study

2024-25

Project - 2025-09

JULY 2025

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1. Executive Summary

*The Hunter River catchment has historically supported strong salmonid fisheries, including land-locked Chinook salmon (*Oncorhynchus tshawytscha*), which remain important for recreational angling. In 2025, the Mata-Au Trust commissioned a study to investigate the primary objective of determining whether and where Chinook salmon are currently spawning in the catchment. The study combined foot-based surveys with environmental DNA (eDNA) analysis at seven sites, during two periods, late May and mid-June. No live or dead salmon were observed—likely due to post-spawning mortality, scavenging by predators such as longfin eels, and the small size of land-locked salmon. However, eDNA results confirmed the presence of salmon at six sites in May, with detections dropping sharply by June, indicating peak spawning occurred in mid to late May.*

Wind Pudding Creek #2 and Green Gully Creek recorded the highest eDNA sequence counts and were the only sites with positive detections in both sampling rounds, suggesting they are key spawning locations. In contrast, the Hunter River mainstem tested positive only in May, likely reflecting salmon passing through rather than active spawning. These findings confirm that land-locked Chinook salmon continue to spawn in the Hunter River catchment and highlight the value of eDNA as a sensitive and non-invasive tool for detecting elusive or low-density populations.

Photo 1. eDNA manifold deployed in Paddock Flat Creek, Hunter River.

2. Introduction

The Hunter River, a major tributary of Lake Hāwea within the Upper Clutha River catchment, holds historical significance for its abundant salmonid populations. It has long supported strong runs of both brown trout (*Salmo trutta*) and rainbow trout (*Oncorhynchus mykiss*), It was once recognised as one of the principal historical spawning grounds for sea-run Chinook salmon (*Oncorhynchus tshawytscha*) in the Upper Clutha system—prior to the construction of the Roxburgh Dam in 1953 (Jellyman, 1989).

Today, land-locked populations of Chinook salmon persist in Lakes Wakatipu, Wānaka, Dunstan, and Hāwea, where they play an important role in the region's sport fishery. Although these fish are smaller than their sea-run counterparts, they are highly prized by anglers for their accessibility, catchability, and eating quality (Court, 2023).

Despite the loss of direct access to the sea following dam construction, otolith microchemistry studies have shown that over 60% of sea-run Chinook salmon captured in the lower Clutha River originated from land-locked populations located upstream of both the Roxburgh and Clyde Dams (Gabrielsson, 2019).

Recent observations have recorded limited spawning activity by land-locked salmon in Hunter River tributaries (Court 2024, van Klink, 2021); however, these populations remain poorly understood. In response, the Mata-Au Trust commissioned this study to identify current spawning locations and assess whether salmon spawning runs are still occurring in these waterways.

The study combined traditional foot-based spawning surveys with environmental DNA (eDNA) analysis—a sensitive, non-invasive method that detects species by isolating genetic material from water samples. This report presents findings from eDNA sampling and spawning surveys carried out in late May and mid-June 2025.

The primary objective was to determine the presence or absence of Chinook salmon at seven key sites through the Hunter River catchment. Secondary aims included identifying the peak timing of the salmon run. Although not a core focus, the eDNA analysis also allowed for broader biological community profiling and baseline water quality assessment via the Taxon Independent Community Index (TICI), produced as part of the analysis.

3. Methodology

Environmental DNA (eDNA) samples and spawning surveys were conducted on seven sites across the Hunter River catchment on two separate occasions between May and June 2025. Six of the sampling sites were located in small tributaries of the main river, while one site was situated on the main stem of the Hunter River. Sites were selected based on a combination of historical spawning records, anecdotal evidence, and communications from anglers and commercial operators familiar with the Hunter River. Habitat suitability, including the presence of clean gravels, appropriate flow conditions, and known accessibility

to migratory fish, also guided the selection of survey locations. The specific locations of all sampling sites are shown in Figure 1.

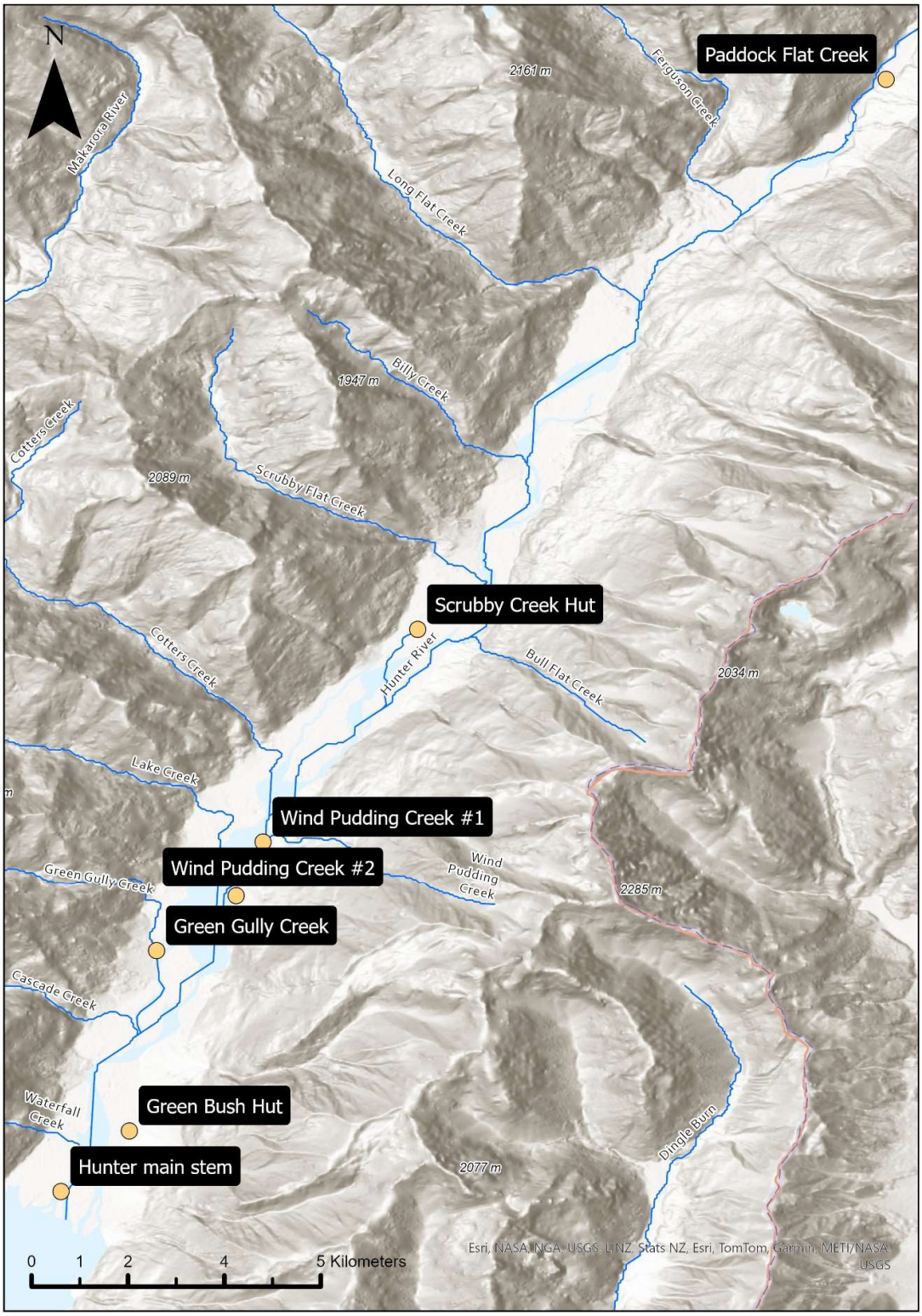

Figure 1: Map showing eDNA sample locations.

Sampling was conducted on 22 May and 14 June 2025, dates selected based on previous observations of Chinook salmon (*Oncorhynchus tshawytscha*) spawning activity. These periods were believed to coincide with the peak of the salmon run. On both days, the river system was running clear and low—providing ideal conditions for both eDNA sampling and visual spawning surveys.

All creeks were initially surveyed by helicopter. This allowed observers to identify potential salmon spawning areas and visually search for salmon, both alive and dead. Key reaches with suitable spawning habitat—such as shallow, gravel-bed riffles—were then selected for follow-up foot surveys. Trained staff carefully walked these sections to conduct spawning assessments, searching for live fish, carcasses, and redds. Special care was taken to avoid entering the water or disturbing the water's edge, in order to prevent contaminating downstream eDNA samples. Spawning surveys were not undertaken at the Hunter River main site, due to the large size of the waterway.

At each site, triplicate passive drogue-type eDNA samplers were deployed and left in place for a 24-hour period before collection in an area with moderate flow. All sampling and sample handling were conducted in accordance with Wilderlab's standard protocols.

Following collection, samples were analysed by Wilderlab using their Comprehensive Freshwater panel, which detects a wide range of aquatic taxa, including vertebrates, invertebrates, plants, and microbes. For this report, a species was considered 'present' at a site if its DNA was detected in one or more of the three replicate samples. While the primary aim was to detect Chinook salmon, data for all identified species were recorded.

The panel also generated a Taxon Independent Community Index (TICI) score for each site. TICI is a modern ecological health metric developed in New Zealand for eDNA data (Wilkinson et al, 2024). Unlike traditional indices such as the Macroinvertebrate Community Index (MCI), which rely on selected indicator taxa, TICI incorporates the full DNA signature of the sampled community—including microbes, fungi, and animals—to provide a more comprehensive measure of ecological condition.

All data from this project have been made publicly available on the Wilderlab website.

3.1. Limitations

Due to the clean gravels found throughout the Hunter River catchment and its tributaries, it is often difficult to definitively identify salmon spawning redds based on physical features alone. As a result, a redd was only recorded as belonging to Chinook salmon if spawning salmon were directly observed in the immediate area. In the absence of such observations, and where brown trout (*Salmo trutta*) were present, redds were conservatively attributed to trout.

Foot-based surveys were prioritised over aerial methods for the detection of spawning salmon. This decision was based on the relatively small size of Chinook salmon in the upper lake's catchments, which makes them difficult to reliably observe from the air. Additionally, previous research has shown that aerial surveys alone can miss significant numbers of

spawning fish, particularly in headwater streams and small tributaries where salmon often conceal themselves under banks or in shaded areas (Van Klink, 2020).

4. Results

4.1. Spawning Surveys

No Chinook salmon (*Oncorhynchus tshawytscha*), either alive or dead, were observed during the foot-based or aerial spawning surveys conducted across the Hunter River catchment (Table 1). In contrast, brown trout (Salmo trutta) and their redds were observed at multiple locations during both survey periods. Brown trout and redds were recorded at Paddock Flat Creek in both May and June. Brown trout were also observed at Wind Pudding Creek in June, and at Green Bush Creek and Scrubby Creek in May.

Table 1: Total Chinook salmon, brown trout and redds detected at six sites in the Hunter River catchment, May–June 2025.

Site	Date	Salmon		Brown Trout	
		Live Fish	Redds	Live Fish	Redds
Paddock Flat Creek	May	0	0	9	3
	June	0	0	6	4
Scrubby Creek Hut	May	0	0	2	0
	June	0	0	0	0
Wind Pudding Creek #1	May	0	0	0	0
	June	0	0	0	0
Wind Pudding Creek #2	May	0	0	0	0
	June	0	0	3	0
Green Gully Creek	May	0	0	0	0
	June	0	0	0	0
Green Bush Creek	May	0	0	9	0
	June	0	0	0	0

4.2. Environmental DNA

The eDNA analysis detected the target species, Chinook salmon (*Oncorhynchus tshawytscha*), at six of the seven sites during the May sampling (Table 2). The only site where salmon DNA was not detected in May was Paddock Flat Creek. In contrast, June results showed a marked reduction in detections, with salmon DNA identified at only two sites: Wind Pudding Creek #2 and Green Gully Creek. Notably, Wind Pudding Creek #1, Green Bush Creek, and the Hunter River – Main Stem all returned negative results in June, despite having tested positive for salmon DNA just weeks earlier in May.

Wind Pudding Creek #2 recorded the highest total eDNA sequence counts for Chinook salmon across both sampling events, with 83,131 reads in May and 8,575 reads in June. This was followed by Green Gully Creek, which recorded 21,661 reads in May and a lower 373 reads in June. Scrubby Creek had the lowest total reads with only 285 reads.

Other salmonid species, brown trout (*Salmo trutta*) and rainbow trout (*Oncorhynchus mykiss*) were detected at all seven sites. The native kōaro (*Galaxias brevipinnis*) was also detected at every site, (Table 3). The longfin eel (*Anguilla dieffenbachii*), a species listed as At Risk – Declining, was detected at only two sites: Wind Pudding Creek and Green Bush Creek. Additionally, the common bully (*Gobiomorphus cotidianus*) was found at four sites

The complete species detection results for each site are presented in Table 3.

Table 2: Total Chinook Salmon eDNA sequence counts detected at seven sites in the Hunter River catchment, May–June 2025.

Site	***May***	***June***	***Total***
Paddock Flat Creek	0	0	0
Scrubby Creek Hut	285	0	285
Wind pudding Creek #1	2828	0	2828
Wind pudding Creek #2	83181	8575	91756
Green Gully Creek	21661	373	22034
Green Bush Creek	2556	0	2556
Hunter River -Main Stem	12320	0	12320

Table 3: Presence (✓) of fish species detected via eDNA analysis at seven sites in the Hunter River Catchment, May- June 2025.

Site	**Month**	**Chinook salmon**	**Rainbow trout**	**Brown trout**	**Kōaro**	**Common bully**	**Longfin Eel**
Paddock Flat Creek	May		✓	✓	✓		
	June		✓	✓	✓		
Scrubby Creek Hut	May	✓	✓	✓	✓		
	June		✓	✓	✓		
Wind Pudding Creek #1	May	✓	✓	✓	✓		
	June		✓	✓	✓		
Wind Pudding Creek #2	May	✓	✓	✓	✓		✓
	June	✓	✓	✓	✓	✓	✓
Green Gully Creek	May	✓	✓	✓	✓	✓	
	June	✓	✓	✓	✓	✓	
Green Bush Creek	May	✓	✓	✓	✓	✓	✓
	June		✓	✓	✓	✓	✓
Hunter main stem	May	✓	✓	✓	✓	✓	
	June		✓	✓	✓	✓	

4.3. The Taxon Independent Community Index

The Taxon Independent Community Index (TICI), an indicator of general ecological health, was calculated for each of the seven sites. Mean TICI scores ranged from 112.2 to 119.5, with an overall average of 115 across all samples. There was minimal variation between the two sampling rounds, with the largest difference in means being 1.2—insufficient to alter any water quality ratings.

The average difference between May and June samples was just 0.2. According to standard Wilderlab classifications, all sites were rated as having Excellent water quality (mean TICI scores between 110 and 120). The Hunter River mainstem, sampled in May, recorded the highest average score at 119.5—just below the threshold for 'Pristine condition', which is set at 120.

5. Discussion

5.1. Spawning Surveys

No Chinook salmon (*Oncorhynchus tshawytscha*), either alive or dead, were observed during the foot-based or aerial spawning surveys conducted across the Hunter River catchment. Like most Pacific salmon species, Chinook die shortly after spawning, and their carcasses are often quickly scavenged by aquatic and terrestrial predators—likely contributing to the absence of any visible remains during surveys. The relatively small size of the land-locked Chinook in Lake Hāwea and the Hunter River, averaging around 0.7 kg, also makes them more vulnerable to complete consumption or removal from the spawning site. Notably, longfin eel (*Anguilla dieffenbachii*) DNA was detected at Wind Pudding Creek #2 and green Bush Creek, and this native scavenger would be more than capable of consuming salmon carcasses post-spawning.

Salmon were previously observed spawning in Scrubby Creek and Green Bush Creek in 2021 (van Klink, 2021); however, no fish were detected in these streams during spawning surveys or eDNA sampling in 2023 (Court, 2023). This highlights the variability of Chinook salmon runs in the Hunter catchment. With limited data, it is difficult to determine the exact cause of this variability, though potential factors include flood events, changes in stream morphology or access, and broader environmental conditions that may have prevented successful spawning in a given year. These gaps in annual stream use may reflect natural fluctuations or failed recruitment events.

The timing of the spawning surveys appears to have been appropriate. On the same day as the initial eDNA and spawning surveys (22 May), several post-spawn salmon carcasses were observed by the author in a spring-fed tributary of the Makarora River, a Lake Wānaka inflow that also supports a population of land-locked Chinook.

5.2. Environmental DNA

The primary objective of this investigation was to determine whether—and where—Chinook salmon were actively spawning within the Hunter River catchment. Environmental DNA (eDNA) analysis detected the target species, Chinook salmon (*Oncorhynchus tshawytscha*), at six of the seven sites during the May sampling. The only site where salmon DNA was not detected in May was Paddock Flat Creek, which is located upstream of Scrubby Creek. This aligns with historical observations indicating that salmon have not been recorded above the Scrubby Creek Hut (van Klink, 2021; Court, 2024).

In contrast, the June sampling showed a marked decline in detections, with salmon DNA found at only two sites: Wind Pudding Creek #2 and Green Gully Creek. Notably, Wind Pudding Creek #1, Green Bush Creek, and the Hunter River – Main Stem all tested negative in June, despite testing positive just weeks earlier. These results suggest that the majority of Chinook salmon spawning activity likely occurred before the June sampling round, with peak presence in mid to late May. This timing is further supported by interviews conducted with anglers during a scheduled Designated Waters survey in early May. At that time, no salmon had been seen in the creeks or captured in the river, indicating that the run had not yet reached its peak.

Wind Pudding Creek #2 recorded the highest total eDNA sequence counts for Chinook salmon across both sampling events, with 83,131 reads in May and 8,575 reads in June. Green Gully Creek followed, with 21,661 reads in May and a significantly lower 373 reads in June. Scrubby Creek had the lowest overall count, with just 285 reads detected. These results suggest that Wind Pudding Creek #2 was likely a key spawning site within the catchment, with high levels of salmon DNA during peak spawning in May and residual traces still detectable in June.

While eDNA sequence counts are not a direct measure of fish abundance, high concentrations, particularly when detected consistently, can provide a useful indication of relative presence and spawning intensity. Based on both the high read counts and the persistence of detections into June, it is reasonable to infer that Wind Pudding Creek #2 and Green Gully Creek supported the most active Chinook salmon spawning during the survey period.

In contrast, the detection of salmon DNA at the Hunter River mainstem in May, followed by a negative result in June, suggests this site may have only registered salmon in transit as they moved upstream toward tributary spawning sites. This is consistent with the known limitations of eDNA detection range in flowing water systems, where DNA can degrade or disperse rapidly, often limiting reliable detection (Yang et al. 2021)

Salmon were detected in the Hunter River catchment this year at the expected spawning time. The eDNA was found in different tributaries than in 2024, suggesting year-to-year variation in tributary uses. The peak of spawning activity appears to be in mid-late May, but the timing of all spawning could not be determined.

What does this mean for salmon below the Roxburgh dam?

It shows there is still a population actively spawning in the Hunter River which feeds Lake Hāwea. It is unclear if Lake Hāwea salmon contribute to the Lower Clutha fishery. The fish Gabrielsson (2019) attributed to Upper Clutha Lakes primarily were linked to Wānaka. However, the sensitivity of the technique meant that discriminating between Wānaka and Hāwea populations was difficult.

6. Acknowledgements

We sincerely thank of the team at Wanaka Helicopters for their exceptional skill, local knowledge, and professionalism, which were critical to the safe and successful collection of data in the Hunter Valley.
This work was made possible thanks to the generous support of the Mata Au Trust and Contact Energy.

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