

How Many Tooth Hops Does It Take To Accurately Measure Saw Blade Teeth-Per-Inch In Bone?

Alicia Grosso Ph.D., Anne Begley, and Sharon Toth B.S. Department of Anthropology, University of Pittsburgh

Introduction

In cases of postmortem dismemberment, forensic anthropologists are often called upon to help with identification of not only the decedent, but the tool used in dismemberment. In many cases, postmortem dismemberment is accomplished with a saw blade. Through microscopic saw mark analysis, the forensic anthropologist can help narrow down a broad list of suspect tools, depending on availability of class and individual characteristics imprinted on the bone. Given the shearing nature of a saw cut, individualizing characteristics, those unique to a specific blade, are rare to find. The majority of features the anthropologist can comment on are general or class characteristics, those unique to a group of tools. One such class characteristic of saw blades is the **distance-between-teeth (DBT**), most often presented as **teeth-per-inch (TPI)** of a blade. This character relays information on saw blade tooth size. For example, a saw marketed as 5 TPI has relatively large teeth, whereas a blade marketed as 18 TPI has relatively small teeth.

From bone, tooth size or TPI can be estimated by a feature known as tooth hop. Typically, as a saw blade shears back and forth across bone, the blade leaves horizontal striations. Sometimes, these striations are wavy and predictable, appearing to "hop" across the cut surface. These waves are **tooth hops** (**TH**) and when measured from either peak to peak or valley to valley (see **figure 1**) can be converted to TPI estimates for a suspect blade (Symes *et al.* 2005; Grosso 2020). THs may appear as isolated hops in bone or may be present in a chain, sometimes presenting with three or four THs in a chain. **Figure 2** provides an example cross-section of bone with an isolated tooth hop as well as double and triple TH chains. **But how many THs do you need to confidently estimate TPI of the suspect blade?**

Results

Table 1. Mean TH, standard deviation, sample size, and outlier count for each of the four groups included in this analysis.

Groups Compared	Mean TH	SD	n	NA
Single THs Only	3.66	0.55	197	2
Double THs Only	3.60	0.46	141	9
Triple Plus (3+) Only	3.83	0.53	58	1
Blade (7 TPI)	3.90	0.08	49	1

Table 2. Example DBT (mm) and relativeTPI conversion (from Symes *et al.* 2005).

DBT (mm)	Blade TPI
3.30	7.70
3.60	7.10
3.80	6.67
4.10	6.25

The p-value from the Shapiro-Wilk test for normality was above the 0.05 threshold, thus the data can be assumed to be normally distributed (W = 0.99, p > 0.05). Mean, standard deviations, and sample distributions are outlined in **table 1** with boxplots presented in **figure 3**. Results from the ANOVA indicate that there is significant difference in at least one of the means (F = 4.19, p < 0.05). From the pairwise comparisons, 95% confidence intervals from three comparisons do not cross zero, indicating statistically significant differences in these groups: 1) double vs. blade; 2) single vs. blade; and 3) 3+ vs. double (figure 4). Levene's test of variance comparing standard deviations of *only bone*-

In personal communication (2011) with Steven Symes, Ph.D. D-ABFA discussing a foundational paper, Symes *et al.* 2005, Symes suggested 3 or 3+ tooth hop chains would likely be the most accurate when estimating blade TPI. *It is hypothesized here that more hops in a chain would increase accuracy and precision when estimating blade TPI*; however, the amount of bone will impact the presence of long chains. In my current research (Grosso 2020), examining TH measurements in pig, deer, and human bone, instances of 3 or 3+ TH chains were extremely rare and completely absent in the human sample (280 THs from two femora).

The research for this poster will evaluate a subset of my dissertation data to evaluate if 3+ TH chains are more effective at estimating blade TPI than single THs or double TH chains.







Figure 2. Bone cross-section with examples of isolated and chained THs (Grosso 2020).

measured TH groups indicated no statistical difference amongst these three groups (F = 2.81, p > 0.05).



Figure 3. Boxplots presenting group TH medians with surrounding quartiles and min/max observations once outliers were removed.

Figure 4. Pairwise ANOVA comparing TH means of all four groups (F = 4.19, num. df = 2.00, denom. df = 156.42, p < 0.05*).

Discussion and Conclusions

From the results, the **3+ TH group has a mean reflective of that of the DBT measurements collected directly from the blade, whereas the single and double TH groups were significantly different.** However, there are important pros and cons to consider when choosing to only analyze 3+ TH chains.

Pros and cons of only using 3+ TH chains



Long TH chains are easier for inexperienced observers to identify.

Materials and Methods

This study used a new 7 TPI hand saw to cut seven pig humeri. Individual hops were measured and sorted into groups based on number of hops in their respective chains, **single** (n = 196), **double** (n = 141), or **triple-plus (3+)** (n = 57). Fifty random DBT measurements were also collected directly from the **blade** for comparison to bone measured THs.

The research question was assessed with the basic null hypothesis that there was no difference in means or standard deviations amongst the single, double, or 3+ groups. All statistical analyses were performed using the Statistical Package R, version 3.5.2 (R Core Team 2018) and package RCommander version 2.5-2. The combined data of all TH measurements were first assessed with the Shapiro-Wilk test of normality to evaluate whether the data needed to be examined in parametric or nonparametric statistical tests. Outliers were removed and replaced with NA. The normality assumption was found not to be violated, so parametric tests could be used.

To test whether 3+, double, or single THs performed significantly different in comparison to each other and to blade measurements, a pairwise one-way analysis of variance test was used. This was followed by Levene's test of variance to determine if the precision of any of the bone-measured groups was significantly better or worse at estimating blade TPI. Long chains may increase any analyst's confidence that these are "real THs" (although this can be true of double chains as well).

When only considering 3+ TH chains, the analyst loses most of the total TH sample size.

The amount of bone present (i.e., cortical thickness) dictates the presence of long TH chains, so only regions thick with cortical bone will be able to present long TH chains.

There is one more vital point to consider in this research. As saw blades are measured in TPI, TH measurements in millimeters should be converted to a usable TPI range to be compared to suspect blades. So, while TH means are found to be statistically different (in millimeters), this difference is masked upon conversion to a TPI range, especially since saw blades are not marketed as having "partial" teeth. Table 2 (above) presents a comparisons of DBT (mm) measurements to blade TPI (Symes et al. 2005). From this table, all bone-measured TH groups in this analysis indicate a blade that is 7 ± 1 TPI or 6 - 8 TPI.

Conclusions

3+ TH chains are more accurate (although not more precise) in estimating blade DBT measurements in millimeters; however, conversion to TPI ranges to compare with suspect blades masks such differences. Thus, single and double TH chains should not be discarded from analysis. When analysts are untrained or new to microscopic saw mark analysis, it may be beneficial to look for TH chains for confirmation of TH, but this could be done with double chains to a similar result as the 3+ group.

Works Cited

- 1. Symes SA *et al.* Knife and saw toolmark analysis in bone: a manual designed for the examination of criminal mutilation and dismemberment. Washington, DC: National Institute of Justice; 2005. Report No.: 2005-IJ-CX-K016.
- 2. Grosso AR. 2020 Tissue variability effects on saw mark evidence in bone. [Dissertation]. Pittsburgh, PA: University of Pittsburgh.
- 3. R Development Core Team (2018). R: a language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.R-project.org/.

Acknowledgements

I would like to thank Dr. Steven Symes for his invaluable guidance, advice, and support not only throughout my Master's research experience, but for also fully investing himself into teaching and training the undergraduates. Without this latter experience, I would not be where I am today. The authors would also like to thank the University of Pittsburgh, Department of Anthropology for access to freezer and laboratory space, as well as Dr. Michael Siegel for use and training in the camera lucida microscope. We would also like to thank the team of mypetcarnivore.com for not only providing the pig bones, but for responding to detailed inquiries of diet, sex, age, and geographic origin of this pig sample.