The evolution of the 9aaTAD domain in Sp2 proteins: inactivation with valines and intron reservoirs

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Abstract

The Sp1 transcription factor has been defined as glutamine-rich activator. The Nine amino acid TransActivation Domains (9aaTAD) have been identified in numerous transcription activators. Here, we identified the conserved 9aaTAD motif in the Sp1 and in all nine members of SP family with broad natural 9aaTAD variations. We showed by the amino acid substitutions that the glutamine residues are completely dispensable for 9aaTADs function. We described the 9aaTAD domains' origin and evolutionary history. The ancestral Sp2 gene with inactive 9aaTAD has duplicated in early chordates and created new paralogs Sp1, Sp3 and Sp4. We discovered that the accumulation of valines in the 9aaTADs correlated with the domain inactivation. The Sp2 activation domain, whose dormancy have lasted over 100 million years during chordate evolution, enabled later diversification in the Sp1-4 clade, including both repressors and activators. The new paralogs Sp1 and Sp3 activation domains have regained their original activator function by loss of valines in their 9aaTADs.

Keywords: activation domain, 9aaTAD, SP, Sp1, KLF, WT1, Gal4, Met4, Gcn4 and p53.

INTRODUCTION

Our longstanding effort has been to determine the pattern of trans-activating sequences in the eukaryotic activators. Previously, we reported successful identifications of the Nine amino acid TransActivation Domains, 9aaTADs, in a large set of the transcription activators that universally recruit multiple mediators of transcription (1–11).

We and others have shown that the activation domains have the competence to activate transcription as small peptides (above 9 to 14 amino acids long) in over 40 activators including Gal4, E2A, MLL and p53 (12–17). Although the activation domains have enormous variability, they are universally recognized by transcriptional machinery throughout eukaryotes (18). Currently, all our tested human 9aaTAD activation domains were shown to be functional in yeast. Therefore we considered universal function of 9aaTAD activation domains in eukaryotes as a further associated property of the 9aaTAD family (12, 14, 18, 19). In addition to the amino acid pattern and universal function in eukaryotes, the 9aaTAD activation domains are further characterized by tandem hydrophobic clusters separated by a hydrophilic region (12, 14). The 9aaTAD domains are well balanced with hydrophilic amino acids, which might be either positively or negatively charged. From the structural data for the E2A and MLL activation domains in complex with the KIX domain, we observed that 9aaTAD domains formed short helices whose length varies from 9 to 12 aa (13). Online 9aaTAD prediction (using a residue position matrix search) is available on www.piskacek.org. The curated 9aaTAD activation domains had been annotated on protein database UniProt (by database search for 9aaTAD).

Earlier, the activation domains have been categorised and their functions were linked to over-represented amino acids (20). The aspartate activation domains were described as acidic (21) or glutamine-rich (22, 23) or proline-rich activation domains (24, 25). Accordingly, the Gcn4, Gal4 and p53 activation domains have been designated as acidic activators (26–29). The next studies revealed some controversies and demonstrated the importance of the hydrophobic amino acids for Gcn4 (30–33) and p53 activators (8, 34–40). Similarly, in the original report for the glutamine-rich activator Sp1(41), the importance of hydrophobic amino acids was already recognized, regardless of the overrepresented glutamines. Nevertheless, the designation as acidic or glutamine-rich activation domains persists to date (42–49).

In the human genome, there are about 1,691 annotated transcription factors, divided into 68 groups according to their conserved DNA binding domain (50). The C2H2-type zinc finger is the largest group (682 members), which includes the evolutionally conserved family of KLF activators (Krüppel-like factors). The SP activators (Specificity proteins Sp1-9) belong to a new evolutionary branch derived from the ancestral KLF family. The SP activators have been linked to cell proliferation, embryonic development, tissue differentiation, Wnt signaling pathway, metabolism, and their dysregulation has been implicated in a number of human diseases and cancers (51–56). This report has focused on the SP family and followed the 9aaTAD domain's evolution.

MATERIALS AND METHODS

Constructs. The construct pBTM116-HA was generated by an insertion of the HA cassette into the *EcoRI* site of the vector pBTM116. The constructs G1-G45 and H1-H45 were generated by PCR and sub-cloned into pBTM116 *EcoRI* and *BamHI* sites. All constructs have a spacer of three amino acids inserted into the *EcoRI* site; peptide GSG. All constructs have been sequenced by Eurofins Genomics. Further detailed information about constructs and primer sequences are available on request.

Assessment of enzyme activities. The β -galactosidase activity was determined in the yeast strain L40 (57, 58). The strain L40 has a chromosomally integrated *lacZ* reporter driven by the *lexA* operator. In all hybrid assays, we used 2 μ vector pBTM116 for generation of the LexA hybrids. The yeast strain L40, *Saccharomyces cerevisiae* Genotype: *MATa ade2 his3 leu2 trp1 LYS::lexA-HIS3 URA3::lexA-LacZ*, is deposited at ATCC (#MYA-3332). The average value of the β -galactosidase activities from two independent transformants is presented as a percentage of the reference with the standard deviation (means and plusmn; SD; n = 2). We standardized all results to the previously reported Gal4 construct HaY including the 9aaTAD domain with the activity set to 100% (14).

Databases used in the study. UniProt, ExPASy, NCBI, KEGG <http://www.genome.jp>, Japanese Lamprey Genome Project <http://jlampreygenome.imcb.a-star.edu.sg/blast/>, Sun Yat-Sen University Lancelet Genome Project <http://genome.bucm.edu.cn/lancelet/blast.php>, Compagen Genomics Platform <http://www.compagen.org/blast.html>, Florida University Neurobase <https://neurobase.rc.ufl.edu/>, UCSC genomic annotation <https://genome.ucsc.edu>.

RESULTS

The 9aaTAD activation domains occur in proteins previously used to define acidic, glutamine-rich (Sp1) or proline-rich activator classes. The Gal4 activation domains have been reported as acidic (aspartic acid-rich), the Sp1 activation domain as glutamine-rich, and the NFIC activation domains as proline-rich (21, 25, 41, 44). However, the importance of the acidic aspartic residues for Gal4 function addressed already by the Johnston group (59). Similarly for Sp1, the authors have demonstrated a greater importance of hydrophobic amino acids, rather than the overrepresented glutamines (41).

Previously, we have identified the 9aaTAD activation domains in the Gal4 (17) and in p53 acidic activators (14). In this study, we aimed to determine the 9aaTAD presence in other members of the SP family, where the 9aaTAD position would correspond with the Sp1 region 467-472 that has been shown to be essential for transcriptional activation (41). Using our online 9aaTAD prediction, we obtained two positive prediction hits for Sp2 (using the most stringent pattern and with 83% and 92% match for the 9aaTAD prediction). Most importantly, the latter match (sequence GEVQTVLVQ in the Sp2 region 361-369) corresponds with the glutamine-rich activation domain of Sp1 (region 467-472).

We have then generated LexA constructs, which included the DNA binding domain LexA and only the 9aaTAD from all nine SP activators and tested them for the ability to activate transcription (**Figure 1**

and 2). The predicted Sp1 activation domain includes glutamines, which are not conserved in Sp5, 6, 7, 8, 9 (**Figure 2**) and are not generally conserved in other 9aaTAD domains. Similarly, the acidic activation domain of the Gal4 activator includes acidic aspartic acids, which are not generally conserved in other 9aaTAD domains (12, 14, 17). In order to prove that the function of the 9aaTADs was not solely dependent on overrepresented aspartates nor on glutamines (which are present in the Gal4 and Sp1 activation domains), we have substituted all Gal4 aspartic residues for glutamines (construct Gal4-Q, non-acidic Gal4 9aaTAD) and all Sp1 glutamines and asparagine for aspartic acid residues (construct Sp1-Ac, acidic Sp1 9aaTAD), and showed their ability to activate transcription (**Figure 1**).

By using our online 9aaTAD prediction, we have searched for the 9aaTADs in the proline-rich activation domain of the NFIC / CTF activator (region 388-487). We have identified two overlapping 9aaTAD motifs (sequences DPLK DLVSL and KDLV SLACD with 83% and 92% match for the 9aaTAD prediction) in the NFIC proline-rich region (the pattern for clusters of less stringent repeats was used). Moreover, we also identified both corresponding 9aaTAD motifs in the very distal orthologs SkoNFI (from *Saccoglossus kowalevskii*, acorn worm), and cinNFI (from *Ciona intestinalis*, sea squirt). Furthermore, in the NF family, prolines are not conserved in any position of the human paralogs (NFA, NFB, NFIC, NFIX), nor in the SkoNFI or cinNFI orthologs, however the 9aaTADs were well conserved in all of them (**Figure 1**). We have generated a LexA construct, which included only the 9aaTAD from the NFIC activator, and showed its ability to activate transcription (**Figure 1**).

The 9aaTAD activation domain in the human SP family. As described above, we have identified the 9aaTAD motif in the human transcription factor Sp2 and consequently, we have aligned all human SP paralogs and found conservation of the 9aaTAD motif in all nine members of the family (**Figure 2**).

The human SP transcription factors share sequence homology in their activation domains and could be divided into two clades (**Figure 2**); i) the Sp1-4 clade with a single tryptophan (single letter code W) in the activation domain (41), excluding the Sp2, whose activation domain lacks tryptophan, and ii) the Sp6-9 clade with two tryptophans in the activation domain, excluding Sp5, the sequence of which differs significantly from other members of Sp6-9 clade.

We have generated LexA constructs h01 - h09, which included only the 9aaTADs from Sp1 to Sp9 proteins, and tested them for the ability to activate transcription (**Figure 2**). The members of the SP family were reported to be activators of transcription (52), with the exception of Sp2, which is a weak activator with little or no capacity for additive or synergistic transactivation (60–66), and functions as a repressor (67). Apart from the h02, h04 and h09, all other constructs h01, h03, h05, h06, h07 and h08 showed strong capacity to activate transcription (**Figure 2**). The deactivated 9aaTADs correlated with the accumulation of valines in the Sp2, Sp4 and Sp9 activation domains and follow a V- Q/H amino acid pattern. Similarly, we found an inactive Sp7 activation domain in the spider mite (*Tetranychus urticae*), where the 9aaTAD deactivation correlated with valine acquisition and followed the V-Q/H amino acid pattern (**Suppl. Figure S1**). We could also identify a 9aaTAD deletion instead of deactivation (**Suppl.**

Figure S2). The prime aim of this study was the identification of functional activation domains. Those which were unable to activate transcription under our experimental conditions are also reported, but without further investigation. Nevertheless, the expression of inactive constructs was monitored by Western blotting (**Suppl. Figure S3**). Of note, in this study, we did not test the entire proteins but only the distinct regions predicted to have activation function. For example, the 9aaTAD from human Sp2 failed to activate transcription in our assay. Our result is compliant with previous reports, finding Sp2 a weak activator with little or no capacity for additive or synergistic transactivation (65). The Sp2 was reported to specifically bind DNA, occupies distal enhancer elements (68–70) and functions as repressor (67). Differently, human Sp1 and Sp3 were reported as activators of transcription (71–73).

Evolution of the 9aaTAD activation domain in SP proteins began in Sea Sponges about 780mil years ago. The SP family is a new branch derived from the KLF family. The ancestral *SP genes* appear in demosponges ~800 million years ago (Mya) (74, 75). The SP family conservation is remarkably strong, particularly in the region of the DNA binding domains. We have followed the diversification of activation domains in SP family proteins in both vertebrates and invertebrates (**Suppl. Figures S4 and S5**) and showed diversification in early-branching metazoan clades Sp1-4 (**Suppl. Figure S6A**), Sp6-9 (**Suppl. Figure S6B**), Sp5 (**Suppl. Figure S6C**) and Sp2 (**Figure 3**) in the following paragraphs.

Using blast searches (see list of Databases used in Materials and Methods), we have identified the 9aaTAD activation domains in human SP activators and their distal ancestors, including in the hemichordate *Saccoglossus kowalevskii* (acorn worm, early deuterostomes), in the crustacean *Daphnia pulex* (water flea, arthropods; branch of ecdysozoans, protostomes), in the cnidarian *Acropora digitifera* (coral; branch of eumetazoans about 700 Mya), in the poriferan *Oscarella carmela* and *Amphimedon queenslandica* (demosponge; early branch of metazoan about 780 Mya) (74) (**Figure 2**).

We generated LexA constructs for the activation domains of ancestral *SP genes*, designated as *SkoSp2* and *SkoSp5* (*Saccoglossus kowalevskii*); *DpuSp2* and *DpuSp5* (*Daphnia pulex*); *AdiSp2*, *AdiSp5* and *AdiSp69* (*Acropora digitifera*); and *OcaSp2*, *OcaSp59* (*Oscarella carmela*) and tested them for the ability to activate transcription (**Figure 2**) (the designation *Sp69* and *Sp59* reflects uncertainty of origin). *SkoSp5* and *DpuSp5* genes are almost identical to human *Sp7*, and therefore omitted. We tested and confirmed that most of constructs showed the capacity to activate transcription. The 9aaTAD of the *Saccoglossus SkoSp2* (construct w00, with accumulated valines within the 9aaTAD domain) was fully deactivated (**Figure 2**).

Conservation of the 9aaTADs in the SP family proteins in vertebrates. Next, we focused on the evolution of the SP family in vertebrates. As representative examples for SP family evolution in vertebrates, we selected the cartilaginous fish *Callorhynchus milii* (elephant shark), ray-finned fish *Danio rerio* (zebrafish), lobe-finned fish *Latimeria chalumnae* (coelacanth), and bird *Gallus gallus* (progenitor of the domestic chicken), and compared their 9aaTAD activation domains with the human ones (**Suppl. Figure S5**). Most surprisingly, we have found a remarkably strong family conservation of

the 9aaTADs in *Sp1*, *Sp3*, *Sp4*, *Sp5*, *Sp6*, *Sp7*, *Sp8* and *Sp9*, but not in *Sp2*. Furthermore, the *Sp7* gene was missing altogether in *Gallus gallus*, but not in all birds. The missing *Gallus Sp7* was substituted by the *Pseudopodoces humilis* ortholog in **Suppl. Figure S5**. The summary of the bird *Sp7* genes, which are missing in some but not all birds, are shown in **Suppl. Table 1**.

Throughout evolution, the loss of the *Sp7* gene has occurred in several bird clades. Importantly, *Sp7* was lost only in some passeriformes. The *Sp7*-less passeriformes members (crow, flycatcher and finch) could have not been the ancestral for other *Sp7*-less clades e.g. falconiformes (76). Therefore, the loss of *Sp7* gene was not a single event during the bird evolution, suggesting a genetic selection in the phylogenetic distribution, rather than simple random events.

The SP1-4 clade diversification. The SP1-4 clade found in early-branching metazoans (**Suppl. Figure S6A**) showed the same preference for a single tryptophan in position p3 of the 9aaTAD activation domains as in vertebrates (**Suppl. Figures S5**). However, there are also exceptions, with twin tryptophan in arthropods, *Strigamia maritima* (Leach) which is typical for the SP6-9 clade (**Figure 2**) and a tryptophan-free activation domain in molluscs *Biomphalaria glabrata*. Thus, the natural occurring 9aaTAD variance has shown that tryptophans, which dominated in the SP family, are not essential for 9aaTAD function. Similar observation was done for the 9aaTAD activation domain in p53 (14).

The SP6-9 clade diversification. The *Sp69* gene (the designation *Sp69* reflects uncertainty of origin, **Figures 2**) has already emerged in radiates and their 9aaTADs have two tryptophans in positions p3 and p4, which are well conserved in vertebrates (**Suppl. Figure S5**). The hemichordate *Saccoglossus kowalevskii* (acon worm) has been the only solitary member of the SP6-9 clade, with the *SkoSp69* gene, which gave rise to the SP6-9 clade (gene duplication). Thus, *Callorhinchus milii* (elephant shark) already has four *Sp69* paralogs, including the *CmiSp6-9* genes. Similarly, the *SkoSp2* gene is a solitary member of the SP1-4 clade in the *Saccoglossus kowalevskii*. Higher in evolution, *Callorhinchus milii* already has four *Sp2* paralogs including *CmiSp1-4* (Phylogenetic tree, **Suppl. Figure S4**).

The Sp5 evolution. From the sequence similarity and from the phylogenetic tree (**Figure 2 Suppl. Figure S4**), we predicted that the SP5 clade has emerged already in the earliest metazoans, before the SP6-9 clade (**Figure 2**). The DNA binding domain signature in the poriferan *Oscarella carmela* *OcaSp59* (**NRCQ**-CPNC, designation *Sp59* in *Oscarella carmela* pointed to a common ancestor of the latter *Sp5* and *Sp6-9* clades) best matches the cnidarian *Acropora digitifera* *AdiSp5* (**RRCR**-CPNC), the protostome *Daphnia pulex* *DpuSp5* (**RRCR**-CPNC), the hemichordate *Saccoglossus kowalevskii* *SkoSp5* (**RRCR**-CPNC) and is conserved up to human *hSp5* (**RRCR**-CPNC). However, it less matches the diverged members of the SP6-9 clade; *AdiSp9* (**ATCD**-CPNC) or *hSp6* (**TVCR**-CPNC), *hSp7* (**SSCD**-CPNC), *hSp8* (**ATCD**-CPNC), and *hSp9* (**ATCD**-CPNC) (**Figure 2**). The members of the SP5 clade also showed a preference for two tryptophans in positions p3 and p4 of their activation domains. The *Sp5* and *Sp69* genes already largely diverged in already in cnidarian (*Acropora digitifera*; corals) and formed a separate clades. In protostomes, the SP5 clade shows the largest diversity we have ever

observed for the 9aaTAD activation domains (**Suppl. Figure S6C**). We have generated constructs for selected members of the SP1-4 (**Suppl. Figure S6A**), SP6-9 (**Suppl. Figures S6B**) and SP5 clades (**Suppl. Figures S6C**). All tested constructs have the capacity to activate transcription.

The Sp2 evolution. Next, we have generated constructs shown in (**Figure 3**) for the Sp2 activation domains including the w63 for *Amphimedon queenslandica* (demosponge, poriferan), constructs w69 for *Acropora digitifera* (coral, cnidarian), w00 for *Saccoglossus kowalevskii* (acorn worm, hemichordate), construct w96 for *Callorhinchus milii* (elephant shark, cartilaginous fish), construct w38 for *Danio rerio* (zebrafish, ray-finned bony fish), w40 for activation domains that are common for *Latimeria chalumnae* (coelacanth, lobe-finned bony fish), to American alligator and to gecko (reptiles), to *Gallus gallus* and egret (birds), to platypus (monotremates) and to Tasmanian devil, opossum and koala (marsupials), construct w37 for exceptional loon Sp2 activation domain (birds), construct h02 for Sp2 activation domains common to elephants and humans (representing two separate clades of placental mammals: atlantogenates and boreoeutheries) and construct w81 for the exceptional gibbon Sp2 activation domain (primates). Furthermore, we generated constructs w22 for the Sp1 activation domain 9aaTAD of *Callorhinchus milii*, which is an early diversified Sp2 paralog in the SP1-4 clade.

Interestingly, not all tested Sp2 constructs showed the capacity to activate transcription. There are periods in metazoan evolution (from hemichordates to chondrichthyes and from early placental mammals to humans), in which the Sp2 activation domains have been deactivated. The deactivation of the 9aaTADs correlated with the accumulation of valines in their activation domains and followed an amino acid pattern of V-Q/N/K. Although tryptophans dominated in the SP activation domains (**Figures 2**), we have also found a tryptophan-less Sp2 activation domain in the sarcopterygians (in the lobe-finned bony fish *Latimeria chalumnae*) and in all their successors (higher vertebrates) (**Suppl. Figure S5**). We have then generated alignments and a simplified phylogenetic tree for *Saccoglossus* *SkoSp2*, *Rhincodon typus* *RtySp2* and *Callorhinchus milii* *CmiSp2* (**Figures 2**). The close orthologs of *SkoSp2* seem to be *CmiSp2* and *RtySp2*, which also correlated with close similarities in their activation domains (**Suppl. Figure S4**).

In summary, we conclude that *Saccoglossus* *SkoSp2* is the ancestral gene for the clade SP1-4. In chondrichthyes (cartilaginous fish) after Sp2 gene duplications, Sp1 regained activator function by *devalinisation* (substitution of valines in the 9aaTAD for other amino acids), which remained during evolution all the way to humans. The Sp2 has regained some activator function later in evolution (in sarcopterygians), but only up to the marsupials, not to the placentals (**Figure 3**).

From the phylogenetic tree (**Suppl. Figures S4**), we have anticipated that the Sp2 gene originated directly from one of two ancestral SP genes found already in demosponges (Sp2 and Sp59; demosponges belong to early branched poriferan branched around ~800 Mya) (**Figure 2**). Also, in the hemichordate *Saccoglossus kowalevskii* (acorn worm, belonging to early branched deuterostome, ~670 Mya), the Sp2 gene is the solitary member of the SP1-4 clade. From above, the Sp2 gene duplication gave rise to the SP1-4 clade found in jawed cartilaginous fish (chondrichthyes) such as *Callorhinchus milii* (elephant

shark) and *Rhincodon typus* (Whale shark). The activation domain of this *SkoSp2* gene with the sequence VNWQ-PVQVQ sustained conserved nearly fully in the *Rhincodon RtySp2* activation domain (VNWQ-AVQVK i.e. 7 identical and 8 similar residues) and almost in *Callorhinchus milii CmiSp2* activation domain with the sequence VNWQ-TLQVK. The activation domain of this *SkoSp2* gene (as well as the entire gene, phylogenetic tree **Suppl. Figures S4**) is less similar to other genes of the *Callorhinchus milii Sp1-4* clade. The *SkoSp2*, *CmiSp2* and *RtySp2* have accumulated valines in their activation domains, which are then associated with the loss of their transcription activating function. After gene duplication, these valines were substituted by other amino acids (*de-valinisation*) in the activation domains of *CmiSp1*, which therefore regained their activation function. However, the *CmiSp2* remained deactivated (**Figure 5**).

In the ray-finned bony fish *Danio rerio* (actinopterygians, see their low diversification in **Suppl. Figure S7**) and in the lobe-finned bony fish *Latimeria chalumnae* (sarcopterygians) we found a common modification of the *Sp2* activation domain (loss of valines in positions p1 and p8 by deletions at p1 and p2, and substitutions of p8). While the modifications are absent in the jawed cartilaginous fishes (chondrichthyes), the modifications must be ancestral for all bony fishes (osteichthyes) but not for all jawed fish (gnathostomes) (**Figure 5**). Both *Sp2* became re-activated, which correlated with a loss of two out of three valines within their activation domains.

The *Sp2* gene duplication in *Takifugu* and *Tetraodon*. A fish-specific whole-genome duplication is present in some ray-finned fish lineages (actinopterygians) that branched from the sister lineage, lobe-finned fishes (sarcopterygians) about 450 Mya but is not present in terrestrial vertebrates (77). We have identified duplicated *Sp2* genes (designated as *Sp2a* and *Sp2b*) in the teleost lineage of the ray-finned fishes takifugu and tetraodon, but not in other teleosts, such as *Danio rerio* (zebrafish) and *Oryzias latipes* (japanese medaka), nor in cartilaginous fish *Callorhinchus milii* (elephant shark), nor in lobe-finned fish *Latimeria chalumnae* (coelacanth), nor in terrestrial vertebrates (reptiles / alligator, birds / chicken, or mammals / opossum, mouse or human) (**Suppl. Figure S8**).

Both *Sp2* genes duplicated in takifugu and tetraodon lost their exons coding for their activation domains. These genes (*Sp2b* genes) were repaired from their intronal DNA, which generated new exons without obvious 9aaTAD activation domains. The origin of the new exons could be well recognized from their ancestral introns (present in takifugu and tetraodon *Sp2a* genes) (**Suppl. Figure S8**). The repairs occurred independently rather than originating from a common ancestor of the tetraodontiformes, because the *Sp2a* intronal sequences of takifugu and tetraodon lack sequence similarity. The relevant *Sp2* exon replacement could also be found in gibbon, in rock hyrax and in crane *Sp2* (**Figure 7** and **Suppl. Figure S9**).

We have investigated the evolution of the new *Sp2* activation domains in detail and found that their intron sequences are reservoirs of activation domains. The introns have full readiness for activation domain repair by presence of i) a copy of exon-intron sequence border, which might promote DNA recombination in a desirable position, ii) a copy of the original 9aaTAD activation domain, which might

be used as a backup for random loss of exonal activation domain and iii) repeats resembling the 9aaTAD domains in all three reading frames, which might facilitate *de novo* formation of another activation domain (the tested construct w35 including activation domain coded by **the tetraodon** intron, for which we have observed the capacity to activate transcription) (**Suppl. Figure S8**).

Although the *Sp2a* gene in tetraodon has two intronal activation domain back-ups ready to use (**Suppl. Figure S8**), these domains were not involved within the *Sp2b* gene rearrangement. We suspect that these events have been rather conditioned by evolutionary pressure to deactivate duplicated genes and not to use the activation domain from takifugu and tetraodon introns.

The deactivated Sp2 turned into activator in gibbon. We have searched for losses of the original activation domains and their replacement by new sequences in *Sp2* genes. We have identified new formations of the *Sp2* exon, coding for activation domains in gibbon, in rock hyrax and in crane (**Figure 5** and **Suppl. Figure S9**). Gibbons are "lesser apes" that belong to the anthropoid primates (hominoidea) superfamily together with the "great apes" (chimpanzees, gorillas, orangutans and humans). The *Sp2* exon, encoding a valine-rich activation domain is well conserved in all eutherian (placental mammals) including primates (**Figure 5**). Differently, the gibbon, rock hyrax and crane *Sp2* exons encoding the activation domain lack homology to the other eutherian *Sp2* exons and their activation domains are not valine-rich. Similar to takifugu, their *Sp2* genes were broken at the same exon/intron junction (corresponding to the exon 3 and intron 3/4 junction in humans) and new exons have risen from their ancestral intron sequence. Therefore, the sequences encoding activation domains differ from those in other eutherian *Sp2* genes (**Figure 5**).

The human *Sp2* intron 3/4 includes multiple putative activation domains in all three open reading frames (WQ-SWL, WQ-LFQV, SWQ-LLF, FWH-LFL, TWN-SW) with similarity to Sp1-4 clade activation domains (Sp1: SWQ-TLQL, Sp3: SWQ-TFQV, Sp4: SWQ-TVQV), that suggest the primates' readiness for activation domain repair of the *Sp2* gene, as we have already found in the tetraodon *Sp2a* intron. We used the human intron sequence for the reconstitution of the ancestral gibbon's gene (**Figure 5**).

We have identified the activation domain in the new gibbon exon 4, which has the 9aaTAD pattern and has no valines. We generated the construct w81 for the gibbon's activation domain and tested the capacity to activate transcription. The rescued gibbon's *Sp2* gene encodes a new 9aaTAD activation domain, whose transcriptional activation capacity is comparable to the Gal4 activation domain (14). Gibbons have therefore recovered a strong activation domain encoded by the *Sp2* gene that has not been seen since the cnidarians. The *Sp2* activation domains were partially active in marsupials, but completely deactivated in placental mammals, including humans. Because of the new gibbon *Sp2* gene with the strong activation domain becoming stable in gibbon population, we suspect that the repair was driven by evolutionary pressure for *Sp2* activation function, which might be beneficial if not essential in gibbons.

In the gibbon's case, the intron provides a new activation domain and the encoded protein regained activator function. From above, we found a similar *Sp2* gene break and repair in another terrestrial

mammal *Procavia capensis* (rock hyrax), which is a close relative of sirenians and elephants (clade atlantogenates). The *Sp2* gene sequence was acquired from the UCSC genomic annotation for rock hyrax Sp2 scaffold_25:102095-130179. In this case, no obvious activation domain was found in their newly-generated exon. The hyrax *Sp2* gene was broken and repaired on the border of exon 3 and exon 4, exactly as in takifugu, tetraodon, crane and gibbon. We conclude that conserved *Sp2* gene repairs, on border of the exon 3 and exon 4, are inborn.

The use of intronal activation domains is not limited to the SP family. Similarly to the *Sp2* gene, we have identified intronal 9aaTAD activation domains in the unrelated human SREBP1 gene, which alternatively engaged exon or intron coding for alternative activation domains. The SREBP1 exon 1 includes part of the activation domain 9aaTAD-I, which could be found only in isoforms 1, 2, 4 and 5. Another alternatively used SREBP1 exon2 includes part of the activation domain 9aaTAD-II, which could only be found in isoforms 3, 4 and 6. In summary, all isoforms of the human SREBP1 include one of the two possible activation domains (**Figure 6**).

KLF homology with the SP family revealed their activation domains. The SP clade is a new branch derived from the KLF family. We have reviewed similarities between the *SP* and *KLF* genes in various metazoans and have found the SP proteins diversified the least from the ancestral KLF proteins in *Strongylocentrotus purpuratus* (Spu, sea urchin) (**Figure 7**). The close similarity of the sea urchin *SP* and *KLF* genes enabled us to localise the 9aaTAD activation domains (from the SP and KLF sequence alignment in **Figure 7**). Next, by comparison of the sea urchin with the human *KLF* genes using simple BLAST search and BLAST generated alignments (not shown), we have identified the 9aaTADs in the human *KLF-1, 2, 3, 4, 5, 6, 7, 8, 12, 15* and *WT1* genes (Wilms tumour protein).

Some of these identified activation domains correspond to previously reported activation domains. The activation domain of the KLF2 was first localised to its short N-terminal region (1-57) (78). Furthermore, the KLF4 activation domain has been characterised by loss-of-function mutations (EEE93/95/96VVV and DDD99/102/104VVV, in which both amino acid substitutions introduced valines in the KLF4 activation domain)(79). We have previously (12) identified the 9aaTAD motif in the KLF4 mutated region (9aaTAD position correlation in the SP and KLF families). Next, two activation domains were reported for the KLF1 (80), which are both also recognized by our 9aaTAD prediction algorithm (with one perfect match ATW **DLD** LLL) (12). Interestingly, we have found the 9aaTAD activation domain in *Crassostrea gigas*, *KLF1* ortholog (9aaTAD sequence ELL **DYD** FIL, gene ID; EKC39171), which closely resembles the first identified 9aaTAD in activator *Oaf1* (9aaTAD sequence DLF **DYD** FLF) (12).

Surprisingly, the 9aaTAD activation domains of KLF3 and KLF8 did not activate transcription, which correlated with their repressor function reported previously (52, 81–84). The accumulation of valines has been shown here again to be associated with the 9aaTAD deactivation (**Figures 7**). Nevertheless, the accumulation of valines in the KLF5 activation domain (in position p1 and p2 of the 9aaTAD) did

not cause the 9aaTAD deactivation, therefore the accumulation of valines by itself is not always sufficient for 9aaTAD deactivation in any of its position.

Similarly to the human KLF6, in which the 9aaTAD domain has accumulated isoleucines, we did not find any capacity to activate transcription for this activation domain. Nevertheless, the evolutionary younger *KLF6* orthologs in *Latimeria chalumnae* (Coelacanth, KLF6 gene ID; H3AK31) and *Branchiostoma floridae* (Florida lancelet, KLF6 gene ID; C3ZT77) have not accumulated isoleucines and hence their 9aaTAD activation domains have the capacity to activate transcription (**Figures 8**).

DISCUSSION

Previously, we have defined a pattern for the 9aaTAD domains that we use in the algorithm in the online Prediction Tool (www.piskacek.org), which has allowed the identification of the activation domains in numerous transcriptional activators. In this study, we have identified the 9aaTAD domains in the glutamine-rich activator Sp1 and in the proline-rich activator NFIC/CTF. We have demonstrated that the aspartic acid and glutamine residues are interchangeable in the activation domains of the glutamine-rich activator Sp1 and in the acidic activator Gal4. Moreover, we have shown that the conservation of glutamines was limited to the SP1-4 clade in vertebrates, but was almost absent in protostomes and in poriferans. Although the SP6-9 clade shares sequence homology with the SP1-4 clade, they also did not accumulate glutamines in their activation domains. Consistently, the proline-rich activation domains of NFIC/CTF activators did not conserve prolines, but rather the 9aaTAD activation domain, through the family. Thus, we united these previously classified acidic, glutamine-rich and proline-rich activators into the 9aaTAD family.

Next, we have described correlation of the 9aaTAD deactivation with accumulation of valines (in human Sp2 and KLF3), leucines (in *Latimeria* and in marsupial Sp2) and isoleucines (in human KLF6). The branched valine or isoleucine amino acids could partially hinder formation of α -helixes and cause their destabilization (85). Therefore, the accumulation of valines and isoleucines, which do not fully support helix formation, might partially explain the 9aaTAD deactivation. Nevertheless, the accumulation of valines at the end of the KLF5 activation domain (in position p1 and p2 of the 9aaTAD) did not cause the 9aaTAD deactivation, therefore the accumulation of valines itself in any position of the 9aaTAD (especially in position p1 and p2 in the KLF5 or in position p3 in Gcn4 or Gal4), is not always sufficient for the deactivation. Similarly, we have identified the accumulation of valines in the 9aaTAD activation domain in a strong activator Met4, which again did not interfere with the activation function (Met4 activation domain was found by the sequence similarity with the deactivated *Sp2* genes; ScanProsite search (ExPASy) for V-[NQDE]-W-[QN] amino acid pattern) (**Suppl. Figure S10**). From the limited number of activation domains with accumulated valines, we could not yet elucidate the amino acid pattern, which is necessary for deactivation of the 9aaTAD domain.

Importantly, we have observed re-activation of the 9aaTAD activation domains after their *de-valinisation* in the SP family. Similarly to the SP family, *de-valinisation* of the Gcn4 activation domain

by substitution with tryptophans has been reported as a great enhancement of the otherwise weak Gcn4 activation domain (AVVE SFFSS → AVwE SLFSS → Awww wLFwS) (86). Additionally, we have previously shown a partial *de-valinisation* of the Gcn4 activation domain by valine substitution for aspartic acid with similar results to increase its function (AVVE SFFSS → DDVE SLFSS → DDVY NYLFD) (14).

In the gibbon, we found surprising recovery of the damaged *Sp2* gene that has reverted into an activator, the very opposite function of the original gene, otherwise found in all other primates. Such dramatic changes in gene regulation in primates were highly unexpected. Nevertheless, the *Sp2* genes are stable in gibbon population and might be a part of their accelerated genome evolution (87). Mouse knock-ins of the gibbon *Sp2* gene coding for an activator might clarify if the Sp2 re-activation could be beneficial for other mammals or would have driven gibbon accelerated evolution.

The most intriguing observation in this study has been the preservation of the deactivated Sp2 9aaTAD domains, which lasted over 100 million of years. After the *Sp2* gene duplication in primitive fish (jawless and cartilaginous fish), the new paralogs were able to diversify into both activators and repressors and have provided a larger diversification of the SP regulatory system (88). After the *Sp2* gene duplication, the newly born paralog *Sp1* has regained its activator function by *de-valinisation* of the 9aaTAD activation domain. The domain deactivation, rather than simple domain deletion, was obviously an advantage during vertebrate evolution.

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Conflict of interest statement. The authors declare that they have no competing interests.

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Figure Legends

Figure 1. The activation domains subfamilies. A) The regions with identified activation domains 9aaTAD in Gal4 (in red), Sp1 (in purpura), their mutants, and NF1C / CTF (in sand brown) were tested in reporter assay with hybrid LexA DNA binding domain for the capacity to activate transcription. The mutants of Gal4 and Sp1 were designed to substitute aspartates (in red) for glutamines (in purpura) and vice versa. B) The NF1 / CTF activator, orthologs and paralogs are shown to demonstrate 9aaTAD motif conservation in their kin (adjacent conserved cysteines are in black). At the bottom of the figure, the entire region of previously reported proline-rich activation domain of the NF1 / CTF is shown; the activation domain 9aaTAD is marked (prolines in sand brown). The activation domains 9aaTAD are coloured for fast orientation. The LexA-Gal4 hybrid constructs assayed in L40 strain for transactivation activity are shown.

Figure 2. The SP family. A) The 9aaTAD activation domains identified in the SP family are shown for humans, for early deuterostomes / hemichordates / *Saccoglossus kowalevskii* (acorn worms), for protostomes / arthropods / crustacea / *Daphnia pulex* (water fleas), for cnidarians / *Acropora digitifera* (corals), and for poriferans / *Oscarella carmela* (demosponges). The designation *Sp69* reflected uncertainty of origin (a single member of the SP6-9 clade in those animals), whereas designation *Sp59* in *Oscarella carmela* pointed to common ancestor of the latter *Sp5* and *Sp6-9* clade. The peptides with capacity to activate transcription are with red ID and those without are in black (five-fold induction below the threshold). The activation domains with similarity are referred to by ~ marks. A link of the *Sp5 genes* and *Sp6-9 genes* is marked in grey boxes and *Sp2 genes* in yellow boxes. The most intriguing variations are in purpura. The dash symbol means amino acid deletion in human *Sp8*. The activation domains 9aaTAD are coloured for fast orientation. Valines in the 9aaTAD are in black and underlined (the pattern V-Q/H correlated here with the deactivation of the 9aaTAD activation domain in *hSp2*, *hSp4*, *hSp9* and *SkoSp2*).

Figure 3. SP2 clade evolution. The 9aaTAD activation domains identified by similarity (BLAST search in metazoans) in the SP2 clade from early branched metazoans to humans are shown. Some of them were tested in a reporter assay with a hybrid LexA DNA binding domain for the capacity to activate transcription. The peptide IDs with capacity to activate transcription are in red and those without are in black (5-fold induction above threshold). The most intriguing variations are in purpura and black. The paralogs (originated from *Sp2 gene* duplication in elephant shark) are in grey and the *Sp2* paralogs of cartilaginous and hemichordates, which show high sequence similarity are in grey boxes. The 9aaTAD activation domains are coloured for fast orientation. Valines in the 9aaTADs are in black. Valine rich (V1 in position p1, V2 in position p6, V3 in position p8) activation domains (AD) with tryptophan (in position p3) are in hemichordates and cartilaginous fish. A link of the first *Sp1-4 genes* with the *Sp2* orthologs and paralogs (in grey) is shown (similarity of hemichordates and cartilaginous fish *Sp2* 9aaTAD domains are underlined). Diversified branches are indicated.

Figure 4. Schema of the SP1-4 clade evolution.

Figure 5. Reformation of the activation domain in the gibbon *Sp2* gene. The *Sp2* activation domain coded by *exon 4* conserved in placental mammals (primates, cats, elephants and mice are shown in grey) was lost in hyrax and gibbon. Their new exons originated from their ancestral introns (in sand brown, exon junction in red, *exon 3* in purpura, *exon 5* in green). This repair took place on the border of the *exon 3* and *exon 4*, exactly as in takifugu and tetraodon *Sp2b* genes and crane *Sp2* gene. In gibbon's case, the intron provided a new 9aaTAD activation domain and their *Sp2* genes render activator function. The missing gibbon ancestral intron was substituted in our figure by the human intron, which is close to all primates and should substitute for the gibbon ancestral intron well. Slashes denote frameshifts in intron sequence. The activation domains 9aaTAD are coloured for fast orientation. The exon junctions are marked by a red hashtag. *UCSC genomic annotation for *Procavia capensis* (rock hyrax) *Sp2* gene in UCSC scaffold_25:102095-130179. We did not identify any obvious 9aaTAD motif in the gained hyrax exon.

Figure 6. Activation domain backup in introns of unrelated transcription factor SREBP. The *exon 1* and *exon 2* junction to *exon 3* of *SREBP1* gene coded for two distinct 9aaTAD activation domains (*exon 1* in red, *exon 2* in sand brown, *exon 3* in purpura). The first activation domain 9aaTAD-I is coded by *exon 1* (used in isoform 1, 2 and 5 but not in 3, 4 and 6) and the second 9aaTAD-II coded by *exon 2* (used in isoform 3, 4 and 6 but not in 1, 2 and 5). The alternative splicing always resulted in the presence of a solitary 9aaTAD activation domain in all isoforms. The peptides with capacity to activate transcription are shown in the chart. The 9aaTAD motif conservation in the SREBP family and the similarity with p53 9aaTAD activation domains are shown in lower panel. The 9aaTAD activation domains are coloured for fast orientation. The exon borders are marked by coloured hashtags.

Figure 7. Alignment of activation sequences of *S.purpuratus* SP and KLF paralogs revealed activation domains in the KLF family. A) *Strongylocentrotus purpuratus* (sea urchin) *SpuSp69* sequence was aligned to *SpuKLF2/3/7/15* sequences (green box for homology region, blue box for 9aaTADs and black box for DNA binding domain). Human and other metazoan SP proteins are shown to have homology regions. The 9aaTAD activation domains in the human KLF proteins were identified by sequence similarity to the activation domain in *SpuKLFs* (simple BLAST search). B) Accordingly to sequence similarity, the KLF and WT1 9aaTAD activation domains were clustered into Sp1-like and Oaf1-like activation domain subgroups (DOI: 10.1016/j.ygeno.2007.02.003). * *Homo sapiens* Hsa, *Saccoglossus kowalevskii* (acorn worm) *Sko*, *Capitella teleta* (annelid worm) *Cte*, *Daphnia pulex* (water flea) *Dpu*, *Acropora digitifera* (acroporid coral) *Adi*, *Oscarella carmela* (slime sponge) *Oca*, *Crassostrea gigas* (pacific oyster) *Cgi*, *Latimeria chalumnae* (coelacanth) *Lch*, *Branchiostoma floridae* (lancelet) *Bfo*. The valines and twin isoleucines (in *HsaKLF6* only) are in black, phenylalanines in positions of valines (in *HsaKLF3*) are in red and tryptophans are in green. Hidden amino acids are

marked with points and numbers. Initial methionines are underlined. The regions with similarity of active and deactivated KLFs are in brown boxes.

Figure 8. Schema of KLF evolution. The KLF genes from *Sarcophilus harrisii* (tasmanian devil) Shr, *Latimeria chalumnae* (coelacanth) Lcm, *Callorhynchus milii* (elephant shark) Cmk, *Branchiostoma floridae* (Florida lancelet) Bfo, *Saccoglossus kowalevskii* (acorn worm) Sko and *Amphimedon queenslandica* are listed in Supp. Table T2. The designation numbers with brackets reflected uncertainty of origin. Sequences in blue fulfil the 9aaTAD pattern but sequences in grey and marked with an asterisk do not. The first 9aaTAD position p1 is the most variable, and therefore not shown in the similarity overview. The valines and isoleucines are in black and tryptophans are in green. * Repressor function for the KLF12 activation domain was only deduced from their reported repressor function and its sequence similarity to KLF3 and KLF6.

Nine amino acids Activation Domains (9aaTAD) in
Acidic Aspartate-rich (Gal4), Glutamine-rich (Sp1) and Proline-rich (NF1c) activation domains

A) 9aaTAD domains enriched for aspartic acids, glutamines or prolines		Activation domain 9aaTAD			Reporter activation tested by peptides
Acidic Aspartate-rich activator Gal4					
Gal4-Ac Wt (D/E-rich, acidic)	acidic Asparte rich activation domain	TM	DD V Y N Y L F D	D	100 ±001%
Gal4-Q mut (Q/N-rich, non acidic)	Asparte to Glutamine substitutions	TM	QQ V Y N Y L F Q	QQ	280 ±048%
Glutamine-rich activator Sp1					
Sp1-Q Wt (Q/N-rich, non acidic)	Glutamine rich activation domain	GQ	VS W Q T L Q L Q	N L Q	224 ±033%
Sp-Ac mut (D/E-rich, acidic)	Glutamine to acidic Asparte substitutions	GD	VS W D T L D L D	D L D	969 ±243%
Proline-rich activator NF1C / CTF					
human NFIC (CTF), P08651	activation domain 9aaTAD		P L K D L V S L	AC D P A	47 ±008%
negative control	empty reporter vector				3 ±001%

B) 9aaTAD domain conservation in Proline-rich activation domain of NF1C / CTF-1

skoNF1, XP006819224	CTF ortholog in Saccoglossus kowalevskii, acorn worm	T P L S D F V Q L VC Q D A
cinNF1, XP002119978	CTF ortholog in Ciona intestinalis, sea squirt	Q D L K D F A Q F AC L S A
humanNFIA, Q12857	CTF paralog in human	E T L K E F V Q L VC P D A
humanNFIB, O00712	CTF paralog in human	D T L K N Y V P S YD P S S
humanNFIK, Q14938	CTF paralog in human	D S L K E F V Q F VC S D G

SP family evolution from porifera to humans

A) Human SP family

SP1-4 clade										SP1-4 clade							
Sp1	TL	QNLQLQAV	PNSGP	IIIR	TPTV			GPN	GQ	<u>VS</u> WQ TLQLQ	N	LQVQN	...EA CTC PYC	h01	244 ±33%		
exceptional Sp2	PS	QNFQIQAAE	PTPTQ	VYIR				TPS	GE	-- <u>V</u> Q TVLVQ	DS	PPATA	...MA CTC PNC	h02	2 ±01%		
Sp3	AL	QNLQLQ	LNPQT	FLIQ	AQTV			TPS	GQ	<u>VT</u> WQ TFQVQ	G	VQNLQ	...VA CTC PNC	h03	35 ±03%		
Sp4	PL	QNVQLQ	AVNPTQ	VLIR	APTL			TPS	GQ	<u>IS</u> WQ TVQVQ	N	IQSLQ	...VA CSC PNC	h04	4 ±02%		
exceptional Sp5	GY	SNLL	PPPPPPPP	PTCR	QLSPN			PAP	DD	<u>LP</u> Ww SIPQA	G	AGP	...RR CRC PNC	h05	335 ±46%		
SP6-9 clade										SP6-9 clade							
Sp6	PF	SKLLQPD	MSHHYE	SWFR	PTH			PGA	ED	<u>GS</u> Ww DLHPG	TS	WMD	...TV CRC PNC	h06	357 ±86%		
Sp7	VY	TSLD	MTHPYG	SWYK	AGIHAGISPG			PGN	TP	<u>TP</u> Ww DMHPG	GN	WLG	...SS CDC PNC	h07	382 ±69%		
Sp8	IY	PRV	GMAHPYE	SWFK	PSHPGLGAAGEV			GSA	GA	<u>SS</u> Ww DV---	GAG	WID	...AT CDC PNC	h08	107 ±04%		
Sp9	LY	PRV	GMAHPYE	SWYK	SGFHSTLAAGEV			TNG	AA	<u>SS</u> Ww DVHSS	PGS	WLE	...AT CDC PNC	h09	8 ±01%		

B) Metazoan SP family

Distal SP relatives in early Deuterostomia / Hemichordata / *Saccoglossus kowalevskii*, acorn worms

SkoSp2	XP006825847	GQTVIQQPAPIFV						RTP	TG	<u>VN</u> WQ PVQVQ	NSTQPL		...VA CSC PNC	w00	2 ±01%
SkoSp5	B5THL2	GHHHPLAITTAHRQVPAF						EEA	SR	<u>AP</u> Ww SVDSH	PSAKGH		...RR CRC PNC	sk5	485 ±36%
SkoSp69	D1LXE7	MY QRMGAHV	GHHYE	PTAWFK	PSPHPGLSGD			VAS	TG	<u>GT</u> Ww DMHAN	PN	WLD	...AT CDC PNC	~h07	

Distal SP relatives in Protostomia / Arthropoda / Crustacea / *Daphnia pulex*, water fleas

DpuSp2	E9GAT7	QQQQQQQQQLQNVSQQITIAGLS						GGN	NQ	<u>LT</u> Mi PASSL	SGLT	RMQ	...VA CTC PNC	w92	22 ±01%
DpuSp5	E9HI52	QQQQQQQQQHQHQ						TES	TL	<u>GS</u> Ww SPASS	AIPAAASVA		...RR CRC PNC	w73	219 ±40%
DpuSp69	E9GTG9	MY SRT	AHHPYE	QAWQFQ	QHVQKEAA			AGV	NG	<u>SS</u> Ww DMHQA	AAAGG	WLD	...AT CDC PNC	~h07	

Distal SP relatives in Cnidaria / *Acropora digitifera*, corals (~700 mil years)

AdiSp2	XP015752653	VY APEVELT	KAVDSG	AWTIK	SDAGEANA			SI	GG	<u>QW</u> WQ GKPLS		WAK	...VA CTC PNC	w69	16 ±01%
AdiSp5L	XP015756270	AF NTRDE	RLTS	STLVK				H	DD	<u>EM</u> Lw GKNGM	QEN	FLP	...SH CVC PNC	w70	21 ±01%
AdiSp5	XP015752723	PA SSRSV	PLSMSC	TAAFK	PEC			KEI	GG	<u>LH</u> Ww SVEPN	KS	VVH	...RR CRC PNC		
Adi4Sp69	XP015752725	MY PRM	PHPYDS	SPWFK	SSI EPRA			QAT	AR	<u>QA</u> Fw EVHSN	PT	WLD	...AT CDC PNC	wa1	32 ±08%

Distal SP relatives in Porifera / *Oscarella carmela*, demosponges (~780 mil years)

OcaSp2	m.85373	WS PPPSSQATVANPVVSA	STAQ	VA				AA	AA	<u>AF</u> Ww SW---	PAPP	SLQ	...IA CTC PYC	oca	421 ±40%
OcaSp59	m.85368	WY SH		PPYQ	VALVS P			HAG	TE	<u>FA</u> Ww AAFvG	PIRT	CIE	...NR CQC PNC	w72	349 ±36%
										SP6-9 clade			SP5 clade		

Evolution + Gene Duplications

Sp2 evolution

9aaTAD

Diversification of the 9aaTAD

ID

Reporter activation

Sp2 evolution

Single gene in the Sp1-4 subfamily

Sp2 *Oscarella carmela*, **Porifera**

m.85373

AA AFWR SWPAP

oca

421 ±01%

Sp2 *Amphimedon queenslandica*, **Porifera**

XP011405146

ST SSWW SAAAA

Duplication in SP group

w63

40 ±14%

Sp2 *Acropora digitifera*, **Cnidaria**

XP015752653

GG QWWQ GKPLS

w69

16 ±01%

Sp2 *Saccoglossus kowalevskii*, **Hemichordata**

XP006825847

TG VNWQ PVQVQ

Valine rich AD, Valines in positions p1, p6, p8

w00

2 ±01%

Sp2 *Branchiostoma belcheri*, **Cephalochordate**

Bb_019380F

NA SNWG MVQLQ

Sp2 *Petromyzon marinus*, **jawless Fish**

S4R950

GQ ITYQ TIQIL

W substitution by Y

wY

4 ±02%

Sp2 duplication, new paralog Sp4

JL2922

GQ IGWQ TIQVQ

Sp2 lamprey paralog Sp4

Sp2 Elephant shark, **cartilaginous Fish**

XP007902582

GQ VNWQ TLQVK

Valine rich AD similar to w00

w96

3 ±01%

Sp2 duplication, new paralogs Sp1, 3, 4 in sharks and in humans

V9KBV2

GQ MGWQ TIQLG

Sp2 shark paralog Sp1, Valine less AD

w22

57 ±14%

human Sp1

GQ VSWQ TLQLQ

AD with Valine in positions p1

h01

224 ±33%

XP007888199

GE ITWQ TFQVQ

Sp2 shark paralog Sp3

human Sp3

GQ VTWQ TFQVQ

Valine rich AD, Valines in positions p1, p8

h03

35 ±03%

XP007901932

GQ INWQ TIQVQ

Sp2 shark paralog Sp4

human Sp4

GQ ISWQ TVQVQ

Valine rich AD, Valines in positions p6, p8

h04

4 ±02%

Sp2 Whale shark, **cartilaginous Fish**

XP020376355

GQ VNWQ AVQVK

Valine rich AD similar to w00

Sp2 *Danio rerio*, **ray-finned bony Fish**

F1Q4L6

GE ΔΔWQ AVQIQ

VN deletion

w38

31 ±04%

Sp2 *Latimeria c.*, **lobe-finned bony Fish** - Sp2 reactivation

H3AC84

GE ΔΔLQ TVLLQ

Leucine rich AD, Valine in positions p6

w40

22 ±01%

Sp2 *Xenopus tropicalis*, **Amphibia**

Q28DC0

GD ΔΔVQ AVVMQ

Valine rich AD, Valines in positions p3, p6 (p7)

Sp2 *Xenopus laevis*, **Amphibia**

A2BDB4

GD ΔΔVQ AVMMQ

Sp2 American alligator, **Reptilia**

A0A151P5I8

GE ΔΔLQ TVLLQ

Leucine rich AD, Valine in positions p6

w40

22 ±01%

Sp2 Gekko, **Reptilia**

XP015267924

GE ΔΔLQ SVLLQ

Sp2 Chicken, **Bird**

H9KYR6

GE ΔΔLQ TVLLQ

w40

22 ±01%

Sp2 Loon, **Bird**

A0A093F1X1

GE ΔΔLQ TVLLQ

w37

5 ±01%

Sp2 Falco, **Bird**

XP014136071

GE ΔΔLQ TVVLQ

Sp2 Mousebird, **Bird**

XP010205758

GE ΔΔLQ TLLLQ

Leucine rich AD, Valine less AD

Sp2 Platypus, **Monotremata**

XP007662554

GE ΔΔLQ TVLLQ

w40

22 ±01%

Sp2 Tasmanian devil, **Marsupialia**

G3VTG8

GE ΔΔLQ TVLLQ

w40

22 ±01%

Sp2 Opossum, **Marsupialia**

F6PI08

GE ΔΔLQ TILLQ

Sp2 Koala, **Marsupialia**

XP020852973

GE ΔΔLQ TVLLQ

w40

22 ±01%

Sp2 Elephant, **Placentalia /Atlantogenata**

G3TNM0

GE ΔΔVQ TVLVQ

h02

2 ±01%

Sp2 Human, **Placentalia / Boreoeutheria**

Q02086

GE ΔΔVQ TVLVQ

Valine rich AD, Valines in positions p3, p6, p8

h02

2 ±01%

mutated Sp2 Human, **Valine substitutions**

L2 artificial

GE ΔΔVQ TVLLQ

Valine in position p8 substitution by L

10 ±02%

L1 artificial

GE ΔΔLQ TVLVQ

Valine in position p3 substitution by L

4 ±01%

LL in w40

GE ΔΔLQ TVLLQ

Valine in position p3, p8 substitutions by L

w40

22 ±01%

Sp2 Gibbon, **Placentalia / Boreoeutheria**

G1QNE4

LT FESQ YLLGW

new 9aaTAD formatted from intron

w81

242 ±12%

Sp2 gene duplication generated SP1-4 Clade

Formation of the activation domain in gibbon *Sp2* gene

Constructs: LexA protein + peptides	ID	Reporter activation
QLDLT FESQYLLG	w81	203 ±20 %
positive control Gal4 9aaTAD	HaY	set to 100 ±12 %
negative control (empty vector)	Hdd	3 ± 1 %

Sp2 orthologs in primates and selected vertebrates

Activation domain backup
in introns of unrelated transcription factor SREBP1

Constructs:	ID	Reporter activation
LexA protein + petides		
TDIE DMLQL	SR1a	105 ±10 %
CTFE DMLQL	SR1c	89 ±08 %
positive control p53 9aaTAD	1p53	set to 100 ±12 %
negative control (empty vector)	Hdd	3 ± 1 %

Human SREBP1 isoforms:

9aaTAD					
Human	SREBP1	P36956-1	PCDLDAALL	TDIE DMLQL	INNQSDSDFPGLF
		P36956-3	MD	CTFE DMLQL	INNQSDSDFPGLF
Chicken	SREBP2	Q12772	TELGDELTL	GDID EMLQF	VSNQVGEFPDLF
	SREBP1	Q90ZM5	ASDIDTALL	SDID DMLQL	INTPDNDFSGLF
	SREBP2	XP015144523	TELGDELTL	GDID EMLQF	VSNQAGDFPDLF
Latimeria	SREBP1	XP014344252	PNEIDTALL	NDID DMLKL	INNQDGDFFPGLF
	SREBP2	XP014353985	TELGDELTL	GDID EMLQF	VSNQAGEFPDLF
Elephantfish	SREBP1	XP007903952	SGEIDNALL	SDID DMLQL	INNQDGEFPGLF
	SREBP2	XP007908491	AALSDELNF	GDID EMLEF	VSGQVGDFPDLF
Lancelet	SREBP1	C3XXF7	NTGFEDGLL	DDID DMLQQ	FGDGNDFLLNA
Human	p53-I			ETFS DLWKL	
	p53-II			DDIE QWFTE	

A)

SP family and the early KLF paralogs

SP/KLF Homology Region HR				9aaTAD	SP/KLF HR	DNA Binding Domain
Hsa Sp1	TL QNLQLQAVPN	SGPI	IIR	TPTV GPNQ	VSWQTLQLQ	
Hsa Sp6	PF SKLLQPDMSHH	YES	WFR	PTH PGAED	GSWDDLHPG	TS WMD
Hsa Sp7	VY TSLDMTH	P YGS	WYK	AGIHAGISPG	TPWDMHPG	GN WLG
Hsa Sp8	IY PRVGMMAH	P YES	WFK	PSHPGLGAAG	SSWWDV	G AG WID
Hsa Sp9	LY PRVGMMAH	P YES	WYK	SGFHSTLAAG	SSWWDVHSS	P GS WLE
Strongylocentrotus purpuratus, Spu						
Spu Sp69	D1LXE7 MY QRMGAHVGGH	YEP TA WFK	PSPHPGLSG	DVASTG	GTWDMHAN	PN WLD
Cte Sp69	R7UUS3 MYSARVPGHH	L YES WPF	GVHSNANPPS	SVAPPASPLKAPSASADAASA	VPWDPVGH	ASS GN WLS
Dpu Sp69	E9GTG9 MYSRTAHH	P YE QA WQF	QQHVQ	EAAAGVNG	SSWDMHQA	AAA GG WLD
Adi Sp69	XP015752725 MYPRMPH	P YDS SP WFK	SSI	EPRAQATAR	QAFWEVHSN	PT WLD
Oca Sp59	m.85368 WYSHP	P YQV A LVS	PHAG	TE	FAWPAAFVG	P I RT CIE
Blast search						
Spu Sp69	W4Y6D0 ILPPHLCGHS	A YES WLK	AATSASMLSR	ENGVHGFS	PA FWSLPGA	Q AS LLD
Spu KLF(3a)	W4YNU4 MA	I YES I WDR	QRGGI	PSPLIKRNYLDP	IEK RVHFFLHML	PCEG NG ALD
Spu KLF(3b)	XP_011668101			...EDQDQDQDEEP	YQTE	25...VDS NG ALD
Spu KLF(6)	E7CQ89 MDALPSGGIFNELEIIGETGCFSALP	S VEE S WSQ	HCL	EMERLLK	SEP CQIRDKQMEPEN	PCQD RV IMD
Spu KLF(4)	W4YVW1 MAAFLGETNHMGHNCDF	S YEI WP		DMEFLQ	EICPPNSFEEP.32.SPESDAFAQVYDD	NN TSD
Spu KLF(15)	W4YJ14 MLDYYRTQS	S VER ES WTL	QRLNSAGGED	EMDSNST	SSMSDIDMSEHSP	LSSNSDD IVD
						...116...PLRKKNVHSC HIPGCGKIYG KTSHLKAH
						...112...HGKRRRVHQC DFAGCNKVYT KSSHLLKAH
						...122...HGKRRRVHQC DFAGCNKVYT KSSHLLKAH
						...124...PDPKRRVHRC QFSGCRKVYT KSSHLLKAH
						...199...GRKRTTSHTC SHPGCGKTYT KSSHLLKAH
						...279...GRGHGNKIAD ELKIHKCTYP NCGKMYSK

B)	KLF family	KLFs 9aaTAD	Peptides tested	Reporter activation
Sp1-like 9aaTADs		SW QTL QLQ		*reported in Figure 2
	Hsa WT1	TW NQM NLG	C M T W N Q M N L G A	283 ±01%
	Hsa KLF6	LW TKI ILA	D L W T K I I L A R	8 ±01%
	Lch KLF6	LW GNF ILT	E D L W G N F I L T C	79 ±18%
	Bfo KLF6	PW NKF LLT	D N P W N K F L L T KE	69 ±02%
Oaf1-like 9aaTADs		LF DYD FLE	D L F D Y D F L F	*reported previously
	Cgi KLF4	LL DYD FIL		
	Hsa KLF4	LL DLD FIL	E F N D L L D L D F I L S N	317 ±97%
	Hsa KLF1	TW DLD LLL	D A T W D L D L L L T N	843 ±13%
	Hsa KLF15	IL DFL LSQ		
	Hsa KLF5	VV DQF FTD	D S A S V V D Q F F T D	193 ±25%
	Hsa KLF2	VL DFI LSM	D L N S V L D F I L S M G	312 ±39%
	Hsa KLF7	AV DIL LSR	K S S A V D I L L S R D	7 ±01%
	Hsa KLF8	PV DLS FHK	Q V E P V D L S F H K	6 ±01%
	Hsa KLF3	PV DLT VNK	Q M E P V D L T V N K	1 ±01%
	Hsa KLF12	PV DLS INK		
positive control	Hsa Sp1		G Q V S W Q T L Q L Q N L Q	set to 100 ±12 %
negative control	empty vector			

9aaTAD activation domains in the KLF family

		Human	Sarcophilus harrisii Tasman. devil	Latimeria chalumnae Coelacanth	Callorhinchus milii Elephant shark	Branchiostoma floridae Lancelet	Saccoglossus kowalevskii Hemichordata	Strongylo centrotus p. Echinodermata	
Sp1-like TAD									
Activator	WT1	SW QTL QLQ TW NQM NLG	TW NQM NLG	TW NQM NLG					
Represor / Activator	KLF6	LW TKI ILA Represor	LW TKI ILA	LW GNF ILT Activator	LL SKI FMA	PW NKF LLT Activator	PW NKF ILP	PW NKF ILP	
Oaf1-like TAD									
Activator	KLF4	LF DYD FLF LL DLD FIL	LL DFD FIL	LL DLD FIL	LL DLD FIL	Gene Duplication	LL DFD FIL	LL DLD FIL	LL DLD FII
Activator	KLF1	TW DLD LLL	CW DLD FFL	FL DLE FIL	YL DLD FLL				
Activator	KLF2	VL DFI LSM	VL DFI LSM	VL DFI LSN	YL DLD FIL				
Represor	KLF7	AV DIL LSR	AV DIL LSR	NV DVL ISP	AV PLA LHR	Gene Duplication			
Represor	KLF8	PV DLS FHK	PV DLS LHK	PV DLS LNK	PV DLS LNK				
	KLF3	PV DLT VNK	PV DLT VNK	PV DLS CRK*	PV DLS LNK		PV DLS MNG*	PL DLS VNG	PV DLT VPR
	KLF12	PV DLS INK	PV DLS INK	PV DLS INK	PV DLS INK				
Activator	KLF5	VV DQF FTD	VV DQF FTD	VV DQY FNE	VV DEF FQE	VV DDF FKE	VV DEF FED		
	KLF15	IL DFL LSQ	LV DNE FLA	IL NYL LSQ	II DFL LSQ	FL DYL FSQ	LL EYL FSK	FL DYL FSR	
<div>← Evolution</div>									