



## An Introduction to Sequential Coded Wire Tags

The Sequential Coded Wire Tag (sCWT) is used to identify individual animals or to allocate a recaptured animal to a particular batch. The sCWT is the same size as the standard CWT (0.042 inches (1.1 mm) long and 0.010 inches (0.25 mm) in diameter), but in addition to the six digit number found on the standard CWT, the sCWT includes a unique sequence number on each tag.

### **Reading Sequential Coded Wire Tags**

Because the machines that cut the tags are not indexed to the coding on the wire, the full code must appear on a tag no matter where along the wire the machine starts cutting. The codes are therefore shorter than 1.1 mm to guarantee that at least one sequential number will occur in its entirety on each tag. However, this means that sequential number “n” does not identify the tag as the n<sup>th</sup> tag to have been cut because some tags will carry two sequence numbers as in the sample tag cut shown below.

The batch code is read from left to right in three two-digit columns. The five digit numbers written around the circumference of the wire are the sequential numbers. They are read from top to bottom.

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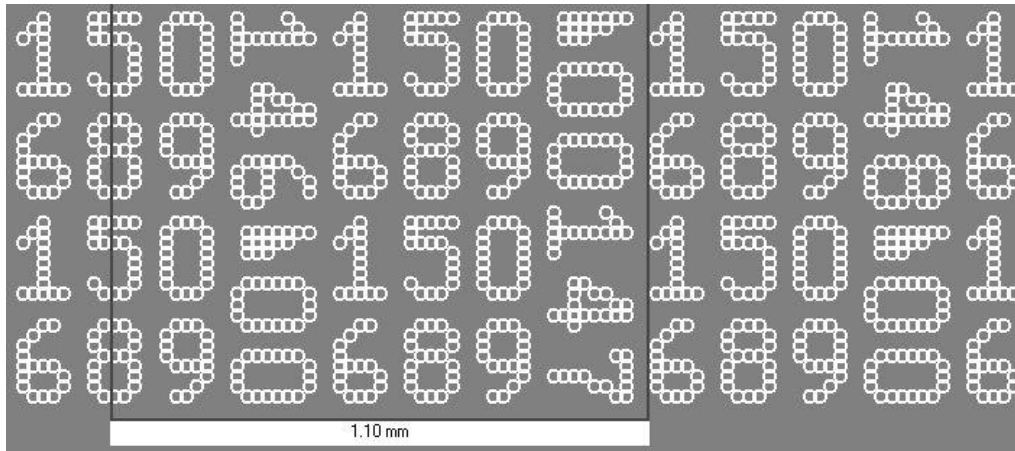


Figure 4: A sample of a Sequential Tag wire. The face of the wire is shown “unrolled” - in practice the wire would have to be rotated through 360 degrees to see all this information. The triangular flag points to the first digit in the batch code (165809) and in the sequential code (00146). starting at the triangular flag and rotating the tag. The sequential numbers are staggered by three digits around the circumference of the wire. This allows for greater reliability if a tag is scratched. The white lines in the figure show the size of the tag, and one possible cut.

For agencies using the traditional data conventions, the Sequential Tag has three static words (Agency, Data 1, and Data 2) and a sequential number. Figure 4 shows Agency = 16, Data 1 = 58, Data 2 = 09, and sequence = 00146 (the lesser of the 2 sequence numbers on the tag).

### Identifying individual fish

With most numbered tag systems the usual practice is to read the tag number as the tag is applied, and to record it alongside other data such as length, weight, date and time. However, although each sCWT bears a unique set of numbers it is usually impractical to read and record the tag number at the time of tagging; therefore other approaches are necessary and some discipline is required to ensure that recaptures are correctly identified.

So how can recaptures be identified? 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 two options:

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1. Reading the tag before placing it in the fish and recording the sequence number. This is normally impractical, but may be feasible where precut tags are used in a Single Shot Injector (see Using Precut Sequential Coded Wire Tags on our website [www.nmt.us](http://www.nmt.us)).
2. The one-in-two option. Here, a reference tag is stored between each one used in a fish; for example, 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. A suggested layout for reference storage sheets for individual identification is shown in Table 1 below.

**Table 1 Suggested tag storage sheet for individual identification, one-in-two option. We recommend laying down a strip of clear silicone in the shaded column. Once the caulking has cured, reference tags can be injected and stored in it.**

Project:		Personnel:		Date:	
Sheet #.....of.....		Tag Code:	Agency:	Data 1:	Data 2:
Line #	Fish #	Reference tag sequence #	Data (customized by project)		

### Identification of batches

Use of sCWT 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.

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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 batch size can be variable, from single fish to many thousands.
- It is not necessary to decide the batch size in advance. A tag is stored before tagging the batch, and the group is bracketed by a reference tag stored at the end of each batch, or at the beginning of a subsequent batch.
- Record the number of tagged animals in each batch by reference to the counter on the injector.
- 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. You may only need to read a few reference tags to locate the recovered tag.

Table 2 shows a suggested layout for reference storage sheets for batch identification.

**Table 2 Suggested reference tag storage sheet for batch identification. We recommend laying down a strip of clear silicone in the shaded column. Once the caulking has cured, reference tags can be injected and stored in it.**

Project:		Personnel:		Date:		
Sheet #.....of.....		Tag Code:	Agency:	Data 1:	Data 2:	
Line #	Batch #	Reference tag sequence #	Counter reading		# in batch	Batch data (customized by project)
			Start	End		

Combining batches in different ways can be very powerful. For example, suppose a hatchery was releasing groups of smolts at four times every day for 3 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 analyze 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

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(batches 4, 8, 12, 16 etc). 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.

### **Suggested designs of sheets for reference tag storage and data recording**

On each sheet, we recommend that you lay down a vertical strip of silicone (indicated by a shaded bar), which can be clear silicon adhesive such as is used for aquarium tank construction or clear silicone caulking. Once cured, this is intended for holding reference tags injected into 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.

### **Contact NMT**

If you have any questions, please contact us by phone at +1 (360) 468-3375 or by email at [office@nmt.us](mailto:office@nmt.us) or [biology@nmt.us](mailto:biology@nmt.us).