# Application of DNA Stock Identification for Estimating Chinook and Sockeye Salmon Run Size in the Upper Fraser River

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## Abstract

Lheidli T'enneh Band is presently evaluating different methods for enumerating sockeye and chinook salmon in the Upper Fraser River. Run size estimation is required to support regional fisheries management and to permit in-season harvest adjustments. DNA analysis of sockeye and chinook was undertaken in the Lheidli T'enneh Fish Area in 2004 to verify the effectiveness of the approach for stock identification. For sockeye, results suggested a strong positive relationship between DNA stock composition data and the known proportions of sockeye in the Upper Fraser watershed based on escapement data. Results demonstrated the effectiveness of DNA analysis for sockeye stock identification in the Upper Fraser Watershed. Coupled with an accurate enumeration method, DNA analysis can be used to estimate stock-specific abundance and to provide a basis for in-season harvest management.

## Introduction

Accurate salmon stock assessments will be required in the Upper Fraser River by a future Joint Fisheries Committee to be established under the Lheidli T'enneh Treaty. During 2004, three different enumeration methods including hydroacoustics, set-netting and a fish wheel (Levy et al. 2005)[4] were tested in the Lheidli T'enneh Fish Area (Figure 1) As a complement to numerical estimation, stock identification will be required so as to scale abundance estimates and to generate stock-specific run size estimates for management.

There are five sockeye stocks which migrate through the LT Fish Area and over twenty five Chinook stocks. DFO Science Branch has developed DNA identification techniques for Fraser River sockeye and chinook populations (Beacham et al. 1995; 2003A; 2003B). These procedures are routinely applied by the Pacific Salmon Commission for identifying the sockeye stock complex at Mission. In the present study, sockeye and chinook stock composition in the Upper Fraser River was determined by DNA analysis to evaluate the utility of the approach for future in-season applications.

Specific objectives were:

1) collect and analyse 1200 sockeye and chinook samples by DNA analysis,
2) evaluate the utility of DNA stock ID procedures for salmon fisheries management in the Upper Fraser River, and
3) train five Lheidli T'enneh Fisheries Technicians to collect, process and maintain fish samples for DNA stock identification purposes

This report summarizes the results from the program.

[4] copies of this report are available upon request

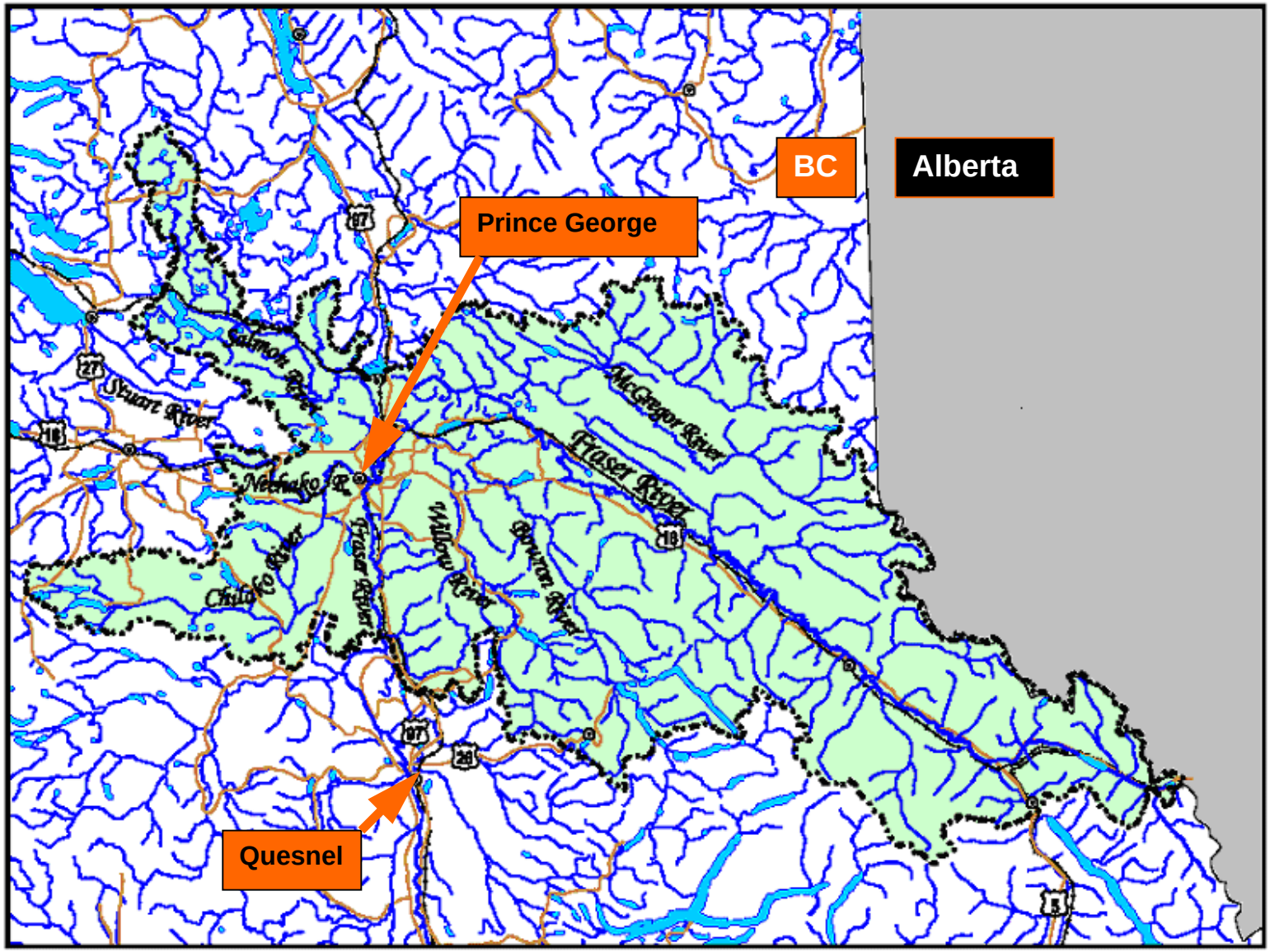



Figure 1. The Lheidli T'enneh Fish Area including the Upper Fraser River and many of its tributaries.

## Methods

Woodpecker (Figure 2) was selected as the fish sampling site. It has an excellent bottom profile for echosounding and there are a number of back eddies for sockeye fishing as well as a site to station a fish wheel. Additionally, the site is road-accessible. All of these factors made Woodpecker the location of choice for sockeye assessment work in 2004.

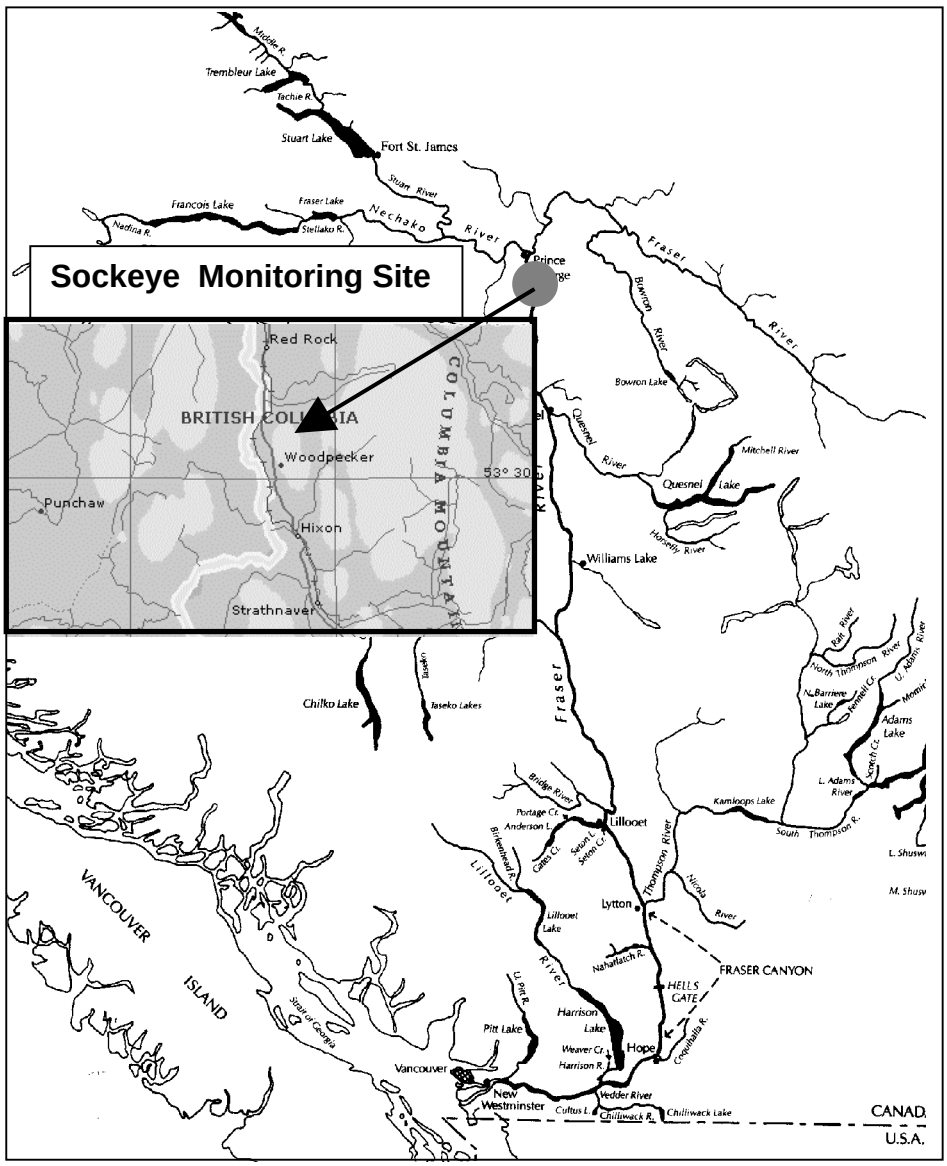



Figure 2. Location of Woodpecker in the Fraser River.

The Woodpecker site is located upstream of the large sockeye runs which return to Quesnel, Chilko and Shuswap Lake tributaries. Sockeye runs which migrate past Woodpecker include the Early Stuart, Late Stuart, Stellako, Nadina and Bowron runs.

The location of Woodpecker relative to Upper Fraser sockeye stocks is shown below.

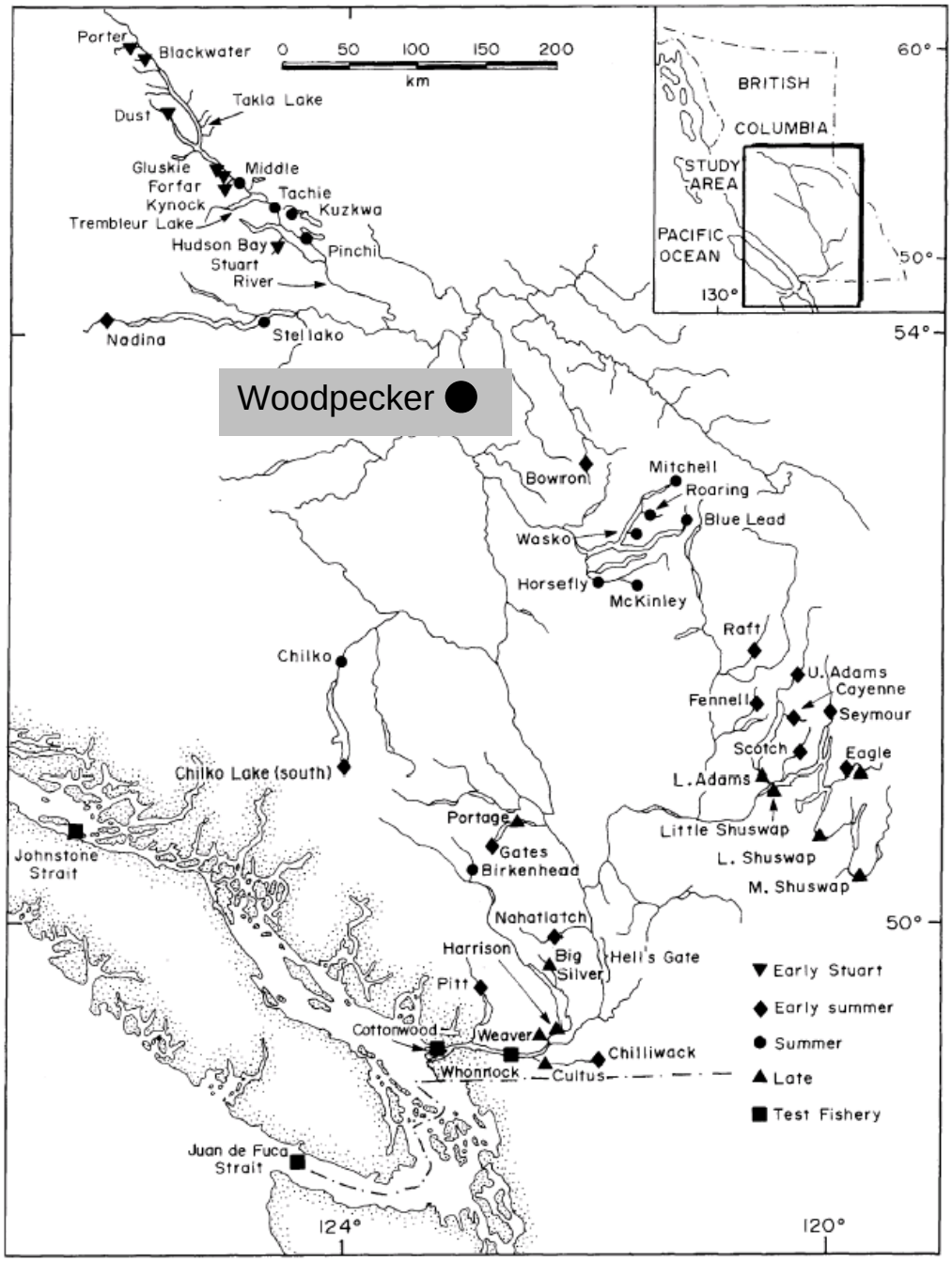



Figure 3. Location of Woodpecker in relation to the Early Stuart (ES), Late Stuart (LS), Stellako (S), Nadina (N) and Bowron (B) spawning grounds. Source: Beacham et al. (2004).

Sockeye and chinook samples for DNA analysis were obtained in set nets using Lheidli T'enneh fishing methods (Levy et al. 2005). Fish sampling was undertaken by four seasonal Lheidli T'enneh fisheries crew members.

DNA samples consisted of a single-hole punch from a sockeye or chinook operculum. The operculum punch was placed in a micro-tube and labeled by date and species. DNA samples were preserved in undiluted anhydrous ethyl alcohol in individual 1.5ml standard conical micro-tubes and stored in polypropylene micro-tube containers (100 micro-tube capacity per container). At the conclusion of the field program, samples were shipped to the Pacific Biological Station for analysis.

Beacham et al. (2004) describe laboratory and analytical procedures for DNA stock identification of Fraser River sockeye. For each sample, polymerase chain reaction products at 14 microsatellite loci were size-fractionated on denaturing polyacrylamide gels and allele sizes determined with an automated DNA sequencer. One of the loci was surveyed by means of denaturing gradient gel electrophoresis, with fluorescent multiplexing. A suite of computer programs were applied to generate statistical parameters. The data were compared statistically to a baseline prepared from 13,000 sockeye from 47 Fraser River spawning populations. Sockeye populations downstream of the Horsefly River were excluded from the baseline since all of the Woodpecker samples were Upper River sockeye. These results provided the basis for stock identification. Raw data for the analysis are shown in Appendix 1.

**Results**

The sockeye stock complex in the Upper Fraser changes during the migration period. Different run timing groups are comprised of the following stocks:

| Run timing group | sockeye stock |
|---|---|
| Early Run | Early Stuart |
| Early Summer Run | Nadina |
| | Bowron |
| Summer Run | Stellako |
| | Late Stuart |

The results of DNA sampling confirmed a progression of the different sockeye runs past Woodpecker (Figure 4).

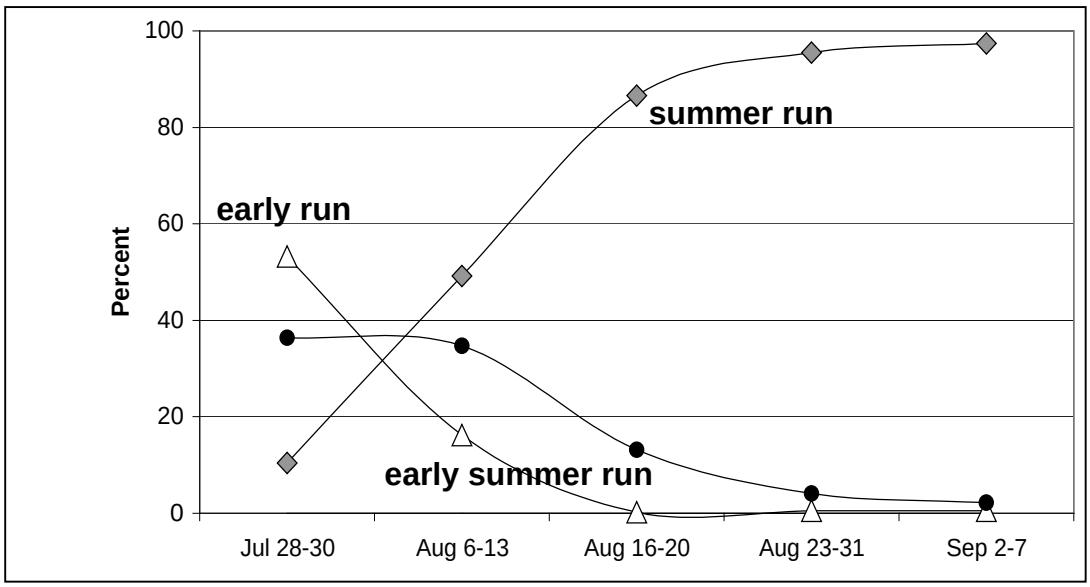



Figure 4. Change in the composition of sockeye run timing groups at Woodpecker during 2004.

Within the Upper Fraser there are five primary sockeye stocks and each can be considered a separate management unit. Figure 5 shows sockeye stock composition at Woodpecker.

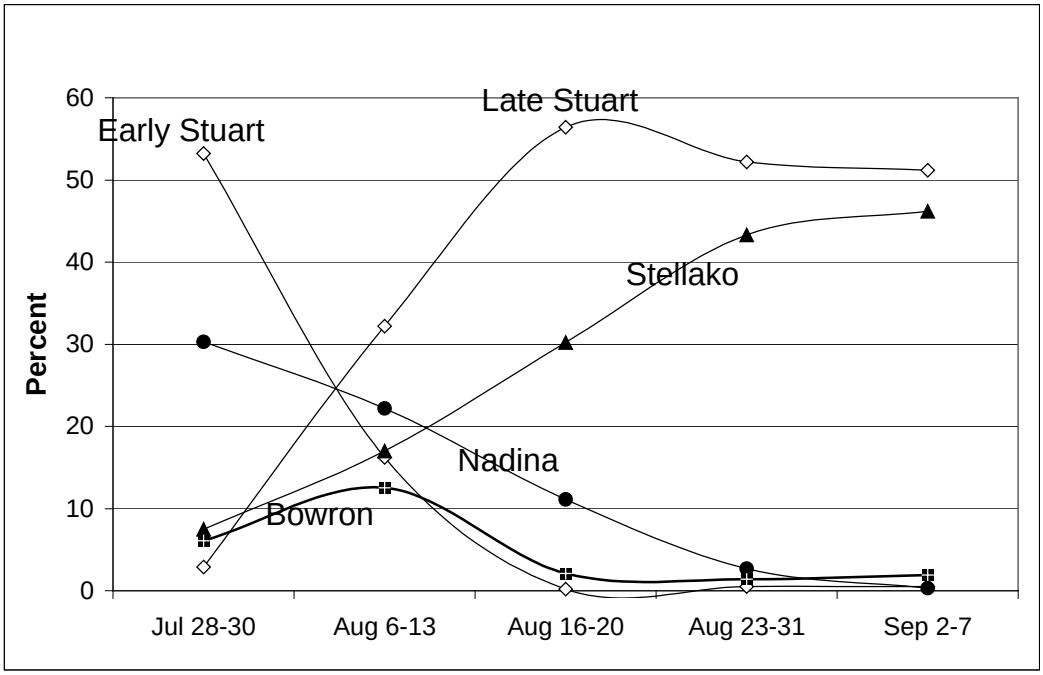
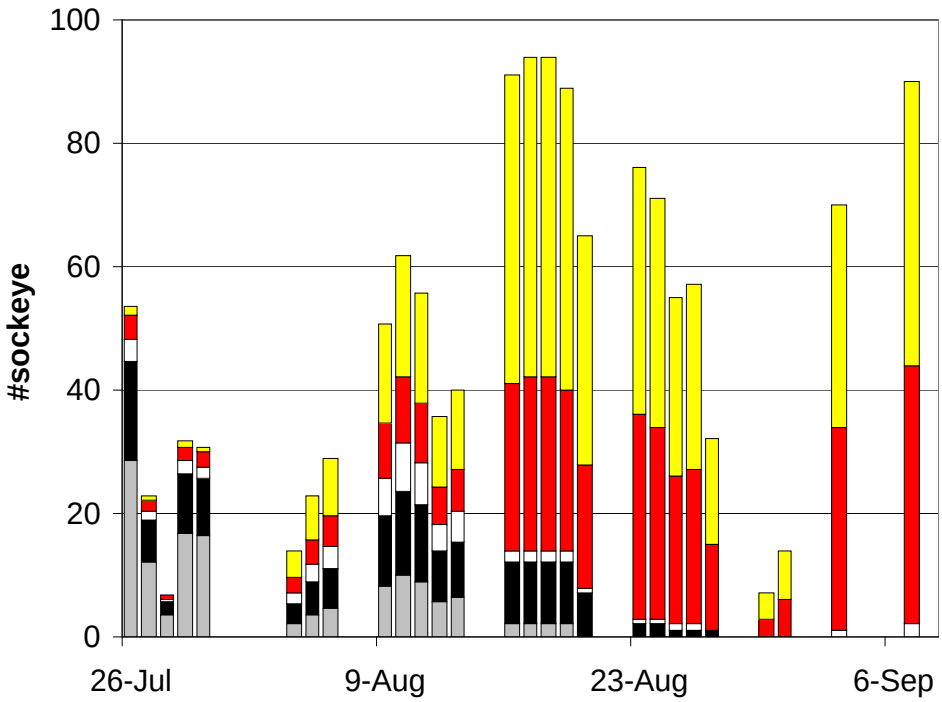



Figure 5. Change in the relative proportion of the five Upper Fraser River sockeye stocks at Woodpecker in 2004.

Figure 6 shows sockeye set-net catches broken down by stock of origin:




Grey = Early Stuart; Black = Nadina; White = Bowron; Red = Stellako; Yellow = Late Stuart

Figure 6. Sockeye stock composition in Woodpecker set-net catches during 2004.

During 27 fishing days at Woodpecker a total of 1361 sockeye were captured. Sockeye escapement in the Upper Fraser Watershed (DFO data) was 205,000 fish in 2004. The following table shows the distribution of stocks at Woodpecker and throughout the watershed.

| | Woodpecker | Upper Fraser Watershed |
|---|---|---|
| Early Stuart | 136 | 9,244 |
| Nadina | 167 | 26,379 |
| Bowron | 64 | 916 |
| Stellako | 404 | 86,688 |
| Late Stuart | 591 | 81,981 |
| **Total** | **1361** | **205,208** |

Because the DNA sampling effort was uniform over the duration of the set-netting period, these data are comparable.

The appears to be a strong relationship between set-net catches and escapement data for the Upper Fraser River (Figure 7).

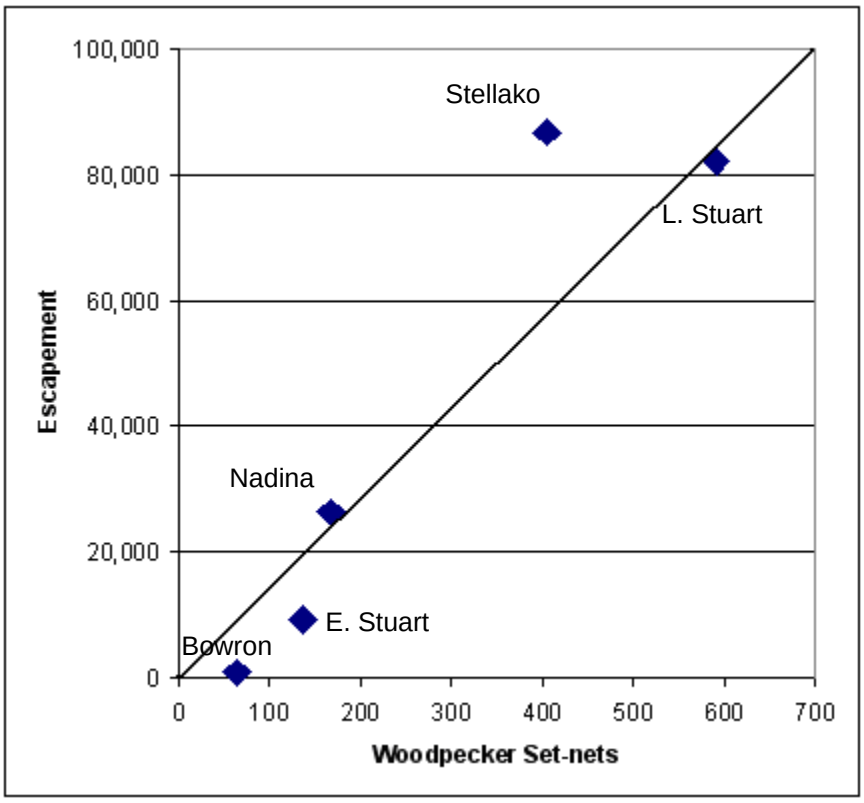



Figure 7. Comparison between Woodpecker set-net catches and sockeye escapement for the 5 Upper Fraser River stocks (diagonal line is 1:1).

These data suggest that Woodpecker set-net catches could be used to predict escapements. The deviations from the diagonal line are due to sampling effects. More data are required to better define the relationship between the two data sets.

These feasibility study results show that DNA analysis, coupled with set net catches, can provide a useful index of salmon abundance. To be useful for in-season management, it will be necessary to develop a set-net catch model that accounts for sockeye migration timing past the monitoring site.

## Discussion

Stock identification is required for fisheries management in the Upper Fraser. The present study demonstrates the utility of DNA stock identification when combined with enumeration programs. Under the Wild Salmon Policy future management will focus on conservation units, which in the case of Fraser River sockeye, equates to a stock-specific management system. This can be accomplished by combining DNA analysis with an accurate numerical estimation method.

Upper Fraser sockeye show cyclic dominance (Figure 8). The observed cyclic patterns are driven by Early and Late Stuart runs, creating large year-to-year variations in sockeye numbers.

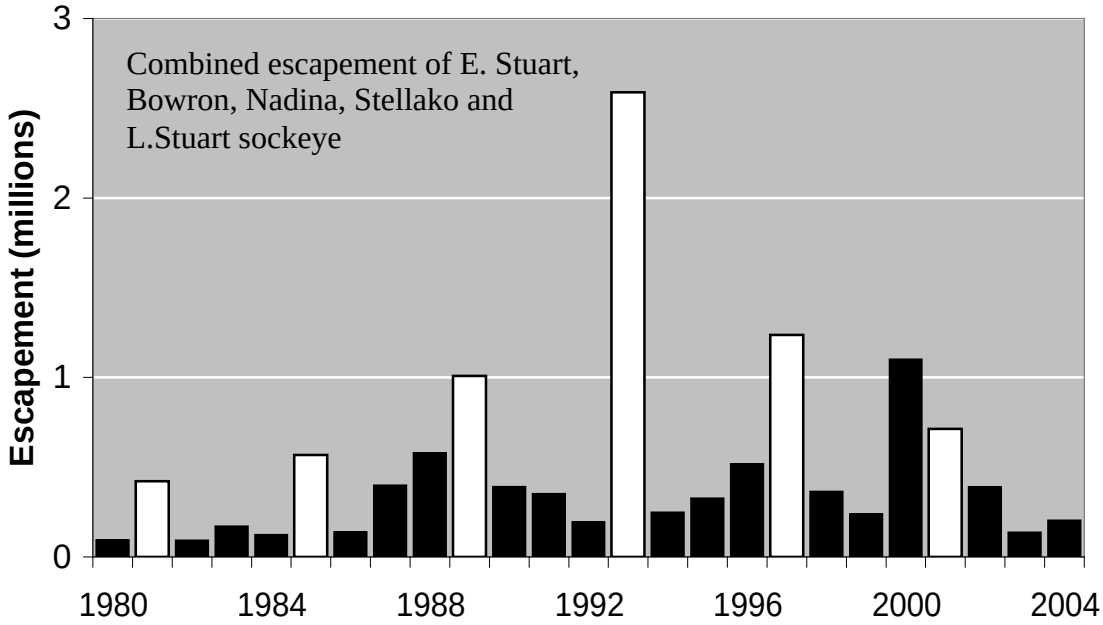



Figure 8. Number of sockeye that spawned in Upper Fraser River tributaries between 1980 – 2004. Dominant return years are shown in white.

In dominant return years, it may be sufficient for a Lheidli T'enneh fish stock identification and enumeration facility to verify the presence/absence of strong dominant runs, thus providing the trigger for additional harvesting. For example, 2005 is a dominant year, and strong returns are anticipated for Late Stuart sockeye. For 2005, there would be minimal in-season management requirements following the detection of Late Stuart sockeye by DNA analysis. LT fisheries could harvest these fish to the highest level specified under a treaty (12,500 fish) with low risk to future run productivity.

During the 3 off-cycle years, higher precision numerical estimates will be required for fisheries management, and accurate stock identification will be critical. The four cycle lines of sockeye in the Upper Fraser are shown as the four colors on Figure 9.

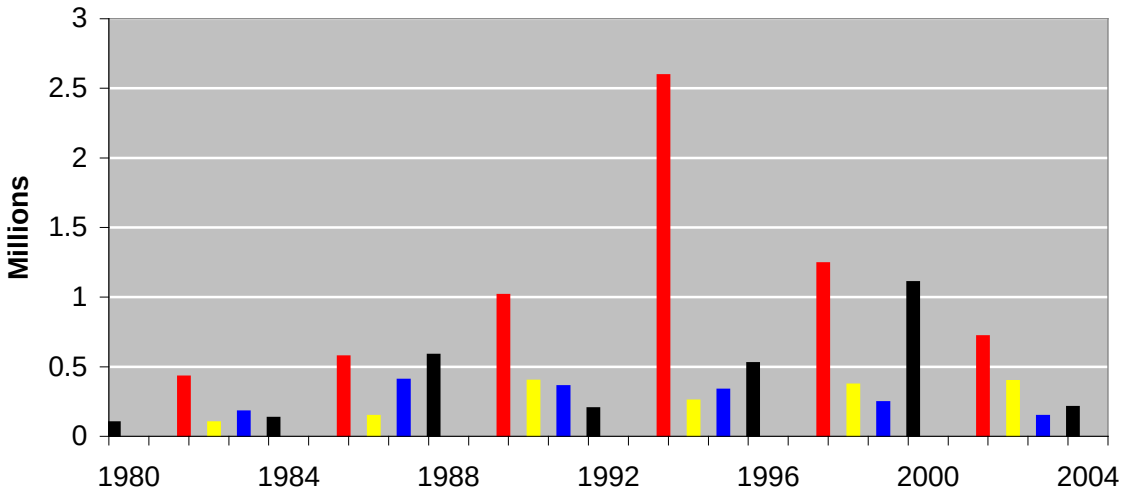



Figure 9. Four cycle lines of Upper Fraser sockeye.

Different management strategies are required on different cycle lines. The mean escapement level for the different cycle lines is shown on Figure 10. Accurate stock identification is especially important on the off cycle years so as to protect weaker stocks e.g. Early Stuart, Bowron.

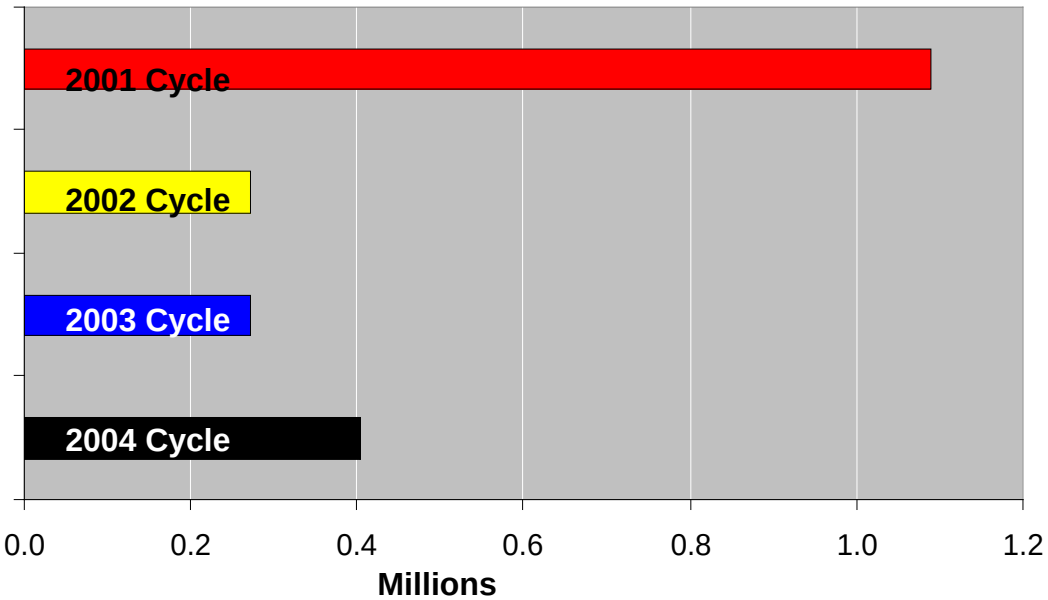



Figure 10. Mean escapements of the four Upper Fraser cycle lines corresponding to the escapements shown in Figure 9.

The Upper Fraser may serve as a useful pilot test for the Wild Salmon Policy. DNA analysis, coupled with quantitative enumeration, provides the necessary data for estimating stock-specific run strength. Compared with lower reaches of the watershed with a greater diversity of sockeye stocks, the Upper Fraser provides a good testing ground for a stock-specific fisheries management system.

## Conclusion

DNA analysis provides an effective means for sockeye and chinook stock identification in the Upper Fraser River. The method can be applied routinely during future in-season stock assessment applications, permitting harvest adjustments based on salmon run strength.

## References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Levy, D.A., P. Nicklin, N. Todd and P. Nealson. 2005. Evaluation of methods for enumerating sockeye salmon in the Upper Fraser River. Prep. for Lheidli T'enneh Band. Prince George, BC.

## Appendix 1: Stock identification data for Upper Fraser salmon (Pacific Biological Station)

### sockeye

**SPAM -minimum number of loci = 8**

| **Baseline** | **Upper Fraser** | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| **Dates** | Jul 28 - 30 | | Aug 6 - 13 | | Aug 16 - 20 | | Aug 23 - 31 | | Sept2-7 | |
| **Fishno** | 2-110 | | 111-219 | | 220-425 | | 426-625 | | 696-867 | |
| **N** | 101(3) | | 109(1) | | 203(3) | | 262(10) | | 166(6) | |
| | | | | | | | | | | |
| **Blackwater** | 0.1 | (0.7) | 0.0 | (0.0) | 0.0 | (0.2) | 0.0 | (0.2) | 0.0 | (0.3) |
| **Dust_____** | 1.9 | (3.2) | 0.0 | (0.2) | 0.0 | (0.1) | 0.0 | (0.3) | 0.0 | (0.3) |
| **Forfar_____** | 17.3 | (7.1) | 0.0 | (2.8) | 0.0 | (0.4) | 0.0 | (0.5) | 0.5 | (0.8) |
| **Gluskie_____** | 29.9 | (7.2) | 16.2 | (4.4) | 0.0 | (0.8) | 0.0 | (0.6) | 0.0 | (0.1) |
| **Hudson_Bay** | 0.0 | (0.3) | 0.0 | (0.1) | 0.0 | (0.0) | 0.0 | (0.1) | 0.0 | (0.1) |
| **Kynock____** | 0.6 | (3.4) | 0.0 | (0.8) | 0.0 | (0.3) | 0.5 | (0.8) | 0.0 | (0.3) |
| **Porter_Creek** | 3.4 | (1.1) | 0.0 | (0.0) | 0.2 | (0.2) | 0.0 | (0.1) | 0.0 | (0.0) |
| **Nadina____** | 30.3 | (4.6) | 22.2 | (4.4) | 11.1 | (2.5) | 2.7 | (1.3) | 0.3 | (1.0) |
| **Bowron_____** | 6.1 | (2.1) | 12.5 | (3.2) | 2.1 | (1.1) | 1.4 | (0.8) | 1.9 | (1.0) |
| **Kuzkwa_Creek** | 0.0 | (1.2) | 2.2 | (3.3) | 12.2 | (3.6) | 7.6 | (3.9) | 3.7 | (3.4) |
| **Middle_River** | 2.9 | (2.9) | 4.0 | (3.5) | 10.6 | (4.1) | 9.9 | (3.8) | 12.5 | (4.3) |
| **Pinchi_Creek** | 0.0 | (1.1) | 0.0 | (1.2) | 0.9 | (2.0) | 1.6 | (1.9) | 3.6 | (2.2) |
| **Stellako__** | 7.5 | (4.4) | 17.0 | (8.0) | 30.2 | (4.6) | 43.3 | (4.7) | 46.2 | (4.9) |
| **Tachie____** | 0.0 | (6.1) | 26.0 | (11.1) | 32.6 | (6.3) | 33.0 | (6.1) | 31.4 | (6.0) |
| | | | | | | | | | | |
| **Early Stuart** | 53.2 | (6.1) | 16.2 | (5.1) | 0.2 | (0.9) | 0.5 | (1.0) | 0.5 | (0.9) |
| **Early Misc.** | 36.4 | (4.9) | 34.7 | (5.0) | 13.2 | (2.9) | 4.0 | (1.4) | 2.2 | (1.5) |
| **Late Stuart** | 2.9 | (5.6) | 32.2 | (10.4) | 56.4 | (4.6) | 52.2 | (4.9) | 51.2 | (5.3) |
| **Stellako** | 7.5 | (4.4) | 17.0 | (8.0) | 30.2 | (4.6) | 43.3 | (4.7) | 46.2 | (4.9) |
| | | | | | | | | | | |
| **Early Stuart** | 53.2 | (6.1) | 16.2 | (5.1) | 0.2 | (0.9) | 0.5 | (1.0) | 0.5 | (0.9) |
| **Early Summer** | 36.4 | (4.9) | 34.7 | (5.0) | 13.2 | (2.9) | 4.0 | (1.4) | 2.2 | (1.5) |
| **Summer** | 10.4 | (5.6) | 49.2 | (6.5) | 86.6 | (2.8) | 95.5 | (1.7) | 97.4 | (1.7) |

# chinook

**SPAM- Baseline Upper Fraser and Mid Fraser above Quesnel. Minimum of 8 loci**

| **Baseline** | **Upper/Middle Fraser** | |
|---|---|---|
| Bowron__ | 0.0 | (1.7) |
| Dome____ | 2.4 | (4.3) |
| Driscoll_Creek | 0.0 | (0.0) |
| Fontoniko | 0.0 | (0.5) |
| Goat____ | 0.0 | (2.0) |
| Holiday_Cr | 0.0 | (0.0) |
| Holmes___ | 1.5 | (5.2) |
| Horsey___ | 0.0 | (0.0) |
| Indianpoint | 0.0 | (1.6) |
| Kenneth_Cr | 0.0 | (1.1) |
| MacGregor | 0.0 | (0.7) |
| Morkill_River | 0.0 | (8.2) |
| Nevin_Creek | 0.0 | (0.2) |
| Ptarmigan | 0.0 | (0.7) |
| Robson_River | 0.0 | (0.0) |
| Salmon@PG | 7.9 | (5.1) |
| Slim_____ | 17.4 | (9.4) |
| Small___ | 0.0 | (0.0) |
| Swift____ | 0.0 | (1.4) |
| Tete_Jaune | 2.0 | (5.4) |
| Torpy_River | 14.5 | (8.3) |
| Walker__ | 0.0 | (0.3) |
| Willow___ | 0.0 | (0.3) |
| Chilako_ | 0.0 | (0.0) |
| Cottonwood | 0.0 | (1.3) |
| Endako__ | 0.0 | (1.1) |
| Nechako_ | 37.7 | (12.0) |
| Stuart__ | 12.8 | (9.3) |
| Westroad | 3.8 | (2.7) |

## Appendix 2: Financial Statement of Expenditures

Provided previously by Vanessa West, Lheidli T’enneh Band