Northwest Marine Technology, Inc.

An Introduction to Sequential Coded Wire Tags

Application Note APC11

Introduction

The sequential coded wire tag (s-cwt) may be used to identify single fish or to allocate recaptured fish to a particular batch. With most numbered tag systems (e.g. VI Alpha) the usual practice is to read the tag number as the tag is applied to the fish, and to record it alongside other data such as length, weight, date and time. Each s-cwt bears a unique set of numbers but it is usually impractical to read and record the tag number as the fish are tagged; therefore, other approaches are necessary and some discipline is required to ensure that recaptures are correctly identified. This note explores this issue in depth. It is assumed that the reader is familiar with the concept of coded wire tags and the way they are cut from a spool and injected, detected, recovered and viewed under a low-power microscope for reading. If not, you should first read our brochure "The coded wire tagging system" on our website (www.nmt.us)

The coding system explained.

With both standard format and sequential format cwt, each and every tag bears a two-digit Agency code (to identify the agency, region or country of origin), a two-digit Data 1 code and a two-digit Data 2 code (to identify the batch of wire from which the tag is cut). Every batch of wire supplied is unique. No two batches will ever duplicate the Agency-Data 1-Data 2 permutation. In this context a "batch" of wire would typically be a spool of 10,000 tags, though several spools bearing the same codes might be supplied to one user for very large groups of fish.

Sequential cwt have in addition one or more incrementing sequential numbers. Every s-cwt tag is unique.

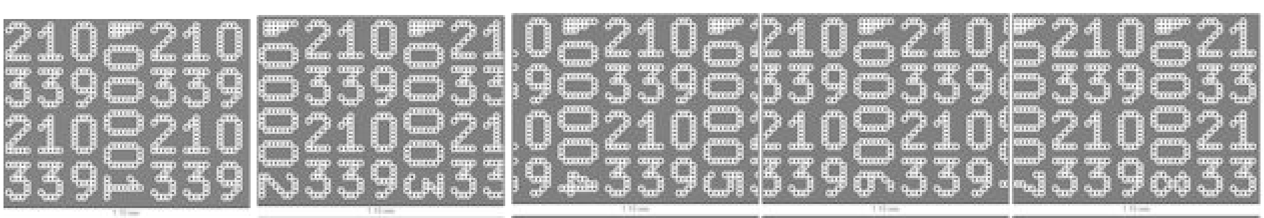

Figure 1. Schematic illustration of the first 5.5 mm of a spool of sequentially coded wire, showing the appearance of the first five tags to be cut. The face of the wire is shown flat - in practice the wire would have to be rotated through 360° to see all this information.

The three two-digit numbers which are repeated twice every 0.65 mm are the Agency code (23), Data 1 (13) and Data 2 (09). The five digit numbers written around the circumference of the wire are the sequential numbers. The triangle at the start of the sequential number indicates where to start reading all numbers.

Where more than one complete sequence number occurs one tag (e.g. the second and third tags in this series) a useful convention is that the lower number is quoted - in this case 00002 for the second tag and 00004 for the third tag .The sequence numbers of these five tags are therefore 00001, 00002, 00004, 00006 and 00008.

The layout of digits on s-cwt wire is shown in Figure 1. This portrays the first few millimetres of a spool, showing how the first five tags to be cut might appear. It is immediately apparent that a complete code sequence occupies less length of wire than is cut to form a single tag. If the code sequences were produced at an interval that corresponded exactly with the tag length, then each tag could, in theory, bear a single sequence number that immediately identified the tag - for example, the 100th tag cut would bear the number 100. However, this is not a practical situation for two reasons:-

- Although the cwt length averages 1.1mm there is some variation between machines and variability between tags cut by one machine. Even the slightest deviation from the standard would quickly lead to a miss-match between the position of the cut and the code sequences.

- Depending upon the age and condition of the cutter in the injector, it can be difficult to decipher digits that are cut or are very close to the ends of the tag.

The codes are therefore printed at 0.65 mm intervals; this guarantees that at least one sequential number will occur in its entirety on each tag, as can be seen from Figure 1. However, this does mean that sequential number "n" does not identify the tag as the nth tag to have been cut. If the injector were cutting tags exactly 1.1mm in length and the first tag showed the sequential number 0001, then the 100th tag cut, for example, would bear the sequence number 00169:-

$$\frac{\textbf{Number of tags x mean length of tags}}{\textbf{Code repeat interval}} = \textbf{sequence number}$$

$$\frac{\mathbf{100 \times 1.1}}{\mathbf{0.65}} = \mathbf{169}$$

Some tags will carry two sequence numbers - for example the second tag cut in Figure 1. A useful convention is to use the lower number, i.e. in this case 00002. Thus the first five tags cut in this example would be identified by the sequence numbers 00001, 00002, 00004, 00006, and 00008. No tags would be identified by the sequence numbers 00003, 00005 and 00007.

Identifying individual fish.

So how can recaptures be identified? Let us first consider a situation where individual identification is required, for example where individual fish length has been recorded at the time of tagging in a growth study. There are basically two options:-

1. Reading the tag before placing it in the fish and recording the sequence number. This is normally impractical, but is feasible where pre-cut tags are used in a single-shot syringe - see our application note "Pre-cut sequential coded wire tags - an inexpensive option for feasibility and small-scale studies".

2. The one-in-two option. Here, a reference tag is stored between each one used in a fish; for example, in Figure 1, the first, third and fifth etc tags cut would be stored, and the second, fourth, sixth etc would be

used in fish. This avoids all possible ambiguity, and recaptures are identified by reading the appropriate archived tags to locate the recovered tag in the sequence. NMT can supply waterproof sheets for storage of reference tags and recording of individual fish details.

It is not of course necessary to read all reference tags to identify each recapture. It is possible to estimate the approximate location in the list of a tag bearing, for example, the sequence code 05000. To start, the first archived tag (the one stored before the first fish) and the last (the one stored before the last fish) would be read. From a typical spool of 10,000 tags the last archived tag cut might be the 10,000th one cut and would represent the 5000th fish tagged (because only one in two tags is put into a fish). If the injector were cutting tags with a mean length of 1.1mm then the sequence number on this tag would be 16,923. However, for the sake of realism let us suppose that the injector was cutting tags on average a little longer than 1.1 mm and that this last archived tag bore the sequence number 17,213. Then the predicted position of a tag with the sequence number 05000 would be:-

$$\frac{05000}{17213} \times 10{,}000 = 2905$$

suggesting that the recovered tag was approximately the 2905th to be cut corresponding to fish number 1452. The reference tag for this fish would then be examined. It might with very good luck be spot on and be the tag immediately preceding the one we had recovered, in which case we have identified our fish in one hit. More likely it will be a few numbers out, but locating the appropriate reference tag will then be a simple iterative process.

A suggested layout for reference storage sheets is shown in Appendix 1.

Identification of batches.

Use of s-cwt for identifying small and variable sized batches of fish is simpler than that for individual identification, but similar care is required in archiving reference tags. In this case, however, it is only necessary to store one tag at the start of each batch, whatever the size of the batch. It is also necessary to store a reference tag at the end of the last batch, and it is prudent to do so at the end of any batch if there is the slightest doubt where and by whom the injector will next be used or if the wire is to be removed from the injector.

Examples of batches might be all fish of a particular length range or weight range in graded samples, or fish released at a particular place or at a particular time. The following points are relevant:-

1. The batch size can be variable, from single fish to many thousands.
2. It is not necessary to decide the batch size in advance. A tag is stored before tagging the batch commences, and the group is bracketed by reference to the tag archived at the start of the next batch or at the end of the last batch.
3. It will be highly desirable to record the number of tagged animals in each batch by reference to the counter on the injector. Although it is possible to calculate the number of tags cut from the sequential numbers on the reference tags, the answer will be approximate only.
4. The batch to which a particular recovered tag belongs is established by locating the two reference tags between which its sequence number lies. It may not be necessary to read all reference tags unless they are adjacent to a batch from which a recovery is made, as the approximate sequence numbers of the reference tags can be calculated from the numbers on the first and last reference tags on the spool, as long as the batch sizes are recorded.

5. Combining batches in different ways can be a very powerful technique. For example, suppose a hatchery was releasing groups of smolts at four times every day for three weeks. If each group comprised a tagged batch, we would have 84 batches (4 x 21). Each batch may in itself be too small to analyse for adult returns, but batches can be combined, for example by day of release (batches 1-4, 5-8, 9-12 etc) or by week of release (batches 1-28, 29-56, 57-84). The effect of time of day of release could also be examined by combining for example all fish released early in the morning (batches 1, 5, 9, 13 etc) or late evening (batches 4, 8, 12, 16 etc). Other possibilities include analysis by flow conditions or by phase of the moon at time of release. An important point is that the way in which batches are combined can be decided when the return results are known, as long as the appropriate data concerning each batch are recorded.

Again, the optimal layout of sheets for storing reference tags and recording data will depend upon the experimental design; one possible design is shown in Appendix 1.

Appendix 1 - Suggested designs of sheets for reference tag storage and data recording when using s-cwt.

On each sheet a vertical strip of tape is shown (indicated by a shaded bar). This is intended for holding reference tags injected onto it; they are visible and readily removed for reading when required. It may be more convenient, especially where every other tag is being archived, to have these strips on a separate sheet from the other data, carefully cross referencing by a numbering system.

a) individual identification, one in two option

SEQUENTIAL DCWT™ REFERENCE TAG STORAGE SHEET

Project…………………… Personnel…………………… Date……………….
Sheet #……of……. Agency………… Data 1……… Data 2…….

Line #	Fish #	Reference tag sequence #	Data

b) batch identification

SEQUENTIAL DCWT™ REFERENCE TAG STORAGE SHEET

Project…………………… Personnel…………………… Date……………….
Sheet #……of……. Agency………… Data 1……… Data 2…….

Line #	Batch #	Reference tag sequence #	Counter reading		No. in batch	Batch data
			Start	End		

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