New genes can arise through duplication of a pre-existing gene or de novo from non-coding DNA, providing raw material for evolution of new functions in response to a changing environment. A prime example is the independent evolution of antifreeze glycoprotein genes (afgps) in the Arctic codfishes and Antarctic notothenioids to prevent freezing. However, the highly repetitive nature of these genes complicates studies of their organization. In notothenioids, afgps evolved from an extant gene, yet the evolutionary origin of afgps in codfishes is unknown. Here, we demonstrate that afgps in codfishes have evolved de novo from non-coding DNA 13–18 Ma, coinciding with the cooling of the Northern Hemisphere. Using whole-genome sequence data from several codfishes and notothenioids, we find higher copy number of afgp in species exposed to more severe freezing suggesting a gene dosage effect. Notably, antifreeze function is lost in one lineage of codfishes analogous to the afgp losses in non-Antarctic notothenioids. This indicates that selection can eliminate the antifreeze function when freezing is no longer imminent. In addition, we show that evolution of afgp-assisting antifreeze potentiating protein genes (afpps) in notothenioids coincides with origin and lineage-specific losses of afgp. The origin of afgps in codfishes is one of the first examples of an essential gene born from non-coding DNA in a non-model species. Our study underlines the power of comparative genomics to uncover past molecular signatures of genome evolution, and further highlights the impact of de novo gene origin in response to a changing selection regime.

Key words: orphan genes, teleost fishes, molecular adaptation.

Introduction

Genomes recurrently acquire new genes, often to take on novel functions in response to a changing selection regime. One notable driver of evolutionary innovation is paleoclimatic changes such as the global cooling and polar icecap formation 10–30 Ma (Kennett 1977; Eastman 1997). This spurred the evolution of the antifreeze proteins (AFPs), which have evolved independently in bacteria, plants (> four times), fungi, insects (> two times), and teleost fish (> seven times) (Cheng 1998; Ewart et al. 1999; Harding et al. 2003; Bildanova et al. 2013; Gupta and Deswal 2014). The most classic way of acquiring new genes is through gene duplications, and many of the AFPs have arisen through neofunctionalization of such duplicates (Liu et al. 2007; Graham et al. 2013). Alternatively, new genes can evolve de novo from non-coding DNA, either by transcripts acquiring an open reading frame (ORF) or consistently transcribed regions of the genome acquiring an ORF (McLysaght and Guerzoni 2015; Schlötterer 2015). De novo gene origin has recently become more widely recognized as a regular source of new genes (Tautz and Domazet-Lošo 2011; Wu et al. 2011; McLysaght and Guerzoni 2015; Schlötterer 2015; McLysaght and Hurst 2016), which often encode novel functions representing lineage specific adaptations to the environment (Khalturin et al. 2009; Tautz and Domazet-Lošo 2011). In notothenioid fishes antifreeze glycoproteins (AFGPs) evolved from neofunctionalization of a duplicate of trypsinogen-like protease (TLP) through a unique recruitment of intronic sequence to form coding DNA (Chen et al. 1997a). In some species within the group of distantly related codfishes (Gadidae) such as Atlantic cod (Gadus morhua), similar AFGP genes (afggs) are the result of convergent evolution (Chen et al. 1997b). Codfish afggs are suggested to be orphans, i.e. not homologous to any other gene, and likely to have originated de novo from non-genic DNA (Zhuang 2014). Although the exact genesis of cod afggs remains unknown, they are most likely relatively young genes. Such tracing their evolutionary history should be possible, making cod afggs good candidates for studying the role of new genes associated with key innovations such as antifreeze properties.

The evolutionary convergence of AFGPs in notothenioids and codfishes is intriguing as AFGPs in both lineages consist of...
nearly identical repeats of Thr-Ala/(Pro)-Ala (in codfishes Thr is occasionally substituted with Arg) (Chen et al. 1997b). These repeats are strung together in large polypeptides that are cleaved after translation yielding isoforms of multiple sizes (Chen et al. 1997a, 1997b), with the shared ability to depress the freezing point of body fluids through thermal hysteresis by binding to ice crystals and preventing them from growing (Kristiansen and Zachariassen 2005). The similar selection pressures imposed by the onset of freezing temperatures in the Arctic and Antarctic have remarkably produced the same function carried out by nearly identical proteins. The independent origin of afgps is evident as the genetic organization and codon usage of afgp are distinctive in the two lineages (Chen et al. 1997b). Codfish afgp has three exons encoding a signal peptide (exon 1, exon 2, and the beginning of exon 3) and the afgp repetitive region (the remainder of exon 3). Notothenioid afgp has two exons, one encoding the signal peptide and another encoding the afgp repeat (Chen et al. 1997b). In addition, notothenioids possess a second AFP known as antifreeze potentiating protein (AFPP) that only exhibits moderate antifreeze activity by itself, but facilitates the function of AFGP (Yang et al. 2013). Especially in species exposed to freezing temperatures year-round, AFPP contributes significantly to a substantial proportion of the total antifreeze activity (Fields and Devries 2015). The evolutionary history of AFPP and how it relates to the appearance of AFGP are not known to date.

There are genetic studies on afgps in a few species in each lineage (reviewed in Cheng 1998; Harding et al. 2003), chiefly on polar cod (Boreogadus saida) in codfishes (Chen et al. 1997b), and the notothenioid Antarctic toothfish (Dissostichus mawsoni) (Chen et al. 1997a; Cheng 2003; Nicodemus-Johnson et al. 2011; Near et al. 2012). However, none of these studies have looked at afgps in a genomic context, except one attempt to assemble the afgp locus in G. morhua (Zhuang et al. 2012). The afgp locus, including its flanking genes, is still not completely characterized in neither codfishes nor notothenioids, probably due to the challenges of assembling repetitive regions such as those in afgp. Whole genome sequencing (WGS) may provide more accurate estimates of copy number variation (CNV), inference of gene losses, pseudogenization, and resolution of genetic organization and synteny (e.g. Goodwin et al. 2016). Moreover, for comparative studies WGS data have the advantage that all homologous sequences can in most cases be detected by BLAST (Albà and Castresana 2007) to give a complete genomic picture of a gene family.

Here, we use a comparative genomics approach to determine when afgps originated in codfishes, as well as resolving the CNV and genomic organization of afgps in both notothenioids and codfishes. Furthermore, for the less studied AFPP genes (afpps) we have addressed their genomic origin and when they arose in the evolutionary history of notothenioids. To achieve this, we sequenced the genomes of eight notothenioid species; Pleuragramma antarctica, Trematomus newnesi, Harpagifer kerguelensis, Artediacrana skottbergi, Gymnodraco acuticeps, and Chaenocephalus aceratus as they represent the main notothenioid lineages that have afgp, the non-Antarctic species Eleginops maclovinus that never had afgp, and Patagonotothen guntheri, that secondarily left the Antarctic and lost afgp (Near et al. 2012; Miya et al. 2016). In addition, we included the published N. coriiceps genome in the comparison of the notothenioids (Shin et al. 2014). For codfishes we took advantage of the already generated genome assemblies for G. morhua (Torresen et al. 2017b), haddock (Melanogrammus aeglefinus) (Torresen et al. 2017a) and 25 additional published codfish genomes (Malmstrøm et al. 2016, 2017). In both lineages, we coupled the presence/absence and copy number of genes in combination with time-calibrated phylogenetic trees (Colombo et al. 2015; Malmstrøm et al. 2016). Our approach reveals that codfish afgp most likely arose de novo from non-genic DNA around 13–18 Ma, which coincides with the onset of freezing temperatures in the Northern Hemisphere (Eastman 1997).

Moreover, afgp has been subsequently lost in one lineage of codfishes, analogous to the loss of afgp in non-Antarctic notothenioids. In notothenioids, afgp coevolved with afgp. In both codfishes and notothenioids there is considerable CNV associated with species living in waters with more severe freezing displaying a higher number of afgps. We here demonstrate the importance of WGS data for comparative genomic studies of molecular evolution, by revealing the complex evolution of afgp involving de novo origin in codfishes, co-evolution of afgp and afgp in notothenioids as well as extensive CNV, gene losses and pseudogenizations in both lineages.

**Results**

**Presence, Copy Number, and Organization of afgps in Codfishes**

To characterize the genomic organization and micro-synteny of afgps we used the high-quality genome assemblies of G. morhua (Torresen et al. 2017b) and M. aeglefinus (Torresen et al. 2017a). Using BLAST we identified four complete copies of afgps on linkage group 6 (Lg06) and one copy on scaffold 9468 (Scf9468) in G. morhua (fig. 1). Based on synteny (see further down) Scf9468 was placed within Lg06. We defined a full-length afgp gene to contain a promoter, 5’UTR, three exons (abbreviated ‘ex’) that contain both the signal peptide sequence (ex1, ex2, and first part of ex3) and afgp tripeptide repeats (ex3), and a 3’UTR (fig. 1 and supplementary table S1, Supplementary Material online). The afgps were named based on partial afgp sequences from Zhuang et al. (2012). In G. morhua afgp2, afgp3, afgp5, and afgp6 are likely functional genes. afgp1 has previously been reported by Zhuang et al. (2012) as a putative pseudogene. We detected a 114 nt insertion in the 5’UTR, a missing 3’UTR and frame-shifting indels rendering the ex3 repeat without the characteristic strings of TAA. Thus, even if this is a functional protein it may not have an antifreeze function.

In M. aeglefinus we identified only one afgp copy on Scf75 (fig. 1). This copy is characterized by a truncated 3’UTR as well as frame-shifting indels and three stop codons in the ex3 repeat; this is a likely pseudogene and homologous to afgp1 in G. morhua based on sequence similarity as well as a shared 5’UTR insertion. The absence of functional afgps in...
**Fig. 1.** *afgps* in codfishes. (A) Gene organization of *afgps* in *G. morhua* and *M. aeglefinus*. The *afgp* genes have been divided up in promoter, 5'UTR, signal peptide, intron, *afgp* repeat and 3'UTR and colored according to legend. The hatched yellow indicates a truncated 3'UTR. The sequences are labeled with species name, a scaffold (scf) or linkage group (LG) identifier, name of *afgp* with Ψ signifying a pseudogene, and the length of each gene given as number of amino acids (aa). The organization of a complete, functional *afgp* gene is shown with triangles indicating cleavage sites of the polyprotein peptide. (B) Presence of *afgp* in a selection of codfishes in a phylogenetic context, showing copy numbers of different parts of *afgps* mapped on a time-calibrated species tree modified from (Malmstrøm et al. 2016) with time given in millions of years (Ma). The time period when freezing temperatures appeared in the Northern Hemisphere is shaded in blue (Eastman 1997). Species shown to have functional AFGP and thermal hysteresis are denoted with (+): *A. glacilis* (Praebel 2005), *G. chalcogrammus* (Tsuda and Miura 2005), and *G. morhua* (Hew et al. 1981). Species shown not to have functional AFGPs or thermal hysteresis are denoted with (−): *M. aeglefinus* (Ewart et al. 2000) and *P. virens* (Denstad et al. 1987). The numbers of putative promoters, ex2, and beginning of ex3 (containing *afgp* repeat) and 3'UTR are given in the colored boxes. The branches where *afgps* originated and pseudogenized according to the most parsimonious explanation are indicated in the tree according to the legend along with the first appearance of an *afgp* 5'UTR sequence.
M. aeglefinus is in concordance with experimental evidence of no thermal hysteresis and no presence of AFGPs in this species (Ewart et al. 2000). In G. morhua afgp3 and afgp6 have two 3’UTRs and there are a promoter and a 5’UTR that no ORF follows before afgp6 (fig. 1). As there are no afgp-repeat-like sequences upstream of these 3’UTRs and no signal-peptide-like sequences downstream of the 5’UTR, we believe these are not the result of pseudogenization, but rather represent incomplete duplications, or complete duplications followed by deletions of the majority of the gene.

In both G. morhua and M. aeglefinus we found only a single genomic region containing afgp (fig. 1A), which is in accordance with previous findings (Zhuang et al. 2012). However, in G. morhua we found four additional sequences with high similarity to afgp in other genomic regions on LG16, LG23, LG19, and Scf4199. These sequences, denoted as afgp-like, include a promoter-like sequence and a signal peptide-like sequence (ex1, ex2, and beginning of ex3). Although similar, these sequences do not contain the characteristic afgp TAA amino acid repeat or an ORF. The afgp-like ex2 sequences have a sequence identity of 85–91% to our query signal peptide ex2 whereas true signal peptide ex2 are 94–98% identical to each other (supplementary table S2, Supplementary Material online). In addition, we found putative 5’UTR-like sequences of varying length at 376 genomic positions outside the afgp region in G. morhua and 290 genomic positions outside the afgp region in M. aeglefinus with BLAST e-values from $4 \times 10^{-6}$ to $5 \times 10^{-7}$5. 3’UTR-like sequences were not detected outside the region containing the true afgps.

The finding of afgp-like sequences outside the afgp locus in G. morhua complicated the estimation of presence/absence and copy number of afgps in the other Gadiformes genomes, particularly where we could not reconstruct syntenies. We located all putative afgp sequences using liberal BLAST searches and then used phylogenetics to determine which sequences were true afgps. All the different components of afgp were found in three codfishes in addition to G. morhua: Gadus chalcogrammus, B. saida, and Arctogadus glacilis (fig. 1B), all of which have been shown to have antifreeze activity in their blood (Hew et al. 1981; Praebel 2005; Tsuda and Miura 2005). Furthermore, we found some segments of afgp in Merlangius merlangus, but just like in its sister species M. aeglefinus a 3’UTR sequence was not detected, suggesting these two species only possess an afgp pseudogene (afgp*1). There are no afgp-like sequences in Brosme brosmes or the 20 codfish genomes investigated outside B. brosmes in the phylogeny (see supplementary table S2, Supplementary Material online). However, we did detect some afgp-like sequences in the species more closely related to Atlantic cod: Pollachius virens, Trisopterus minutus, and Gadilicus argenteus. To determine whether the sequences with some similarity to afgp are homologous to the true afgps or the four afgp-like sequences detected in G. morhua we carried out phylogenetic analyses.

We included sequences where ex1, ex2, and parts of ex3 were located on one unitig (utg) denoted by a letter (for full utg identifier see supplementary table S3, Supplementary Material online). The un-rooted phylogenetic tree in figure 2 shows that putatively functional afgps together with putative afgp-pseudogenes form a well-supported cluster (posterior probability = 0.99, bootstrap support = 78%). Most of the afgp-like sequences form a single cluster, except G. argenteus_a and P. virens_a; however, these are still outside the cluster of true afgps. Only sequences from G. morhua, G. chalcogrammus, B. saida, A. glacilis, M. merlangus, and M. aeglefinus cluster with true afgps, whereas all sequences from P. virens, T. minutus, and G. argenteus appear to be afgp-like (fig. 2). Furthermore, the afgp-like sequences are located in the G. morhua assembly at LG16 (between calm and kalm), LG23 (between aloxi and arhgap21), LG19 (between npur12 and vldlr), and Scf4199, which contains no genes nor ORFs. In Gasterosteus aculeatus, these genes are not linked, i.e. synteny is not conserved in these regions. The distance between the afgp-like sequence and the closest gene is quite large, ranging from 40 to 160 kb, on average 80 kb. Taken together with the absence of afgp-like sequences outside Gadidae, the evidence for the gadid-specificity of these afgp-like sequences is quite strong, especially considering that the Gadiformes genome assemblies are not repeat-masked, so we would detect these sequences if present.

We estimated copy numbers for the different components of afgp independently, as we did not have complete full-length afgp sequences for many of the species. For signal peptide ex2-like sequences we reconstructed a phylogeny revealing that copies of true afgp ex2 ranges from one in M. aeglefinus and M. merlangus, and 11 in B. saida (supplementary fig. S1, Supplementary Material online). For the other components of afgp it was not feasible to construct phylogenies so we inspected the sequences manually and counted the number of copies. The number of different afgp segments varies somewhat within each species (fig. 1), which is not unexpected given the finding that the number of different segments is not equal to the number of complete genes in G. morhua and M. aeglefinus (fig. 1B). Based on the number of signal peptide ex2 sequences there is still a clear pattern in the number of copies, with a higher number in the lineage with functional copies of afgp, ranging from five in G. morhua to B. saida’s estimated copy number of 11 (fig. 1B). Furthermore, we find no afgp genes in P. virens, T. minutus, and G. argenteus (fig. 1B) based on the absence of afgp repeats and 3’UTR sequences in these species, and that ex2-like sequences found in P. virens, T. minutus, and G. argenteus are not homologous with afgp ex2 (fig. 2 and supplementary fig. S1, Supplementary Material online). The absence of afgp in P. virens is concordant with the finding of no thermal hysteresis in the blood plasma (Denstad et al. 1987).

We were not able to count and map the number of afgp 5’UTRs as we could not determine which 5’UTR BLAST hit belonged to afgp or not. This was due to the many copies of 5’UTR-like sequences in the G. morhua genome, which were indistinguishable from the afgp 5’UTR (see supplementary notes, Supplementary Material online for more information). We did not locate 5’UTR-like sequences in species outside Gadidae, suggesting this is a repeat-specific trait for this family (figs. 1 and 2, and supplementary table S2, Supplementary Material online). Moreover, we did not identify any matches to the signal peptide ex2, 5’UTR, 3’UTR, or the antifreeze
Phylogeny of afgps and afgp-like sequences in codfishes. Sequences from the genomes of *G. morhua*, *M. aeglefinus*, *G. chalcogrammus*, *B. saida*, *A. glacilis*, *M. merlangius*, *P. virens*, *T. minutus*, and *G. argenteus* are included. The sequences from *G. morhua* and *M. aeglefinus* have a scaffold (scf) or linkage group (LG) identifier and sequence annotation (either afgp or afgp-like). Ψ is signifying a pseudogene. The remaining sequences have an assigned letter following the species name (details regarding content and genomic position of each sequence is given in supplementary table S3, Supplementary Material online). The tree topology was constructed with MrBayes. Posterior probabilities are shown for the main branching patterns in addition to bootstrap support for a maximum likelihood topology (using MEGA 7). Putatively functional afgps and afgp-like sequences are highlighted in blue and green, respectively, according to legend.

Fig. 2. Phylogeny of afgps and afgp-like sequences in codfishes. Sequences from the genomes of *G. morhua*, *M. aeglefinus*, *G. chalcogrammus*, *B. saida*, *A. glacilis*, *M. merlangius*, *P. virens*, *T. minutus*, and *G. argenteus* are included. The sequences from *G. morhua* and *M. aeglefinus* have a scaffold (scf) or linkage group (LG) identifier and sequence annotation (either afgp or afgp-like). Ψ is signifying a pseudogene. The remaining sequences have an assigned letter following the species name (details regarding content and genomic position of each sequence is given in supplementary table S3, Supplementary Material online). The tree topology was constructed with MrBayes. Posterior probabilities are shown for the main branching patterns in addition to bootstrap support for a maximum likelihood topology (using MEGA 7). Putatively functional afgps and afgp-like sequences are highlighted in blue and green, respectively, according to legend.
repeat sequence in ex3 in our searches in RepBase (Bao et al. 2015), indicating that these sequences are unique to the Gadidae family (fig. 1).

For G. morhua and M. aeglefinus we also have lower coverage draft assemblies constructed in the same way as the codfish genomes (G. chalcogrammus, B. saida, A. glacilis, M. merlangus, P. virens, T. minutus, G. argenteus, and B. brasme) (Malmstrøm et al. 2016). We therefore ran the annotation pipeline on these genome assemblies as a proof of principle on our copy number estimation criteria. The estimated numbers were in concordance with the copy-number estimates from the high-quality genome assemblies for both G. morhua and M. aeglefinus, respectively (supplementary table S2, Supplementary Material online).

Genomic Organization and Synteny of Codfish afgps and Flanking Regions
The synteny surrounding the afgp locus is relatively conserved across a selection of teleost fish genomes (fig. 3). This is particularly evident between the phylogenetically close relatives G. morhua and M. aeglefinus; T. nigroviridis, and T. rubripes; and O. niloticus and X. maculatus (fig. 3A). The G. morhua afgp genes are found on LG6 and Scf9468. However, previous studies indicate that there is only one contiguous afgp locus in this species (Zhuang et al. 2012). On LG6, between the genes spinw and dmtn (position LG6: 1941982–1942081), there is a gap—of unknown size—originating from the ordering and orientation of scaffolds into linkage groups (Tørresen et al. 2017b). Based on the conserved synteny between M. aeglefinus and G. morhua we were able to place Scf9468 in this gap, resulting in the complete, contiguous afgp locus in G. morhua (figs. 1A and 3A). Vista plotting was used to detect short stretches of similar sequences likely to be undetected by BLAST for the region between mak16 and rsph14 in G. morhua, M. aeglefinus, G. aculeatus, O. niloticus, and T. rubripes (supplementary fig. S3, Supplementary Material online). Only the regions containing the flanking genes around afgp (i.e. mak16, rsh14, dmtn, and rsph14) are conserved between codfishes and G. aculeatus, O. niloticus, and T. rubripes. There are no regions similar to the afgps in the species outside codfishes, or any conserved non-coding elements. The similarity between G. morhua and M. aeglefinus is high, especially at the flanking genes and the shared afgp Y1. Furthermore, M. aeglefinus differs from G. morhua at non-coding regions as well as in sequences encoding afgp2, afgp3, afgp5, and afgp6 in G. morhua.

De Novo Origin of Codfish afgp
afgps either evolved from non-coding DNA or pre-existing genes encoding proteins. We did not get any BLAST hits against any part of afgp in genes or ORFs in the high-quality G. morhua and M. aeglefinus genomes, or in the other codfish draft genomes, even with an E-value of 0.1. Furthermore, BLAST got no hits to afgp in Uniprot, the Ensembl genomes or Genbank (except other afgp sequences).

De novo genes are more likely to arise in GC-rich genomic regions as these regions are more transcriptionally active and these areas are more likely to obtain an ORF because stop codons are AT-rich (McLysaght and Hurst 2016). Consistent with this we find that the nucleotide composition is indeed skewed towards a high GC-content in the functional afgp copies in G. morhua (table 1). In fact, the GC-content in the afgp copies was as high as 71% vs. 56% on average for all annotated genes in the G. morhua genome assembly (Torresen et al. 2017b), implicating that the high alanine content strongly influences the GC-content of afgps (supplementary fig. S4, Supplementary Material online). In addition, by calculating the relative synonymous codon usage (RSCU) we found a significant codon usage bias (RSCU significantly <1 or >1) for the amino acids in the repeats (Thr, Pro, and Ala) across all the afgps in G. morhua and M. aeglefinus, which is consistent across the genes (supplementary table S4, Supplementary Material online). This finding, together with the occurrence of all afgps on a single linkage group and the well conserved synteny (figs. 1 and 3) between G. morhua and M. aeglefinus strongly suggests a common origin of codfish afgps, with subsequent gene duplications.

One feature that distinguishes natural proteins from a hypothetical protein product of translated non-coding DNA is that the latter is intrinsically more disordered (Romero et al. 1998). We therefore calculated degree of intrinsic structural disorder (ISD) using IUPred (Dosztányi et al. 2005) for all four putatively functional afgps in G. morhua, including all three potential ORFs for the complete coding sequence and the repetitive region separately. To account for the variation in ISD over the entire ORF we calculated both mean and median ISD for each gene. For the primary ORF, mean ISD ranged from 0.37 to 0.89 with an average of 0.68 and median ISD ranged from 0.40 to 0.98 with an average of 0.75 (supplementary table S5, Supplementary Material online). The level of ISD is consistent across the length of the protein for each afgp gene (supplementary fig. S5, Supplementary Material online), except for afgp2 (supplementary fig. S5A, Supplementary Material online). These values were even higher when only looking at the repetitive region, and the values were consistent even considering alternative ORFs (supplementary table S5, Supplementary Material online). For comparisons, we also calculated ISD for all annotated genes in the G. morhua genome assembly (Torresen et al. 2017b), where the average mean ISD was 0.36, and the average median ISD was 0.35. These values are clearly much lower than the average mean and median found in afgp (0.68 and 0.75, respectively) (fig. 4 and supplementary fig. S6, Supplementary Material online).

Copy Numbers of afgp in Notothenioids
In notothenioid species known to harbor AFGPs (Near et al. 2012; Miya et al. 2016), we identified the afgp repeat in the genomes of P. antarctica, T. newnesi, N. coriceps, H. kerguelensis, A. skottsbergi, G. acuticeps, and C. acutus. The presence of afgp, together with data on presence/absence of functional AFGP and thermal hysteresis obtained from the literature, was mapped onto a time-calibrated phylogenetic tree from (Colombo et al. 2015) (fig. 5). As expected from previous studies, we did not detect afgp in the non-Antarctic species E. maclovinus (Cheng and Chen 1999) and P. guntheri
Based on the number of signal peptide sequences we estimated the copy number of afgp, its evolutionary precursor trypsinogen-like protease gene (tlp) (Chen et al. 1997a), trypsinogen-1 (tryps1), and trypsinogen-3 (tryps3) (fig. 5). In N. coriiceps, the afgp region is poorly assembled, and estimation of copy numbers was unmanageable, but at least one copy is present. In T. newnesi and the lineage containing H. kerguelensis, A. skottsbergi, G. acuticeps, and C. aceratus there are four copies of afgp. The highest copy numbers are seven in P. antarctica and eight in D. mawsoni.

**Copy Numbers and Evolutionary Origin of afpp in Notothenioids**

The AFPP protein sequence available from (Yang et al. 2013) was found to be highly similar to a c1q-like gene (a3ffr1 in D. mawsoni) based on a BLAST search against Uniprot (E-value: $5 \times 10^{-48}$, alignment shown in supplementary fig. S7, Supplementary Material online). Based on BLAST alignments with notothenioid genomes there appear to be two exons encoding from 1 to 40 aa and from 40 to 130 aa, which have a high sequence identity with a c1q-like gene (supplementary fig. S7, Supplementary Material online). The first exon seems to be more conserved, yet sufficiently different to distinguish afpp from c1q-like genes (supplementary fig. S7, Supplementary Material online). Therefore, the first exon was used for the detection of afpp presence in notothenioids and for afpp copy number estimation. Echoing the pattern of afgp, afpp is present in the genomes of P. antarctica, T. newnesi, H. kerguelensis, A. skottsbergi, G. acuticeps, and C. aceratus and not present in E. maclovinus and P. guntheri (fig. 5, supplementary table S7, Supplementary Material online). We detected afpp in N. coriiceps, but only in the raw reads and

![Fig. 3](https://example.com/fig3.png) Synteny of genes flanking afgp and tryps in codfishes and notothenioids. Scaffold (scf), linkage group (LG), or chromosome (chr) is specified under each species, orientation of genes is indicated as arrows, grey triangles denote unidentified ORFs and truncated lines indicate regions containing genes not shown for practical purposes. (A) Synteny of the afgp genomic region in G. morhua (gadMor2) and M. aeglefinus (melAeg) compared with the following teleosts lacking afgps: G. aculeatus, T. nigroviridis, T. rubripes, O. niloticus, X. maculates, and E. lucius. Scf9468 in G. morhua has been placed in a gap in LG06 based on syntenic context and overlap at the afgp locus. (B) Genomic organization of the afpp locus in N. coriiceps. (C) Synteny of the trypsinogen locus in N. coriiceps and G. aculeatus, T. nigroviridis, T. rubripes, O. niloticus, and E. lucius.

(Yang et al. 2013). Based on the number of signal peptide sequences we estimated the copy number of afgp, its evolutionary precursor trypsinogen-like protease gene (tlp) (Chen et al. 1997a), trypsinogen-1 (tryps1), and trypsinogen-3 (tryps3) (fig. 5). In N. coriiceps, the afgp region is poorly assembled, and estimation of copy numbers was unmanageable, but at least one copy is present. In T. newnesi and the lineage containing H. kerguelensis, A. skottsbergi, G. acuticeps, and C. aceratus there are four copies of afgp. The highest copy numbers are seven in P. antarctica and eight in D. mawsoni. The numbers of trypsinogen genes vary even more, between 1 and 12 (fig. 5).
There is considerable variation in the number of afpp copies, from one copy in *P. antarctica* and *H. kerguelensis* to six copies in *T. newnesi* and *G. aculeatus* (fig. 5). Together, these results indicate that afpp evolved from a c1q-like gene at the root of the Antarctic notothenioids. This coincides with the cooling of the Southern Ocean and the evolutionary origin of afgps (Chen et al. 1997a) (fig. 5).

### Genomic Organization and Synteny of afgps in Notothenioids

In the notothenioid *N. coriceps*, we identified only a single large scaffold, Scf4413, containing afpp where synteny could be reconstructed (fig. 3B). The genes flanking afpp were not syntenic with other teleost genome assemblies such as *G. aculeatus*, *T. nigroviridis*, *T. rubripes*, *D. rerio*, *O. niloticus*, and *X. maculatus* (data not shown). Afpp is juxtaposed with *tlp*, its evolutionary precursor. *tlp* is a gene encoding an enzyme which belongs to a larger family of trypsins, and we also identified a larger scaffold containing a trypsorgen gene (*tryps1*), Scf36400 (fig. 3C). This region is quite conserved across teleosts (fig. 3C). However, a higher genomic resolution is needed to pinpoint the genomic origin of the tryps gene ancestral to the afgps.

### Discussion

Here, we show that AFGPs evolved around 13–18 Ma in codfishes ancestral to the lineage including by *M. aeglefinus* to *G. morhua* in figure 1B, congruent with the cooling of the Northern Hemisphere and first glaciations 10–15 Ma (Eastman 1997). As the oceans cooled in the Northern Hemisphere, organisms faced three possibilities: migrate south to warmer waters, die out, or adapt to the new, freezing conditions. The birth of an entirely new gene, afpp, from previous non-genic DNA allowed the ancestor of afgps to evolve at a high rate and regulatory sequences are still highly similar (Chen et al. 1997a) in *G. morhua*.

Table 1. Nucleotide Composition of afgps in *G. morhua*.

<table>
<thead>
<tr>
<th>Sequence</th>
<th>Percentage of Nucleotide</th>
<th>Total Number of Nucleotides</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>T</td>
<td>C</td>
</tr>
<tr>
<td>afgp2</td>
<td>14.1</td>
<td>39.6</td>
</tr>
<tr>
<td>afgp3</td>
<td>5.4</td>
<td>49.8</td>
</tr>
<tr>
<td>afgp5</td>
<td>6.2</td>
<td>47.1</td>
</tr>
<tr>
<td>afgp6</td>
<td>10.3</td>
<td>43.3</td>
</tr>
<tr>
<td>afgp2—ex3</td>
<td>7</td>
<td>47.5</td>
</tr>
<tr>
<td>afgp3—ex3</td>
<td>2.1</td>
<td>53.4</td>
</tr>
<tr>
<td>afgp5—ex3</td>
<td>3.9</td>
<td>49.2</td>
</tr>
<tr>
<td>afgp6—ex3</td>
<td>7.5</td>
<td>46</td>
</tr>
</tbody>
</table>

Note—For each complete, putatively functional afpp, the percentage of each nucleotide for the complete cds and for only the repeat in ex3 is given, as well as the total number of nucleotides.

![Fig. 4. ISD for all genes in the *G. morhua* genome assembly. A histogram of the distribution of mean ISD for all annotated genes in *G. morhua* with the average mean ISD for afpp is shown. Average mean ISD for all genes in the *G. morhua* genome assembly was 0.36. ISD was calculated using IUPred for each amino acid position in each annotated gene in *G. morhua.*](https://academic.oup.com/mbe/advance-article-abstract/doi/10.1093/molbev/msx311/4693805/fig-4)
although the presence of \( \text{afgp} \) or \( \text{afpp} \) first (McLysaght and Guerzoni 2015; Schloëtterer 2015; McLysaght and Hurst 2016). Evolution of \( \text{afgp} \) and \( \text{afpp} \) genes can thus take two alternative routes, transcription first or ORF first (McLysaght and Guerzoni 2015; Schloëtterer 2015; McLysaght and Hurst 2016). We found no conserved non-coding elements or \( \text{afgp} \) sequences in the genomic region syntenic to \( \text{afgp} \) in figure 3A and supplementary figure S3a, Supplementary Material online. Together with the absence of orthologous genes to \( \text{afgp} \) in species closely related to \( \text{afgp} \)-bearing codfishes this is strong evidence that \( \text{afgp} \)s are \textit{de novo} genes (fig. 1B).

For a non-genic region to evolve into a gene, two key evolutionary events must occur: the region must be consis-
tently transcribed and translated into a protein, and it must 
proceed through a stretch of the \( \text{afgp} \)-repeat. In the 
ancestor of \( \text{afgp} \)-bearing codfishes, the \( \text{afgp} \)-like ex2 sequence evolved together with a stretch of the \( \text{afgp} \)-repeat. In the 
ancestral state this repeat did not have to be long, as the 
smallest functional AFGP is only 14 amino acids long in \( \text{G. morhua} \) (Hew et al. 1981). If this ancestral \( \text{afgp} \) sequence then 
became transcribed (either by utilizing another gene’s regu-
late sequence or acquiring its own) and translated, it be-
came subject to selection. The small, ancestral AFGP probably 
had a rudimentary ice-binding activity giving its carrier a fit-
ness benefit, leading to \( \text{afgp} \) eventually becoming fixed in 
the population as a new gene. If the \( \text{afgp} \)-like sequences in \( \text{P. virens} \), \( \text{T. minutus} \), and \( \text{G. argenteus} \) are true pseudogenes, 
meaning \( \text{afgp} \) first appeared in the ancestor of Gadidae 27 
Ma (fig. 1), our \textit{de novo} origin hypothesis still holds water as 
there are no \( \text{afgp} \) homologs outside Gadidae. Furthermore, 
the evolution of antifreeze function more than 10 Ma before 
the onset of freezing temperatures in the Northern 
Hemisphere is a less plausible scenario.

Two hypotheses have been proposed to explain \textit{de novo} 
gene birth; either new genes evolve through a series of 
intermediate stages between non-coding DNA and gene 
(‘continuum hypothesis’) (Carvunis et al. 2012), or arise 
from non-coding DNA that happens to be gene-like (‘pread-
aptation’ hypothesis) (Masel 2006; Wilson and Masel 2011).
Preadaptation of \textit{de novo} genes does not invoke selection on 
noncoding DNA, but refers to the conditional probability 
that given that a gene was born it likely originated from a 
noncoding sequence with more favorable characteristics for gene 
birth than the average noncoding sequence (Wilson and 
Masel 2011).
Thus, the preadaptation hypothesis of de novo gene appearance predicts that young genes are more disordered (higher ISD) than older genes, and the continuum hypothesis predicts that older genes are more disordered than younger genes. ISD in genes of different ages of origin in vertebrates ranged from 0.35 in pre-vertebrates to 0.55 in rodents, using mouse as a focal species (Wilson et al. 2017). For afgp ISD is very high (on average 0.68, supplementary table S5, Supplementary Material online) compared to the average ISD of 0.36 in the annotated genes in G. morhua (fig. 4), consistent with being young genes. Furthermore, the high GC-content in afgps (63–75%, table 1) increases the chances of obtaining a coding sequence uninterrupted by stop codons, which are TA rich, and increases the chance of transcription. Taken together with the presence of signal-peptide like sequences in Gadidae the sequences ancestral to afgps seem to have been preadapted to become genes.

The genomic processes leading to the genesis of afgp in notothenioids and codfishes seem to have been quite different. The evolution of afgp did not result in any major genomic rearrangements in codfishes as judged from the conserved synteny of the genes flanking afgp across teleosts (fig. 3A). In contrast, the evolution of notothenioid afgp seems to have involved genome rearrangements since the afgp locus is not syntenic with other teleosts (fig. 3B). afgp together with tlp—its evolutionary precursor—is flanked by genes that are not linked in other teleosts examined (fig. 3B). On the other hand, tryps, which is paralogous to tlp and afgp, is in a region with high degree of synteny with other teleosts (fig. 3C). This suggests that in the ancestor of afgp-bearing notothenioids tryps got duplicated to a new genomic location to form at least two copies of tlp, and afgp subsequently evolved from one of the tlp copies (Chen et al. 1997a). The event that resulted in the duplication of tlp may have caused reshuffling of other genes as well, ensuing the lack of synteny in the afgp locus in the notothenioid N. coriiceps.

Our data demonstrate that WGS is essential to get a complete overview of the afgp gene family, especially due to their repetitive nature and the presence of multiple copies (fig. 1), pseudogenes, incomplete duplications (fig. 1), and afgp-like sequences (fig. 2). To get complete afgp sequences suitable for resolving the organization of afgps (fig. 1A) and their syntenic context (fig. 3), long-read sequencing technologies such as PacBio is an advantage because short reads from e.g. Illumina do not span repetitive regions longer than the read length, leading to collapsed repeats and assembly gaps. The assembly challenge associated with such complex repeats may explain why afgps were not properly assembled in the first version of the Atlantic cod (G. morhua) genome (Star et al. 2011). Yet, for detecting the presence/absence and CNV of afgp, we have shown that genomes generated from short-read sequencing are sufficient.

Shared features in notothenioids and codfishes—revealed by WGS—are a common origin of afgp and high CNV, resulting from gene duplications and losses leading to unique afgp repertoires in different species (figs. 1 and 5). Since afgps consist mainly of repeats, unequal crossing over events are likely to be the driver in CNV—and further reinforced by selection in the various species (figs. 1 and 5). Furthermore, there have been pseudogenization and loss of functional afgps in both codfishes (fig. 1) and notothenioids (fig. 5) (Miya et al. 2016). In both lineages there seems to be a gene dosage effect related to the harshness of climate different species are exposed to, yet there are still some notable differences. In notothenioids, the evolution of afgp was a matter of survival, as they became isolated in the freezing Antarctic waters at the onset of the circumpolar current. In the Antarctic notothenioids, the number of afgps ranges from at least one to eight (fig. 5). Most notothenioid species are demersal or benthopelagic, including the species in figure 5, except for the two pelagic species P. antarctica and D. mawsoni. These species have about twice as many afgps as the other species (fig. 5), indicating that a larger afgp repertoire is associated with a pelagic distribution. This could be because pelagic species are exposed to more variable abiotic factors requiring more diverse afgps, or a larger diversity of afgps is associated with the physiology of more active, pelagic species. However, the high-Antarctic species T. newnesi and G. acuticeps have the same number of afgps as the sub-Antarctic H. kerguelensis. To fully determine if there is a gene dosage effect, CNV data for more taxa are required. Given that gene dosage effects have been demonstrated in freeze-preventing zona pellucida proteins in notothenioids (Cao et al. 2016), an analogous scenario for afgps seems plausible. The notothenioid P. guntheri has completely lost afgp (Miya et al. 2016), and we cannot find trace of any afgp pseudogene in its genome (fig. 5).

This species has colonized waters north of the polar front and is not exposed to freezing temperatures (Miya et al. 2016). In contrast, the Arctic is not an isolated system and it is possible to escape freezing waters by swimming south or down to deeper waters. Furthermore, many teleost species thrive in the Arctic without afgps. The main advantage of afgps might be allowing its bearer to escape both predation and competition in freezing waters unavailable to animals without special adaptations. Consequently, as A. glacialis and B. saisda are Arctic specialists occupying latitudes north of 60 and 70°N, respectively, they possess more afgps than G. morhua and G. chalcogrammus, which are not restricted to the high Arctic and have a broader thermal niche (Eschemeyer and Fricke 2017). In the most parsimonious scenario, the loss of AFGP function of M. merlangius and M. aeglefinus was a single event in the ancestor of these species (fig. 1B). Their distribution ranges between latitudes of 72–35°N for M. merlangius and 79–35°N for M. aeglefinus (Eschemeyer and Fricke 2017). Part of these regions can have freezing temperatures, but not throughout the water column. If the ancestor of these species had a more southerly distribution or avoided freezing waters by for instance swimming deeper, relaxed selection on afgp could have led to pseudogenization. There could also have been selection against this gene due to a harmful effect of ice build-up, which has been demonstrated in notothenioids (Cziko et al. 2014), or simply because of energy expenditure associated with production and circulation of AFGP. Alternatively, it could be lost due to genetic drift. However, given the large effective
population sizes observed for *M. aeglefinus* (Tørresen et al. 2017a) we find this a less likely scenario.

In notothenioids, antifreeze activity is enhanced by the presence of AFPP. Although not essential, AFPP can contribute significantly to the total antifreeze activity, especially in species exposed to freezing temperatures year-round (Fields and Devries 2015). Here, we show that *afpp* most likely evolved from a *c1q*-like gene concurrently with *afgp* 13–20 Ma (fig 5). This coevolution makes the evolution of antifreeze more complex and raises the question whether *afpp* evolved just after or simultaneously as *afgp*. In codfishes *afpp* is not present, according to a PhD thesis abstract (Jin 2003) and given the independent origin of *afgp* in these lineages it seems unlikely codfish should possess *afpp*, although codfishes could have a protein with an analogous function to *afpp*.

Most likely, codfish *afgp* arose from entirely non-coding DNA making them type I de novo genes, according to the classification in McLyasgh and Hurst (2016). Nototheniid *afgp* is a type II de novo gene, as part of its sequence, the signal peptide, has previously been under selection, but not the region with an acquired new function (i.e. antifreeze). The *afgp*-repeat of the sequence arose from intronic, non-coding DNA (Chen et al. 1997a). Intriguingly, genes encoding AFP type I (AFPI) in cunner, snailfish, sculpins, and flounder has no homologous gene (Graham et al. 2013) and are therefore also candidates for de novo gene evolution. As antifreeze is a completely new function in these organisms even a protein with rudimentary antifreeze function can become selectively advantageous and set off the process of evolutionary tinkering, finally ending up with the plethora of AFPs detected to date. De novo genes are often involved in response to biotic and abiotic stress, being related to functions that require rapid change to a new selective regime (Schlötterer 2015). This could explain the apparent prevalence of *de novo* gene evolution in freeze avoidance in teleosts. Interestingly, in animals there is a peak of emergence of new genes around 800 Ma, which precedes the major radiations of animals in the time period Earth underwent a series of freezing cycles (Tautz and Domazet-Lošo 2011).

This is the first study employing WGS data in a phylogenetic context to shed new light on the evolution of antifreeze genes in codfishes and notothenioids. Using different types of genomic data we have been able to fill some of the gaps in the intriguing evolutionary history of *afgps* in codfishes and notothenioids and compare two paths of *de novo* gene birth. Even though *de novo* origin of genes is currently seen as more prevalent than previously thought, examples of new genes being essential for survival such as *afgp* in codfishes and notothenioids are few. As more high quality genomes are being sequenced we will get a better picture of which functions are underpinned by *de novo* genes across species.

**Materials and Methods**

**Annotation of *afgp*** in *G. morhua* and *M. aeglefinus*

For *G. morhua* and *M. aeglefinus* we have annotated genomes assemblies of high contiguity denoted as gadMor2 (Tørresen et al. 2017b) and melAeg (Tørresen et al. 2017a), respectively. To determine the organization of *afgps* in these genomes we used BLAST (v. 2.2.26+) (Altschul et al. 1990) with queries from *G. morhua* and *B. saida* (Zhuang 2014). Our query sequences contain both non-coding sequences like the putative promoter, 5’UTR, and 3’UTR sequences, as well as protein-coding sequences divided into the signal peptide in ex2, and the ex3 which contains 84 nt of non-repetitive sequence and sequences encoding the tripeptide-repeats in the mature *afgp* (annotation of gene organization based on gene-prediction in Zhuang 2014). Using these different parts of *afgp* also allowed us to identify potentially homologous regions in the genomes. We BLASTed using both proteins (tBLASTn) and nucleotides (BLASTn) as queries against nuclear databases for each species. We also used the option BLASTn-short, which is more optimal to detect the short sequences used as queries (Altschul et al. 1990). For all BLAST searches we used an E-value cutoff of 0.1 and otherwise default options, unless explicitly noted.

We analyzed codon usage bias and GC-content of the *afgps* using MEGA v.7 (Kumar et al. 2016). We also calculated the GC-content of all annotated genes in the *G. morhua* genome assembly (gadMor2) (Tørresen et al. 2017b). Codon usage bias was calculated as the observed frequency of a codon divided by the expected one (RSCU values).

The degree of ISD was calculated using IUPred (Dosztanyi et al. 2005) for *afgps* and all other annotated genes in the gadMor2 assembly. We calculated ISD for sequences translated into proteins using all three ORFs.

**Copy Number Estimation and Evolutionary Origin of *afgp*** in Codfishes

We used BLAST to annotate *afgp* in the genomes of 23 codfishes available (Malmström et al. 2016, 2017). However, as these genomes are assembled from only short reads, *afgps* with their long repetitive regions are not in contiguous sequences in these species. Hits against *afgp* repeats were thus only used to detect presence/absence of *afgp*. To establish *afgp* copy number we used the signal peptide sequences, as well as the non-coding sequences of the promoter, 5’UTR and 3’UTR. However, gadMor2 5’UTRs gave significantly more hits than 3’UTR and were excluded from the analysis. Annotation was validated by aligning the reported BLAST hit regions and generating phylogenetic trees using maximum likelihood (Tamura-Nei model, partial deletion of missing data, 1,000 bootstraps) in MEGA v.7 (Kumar et al. 2016).

To distinguish between *afgps* and *afgp*-like sequences, a phylogenetic tree was constructed with all putative *afgp* sequences which included ex1, ex2, and the start of ex3 from *G. chalcogrammus*, *B. saida*, *A. glacilis*, *M. merlangius*, *P. virens*, *T. minutus*, and *G. argenteus*, and *afgps* and *afgp*-like sequences from *G. morhua* and *M. aeglefinus*. The main topology of the phylogenetic tree was constructed using a Bayesian method in MrBayes 3.2.2 (Ronquist and Huelsenbeck 2003) with standard priors, four chains of simulations for 1×10⁶ generations sampling every 1×10⁵ generation. For each run convergence was considered reached when the likelihood scores leveled off asymptotically. Trees
sampled before convergence were discarded and support (posterior probability) was calculated based on a consensus of the remaining 1,502 trees. Bootstrap support values were obtained by constructing a phylogenetic tree with maximum likelihood (Tamura-Nei model, partial deletion of missing data, 1,000 bootstraps) in MEGA v.7 (Kumar et al. 2016).

To determine evolutionary origin the presence of afgp repeat as well as copy number of promoter, signal peptide ex2, beginning of ex3 and 3′UTR were mapped on a time calibrated phylogeny from (Malmstrøm et al. 2016). Furthermore, we searched for the presence of signal peptide ex2, beginning of 5′UTR, 3′UTR, and the antifreeze repeat sequence in ex3 in RepBase (Bao et al. 2015).

Assembly of Notothenioid Genomes
To obtain representatives from most lineages of notothenioids (Colombo et al. 2015), we did WGS for the following eight species; E. maclownus, P. antarctica, P. guntheri, T. newnesi, H. kerguelensis, A. skottbergi, G. acuticeps, and C. aceratus. We sequenced paired end libraries with an average insert size of 350 bp (2 × 150 bp reads on Illumina HiSeq 2000) with coverage ranging from 31 to 67× (average coverage 44×). The Celera assembler (Miller et al. 2008) was used to assemble the genomes, with contig N50 ranging from 5 to 9.6 kb with an average of 6.3 kb. CEGMA (Parra et al. 2009) and BUSCO (Simão et al. 2015) were used to evaluate gene completeness; CEGMA gave, on average, complete or partial hits for 69% of the conserved eukaryotic genes included in the CEGMA analysis and BUSCO gave, on average, 68% of the conserved genes belonging to the Actinopterygii lineage in the BUSCO analysis. A list of species with relevant genome statistics is given in supplementary table S6, Supplementary Material online. Sequences are deposited in ENA.

Copy Number Estimation in Notothenioids
The afgps in notothenioids consist of a signal peptide (ex1) and tripeptide repeats of various lengths (ex2). We used both exons to BLAST against the genomes of E. maclownus, P. antarctica, P. guntheri, T. newnesi, H. kerguelensis, A. skottbergi, G. acuticeps, and C. aceratus, as well as the published genome of Notothenia coriiceps (Shin et al. 2014). The hits against ex2 were only used to determine presence/absence of afgp. Because afgp are homologous with tlp, we used the signal peptide from tlp, as well as the related sequences encoding trypsinogen-1 (tryp1) and trypsinogen-3 (tryp3), as query sequences. Query sequences were obtained from D. mawsoni (Nicodemus-Johnson et al. 2011). We then mapped the number of signal peptide copies from these genes on a phylogeny from (Colombo et al. 2015), together with copy number estimates from (Nicodemus-Johnson et al. 2011) for D. mawsoni. According to Nicodemus-Johnson et al. (2011) there are two haplotypes in D. mawsoni with different copy numbers of afgp, tlp, tryp1, and tryp3. We chose copy numbers from haplotype 2 (accession number HQ447060) (fig. 5), as we do not trust the evidence for haplotype 1.

We estimated the number of afgps using BLAST hits against AFPP amino acid sequence from G. acuticeps (Yang et al. 2013). As the different exons were usually on different utgs, we used the putative first exon to count the number of copies of afpps, using BLAST sequence identity to distinguish afpp from related gene sequences. Copy number for each species was then mapped onto the phylogeny in figure 5.

Synteny of afgp and Trypsinogen Locus
We investigated the flanking sequences of afgp in G. morhua (gad/Mor2), M. aeglefinus (melAeg) and N. coriiceps (Shin et al. 2014); in the N. coriiceps we also investigated sequences flanking tryp1 and tryp3. In codfish we delimited synteny analyses between the genes ppp2ca and adam19; in N. coriiceps we delimited synteny analyses between the genes nr2f6 and nkap5l for afgp and lipeb and apoea for tryp3. We then identified homologous regions in release 86 of the Ensembl database (Yates et al. 2016) for the following species; tilapia (Oreochromis niloticus), platyfish (Xiphophorus maculatus), three-spined stickleback (Gasterosteus aculeatus), tetrodon (Tetraodon nigroviridis), and fugu (Takifugu rubripes), as well as the genome of the northern pike (Esox lucius) (Rondeau et al. 2014). In cases where the automatic annotation was incomplete we manually annotated genes by BLASTing against the Uniprot and Ensembl databases.

mVista comparisons between species were carried out using LAGAN alignments (Frazer et al. 2004).

Supplementary Material
Supplementary data are available at Molecular Biology and Evolution online.

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Author Contributions
S.J. and H.T.B. initially conceived and designed the study, with input from K.S.J. and W.S. Samples for the eight notothenioid genomes were provided by W.S. and R.H. The genome assembly pipeline was set up by O.K.T. and carried out by O.K.T. and H.T.B. Annotation of afgp genes in codfishes was carried out by H.T.B. with assistance from M.H.S. Genome-mining, phylogenetic analyses and construction of all figures and tables were done by H.T.B. Synteny analyses were carried out by H.T.B. and O.K.T. The manuscript was written by H.T.B. together with S.J. and K.S.J, with additional input from all other authors.

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References


