Possible identification of CENP-C in fish and the presence of the CENP-C motif in M18BP1 of vertebrates. [version 1; peer review: 1 approved with reservations]

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Abstract
The centromeric protein CENP-C is a base component of the kinetochoore. This protein, along with CENP-A has been shown to adaptively evolve in a number of animal and plant species. In order to determine if CENP-C also evolves in fish species, I attempted to retrieve fish CENP-C sequences from GenBank. No Teleostei CENP-C sequences were found either by name or by BLASTP searches with the vertebrate CENP-C motif sequence. A number of putative Teleostei protein sequences were identified in GenBank that have homology to the C-terminal cupin domain of vertebrate CENP-C. These proteins only have partial homology to the CENP-C motif, but evidence is presented that makes it likely that these fish proteins are orthologs of CENP-C. Interestingly, it was also discovered that the CENP-C motif sequence is also mostly present in M18BP1 proteins of fish and some other vertebrates but not in mammals. This finding may have implications for CENP-C and M18BP1 assembly in centromeric regions of different vertebrate taxa.

Keywords
CENP-C, M18BP1, centromeric proteins, teleostei, kinetochoore, CENP-C motif, cupin domain protein
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Introduction

The kinetochore is a structure that connects chromosomal centromeric DNA to microtubules during mitosis and meiosis. The centromere is epigenetically defined by the deposition of nucleosomes that contain the histone H3 variant CENP-A. Centromeric protein CENP-C is required for both the recruitment of new CENP-A to the centromeric region as well as the initial assembly of the kinetochore. The CENP-C protein is generally considered to be ubiquitous in all eukaryotic taxa since homologs of CENP-C have been identified in yeast and Drosophila as well as many plants and vertebrates. While CENP-C evolves so rapidly that very little homology is observed between distantly related taxa, a conserved CENP-C motif has been identified across all lineages studied. This conserved motif should, therefore, be of utility to identify CENP-C orthologs in other species.

CENP-A has been initially shown to evolve adaptively in Drosophila, in members of the Bressicaceae family and more recently in primates and in percid fishes. CENP-C has also been shown to evolve adaptively in a number of animal and plant species as well as in primates. In an effort to determine if CENP-C also evolves adaptively in fish species, searches were conducted in GenBank for Teleostei proteins that had been already identified as CENP-C or for genes that had been annotated as coding for CENP-C. No such fish proteins or genes were found. BLASTP searches of just the Teleostei subset of GenBank were performed with the conserved vertebrate CENP-C motif and these too failed to find identified fish CENP-C proteins or genes. However, these searches did identify fish M18BP1, which, as will be discussed below, contains a sequence homologous to the CENP-C motif. A search of the Chondrichthyes for proteins that had been already identified as CENP-C, or for genes that had been annotated as coding for CENP-C, found one gene annotated as CENP-C in the elephant shark (Callorhinchus milii) genome. Interestingly, while this putative shark CENP-C protein contained a cupin domain at the C-terminal end homologous to the cupin domain found at the C-terminal end of other vertebrate CENP-C proteins, the conserved CENP-C motif was not found in the expected location upstream of the cupin domain. However, a region further upstream does have homology to some of the most conserved amino acids of the CENP-C motif.

BLASTP searches of the Teleostei subset of GenBank with the putative shark CENP-C protein sequence identified a number of genes that were primarily homologous to the C-terminal cupin domain. However, none of these fish sequences were annotated as CENP-C in GenBank. Upon closer analysis, as will be discussed below, these C-terminal cupin domain containing fish proteins do contain sequences that are partly homologous to the conserved CENP-C motif and, therefore, these fish genes could be CENP-C orthologs.

Results and discussion

BLASTP searches with the vertebrate CENP-C motif identified CENP-C proteins from a variety of taxa, including plants, but did not identify any CENP-C in fish lineages. It is possible that CENP-C may be absent in fish, but the ubiquity of this protein in other lineages and the central role of this protein in centromeric function make this unlikely. A C-terminal cupin domain protein encoded by a shark gene annotated in GenBank as CENP-C was used to identify homologs in Teleostei genomes by BLASTP. The retrieved teleost fish homologs were annotated as either calponin homology domain containing protein, neurofilament heavy polypeptide-like protein, or myb-like protein. Within vertebrate CENP-C proteins the RxRxRxxxPLxYWxGERxxY sequence defines identities within the CENP-C motif located within about 100 amino acids upstream of the cupin domain (Figure 1). However, within the shark and teleost fish C-terminal cupin domain-containing protein sequences, only some of these CENP-C motif sequence identities were present (Figure 2) and, therefore, unambiguous identity of these proteins as CENP-C was not obvious.

In a recent study that examined the interaction between CENP-C conserved domains and CENP-A containing nucleosomes (or

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**Figure 1. Conserved domains and sequences in vertebrate CENP-C.** (A) Diagram of human CENP-C. (B) Amino acids that are identical in the CENPC motif in vertebrates in which CENP-C has been identified. (C) Conserved sequence in the CEN-P-C central region that is homologous to part of the CENP-C motif. Amino acid locations within human CENP-C protein of conserved sequences are indicated at the beginning and end of each sequence.
nucleosomes containing histone H3 modified with a CENP-A C-terminal tail), Kato et al.\textsuperscript{11} identified within the conserved central region of CENP-C a RxSxxPSxWW consensus sequence (Figure 1) that is similar to the core portion of the CENP-C motif. Mutations of the arginine to alanine or the tryptophans to alanine in this sequence prevented the binding of this central region to the nucleosomes. So, functionally, the RxxxxPxxWW portion of the central region sequence is important to centromeric binding of CENP-C. Furthermore, mutations of the arginine, tyrosine and tryptophan in the core CENP-C motif RxxxxPxyYW also reduce the binding affinity the CENP-C to the nucleosomes\textsuperscript{11}. A mutation of arginine to alanine in this core portion of the CENP-C motif was previously shown to prevent the binding of Xenopus CENP-C to centromeres\textsuperscript{12}.

An alignment of the putative shark and teleost fish CENP-C proteins identified two conserved regions that contained the RxxxxPxxWW sequences (Figure 2). The placement of these sequences corresponds roughly to the locations of the central portion and the CENP-C motif of the vertebrate CENP-C (Figure 1). Therefore, it is likely that the combination of the C-terminal cupin domain and the presence of these centromeric nucleosome binding regions in positions generally corresponding to the locations of the central region and the CENP-C motif identifies these teleost genes as possible CENP-C orthologs. It will be necessary, of course, to verify if this protein is actually found at fish centromeres. It should be noted, however, that the distance between the cupin domain and the “CENP-C motif” position is about twice as long in the putative fish CENP-C in comparison to this distance in CENP-C of other vertebrates. It is interesting that the putative shark “CENP-C motif” location lacks the tryptophans of the RxxxxPxxWW sequence and that Poecilia reticulata has a replacement of the first tryptophan in the conserved central region sequence (Figure 2). However, depending on other factors acting in the assembly of the centromere in various taxa, it may be possible that just one of those conserved RxxxxPxxWW sequences may be necessary for centromeric binding of the putative fish CENP-C. Interestingly, no homology to the RxxxxPxxWW portion of the conserved central region is detectable in CENP-C of reptiles and birds.

Interestingly, BLASTP searches of the Teleostei subset of GenBank retrieved centromeric protein M18BP1 sequences. This protein is recruited to centromeres by CENP-C\textsuperscript{13,14} and along with centromeric proteins Mis18\textalpha{} and Mis18β functions in the recruitment of CENP-A to centromeres\textsuperscript{15}. The M18BP1 protein contains almost the entire vertebrate CENP-C motif in all vertebrates examined except in mammals (Figure 3). It appears that the
CENP-C motif sequence is not exclusive to just CENP-C. Since both CENP-C and M18BP1 associate with centromeres and with each other, it is tempting to speculate that what has generally been regarded as a CENP-C motif sequence facilitates the interaction of both of these proteins with centromeric nucleosomes. Furthermore, since mammalian M18BP1 lacks this CENP-C motif, it is possible that mammalian M18BP1 may be more dependent on association with CENP-C to localize to the centromere than the M18BP1 of other vertebrate taxa.

**Competing interests**
No competing interests were disclosed.

**Grant information**
This study was supported by a Faculty Research Grant funded by the University of West Georgia.

*I confirm that the funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.*

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**Supplementary material**

**Supplementary file S1. Alignment of the C-terminal portion of vertebrate CENP-C proteins.**

The vertebrate CENP-C motif containing consensus sequence utilized in BLASTP searches spans amino acids 11 to 33 and is highlighted in red.

*Click here to access the data.*
References


The centromere protein CENP-C is well known as an essential component for functional kinetochore assembly. Due to importance of this molecule, CENP-C must be conserved in Fish species. The author performed BLASTP searches with the conserved CENP-C motif sequence, but any CENP-C homologues in Fish lineages were not identified with this sequence. However, as there is a putative CENP-C sequence in shark genome, BLASTP searches were carried out with C-terminal domain sequence of putative shark CENP-C. Then, the author identified CENP-C candidates from various teleost genomes. Although the author does not show that candidate proteins localize to centromeres, these candidates contains related sequences of CENP-C motif, which were a little divergent from the vertebrate consensus sequences. Interestingly, the authors found that various vertebrate M18BP1s, which are recruited to centromeres by CENP-C, contain the CENP-C motif sequence, but mammalian homologues do not contain the motif sequence.

This is an observation article and finding of the CENP-C motif in the M18BP1 sequence is interesting. However, to improve the quality of the paper, the author should revise the manuscript. My specific concerns are following.

1. As the author recognizes, it is necessary to verify whether CENP-C candidates from teleost genome really localize to Fish centromeres. As the author obtained a candidate from Zebrafish genome, such an experiment is not difficult with the Zebrafish experimental system. If the author added localization data, Figure 2 would be interesting.

2. Related to Figure 2. If the author shows sequence comparison of Cupin domain in teleost sequences, it would be helpful.

3. When the author discuss about central region of human CENP-C, it may be better to cite a recent paper by Nagpal et al. (Mol. Biol. Cell, 2015), which says that central region sequence does not exist in chicken CENP-C. Then, the author can emphasize that the central motif is really important for CENP-A binding.
4. The author described some results of the analysis in the Introduction. This is not necessary and it would be better to cut of redundant description.

**Competing Interests:** No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 12 Jan 2016

**Leos Kral,** University of West Georgia, Carrollton, USA

I have revised the manuscript to address concerns #2, #3 and #4. Unfortunately, I do not have the resources to carry out the localization experiment (concern #1). My main motivation in publishing these observations is to bring awareness of this issue to individuals who may have the resources and interest to follow up with the relevant experiments.

**Competing Interests:** No competing interests were disclosed.

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