# Family descriptions newly added TAP families

**1. ALOG**

“Arabidopsis thaliana LSH1 and Oryza G1” proteins are abbreviated with “ALOG” and also referred to as light-dependent short hypocotyl (LSH) proteins (Lee et al., 2020). These proteins represent a family of TFs which can be found in all land plants and some streptophyte algae (Naramoto et al., 2020). ALOG proteins are involved i.e. in the elongation of the hypocotyl, in the determination of the lateral organ identity and in the conservation of the apical meristems (e.g., (Cho & Zambryski, 2011; Naramoto et al., 2020; Zhao et al., 2004)). (Naramoto et al., 2020) identified, based on the occurrences of ALOG proteins in some streptophyte algae, that the ALOG TF family emerged before the evolution of land plants and is present in species that feature traits like apical growth, plasmodesmata and rhizoids (Naramoto et al., 2020).

**2. C2H2-IDD**

The Cys2-His2 (C2H2) zinc-finger protein family is present in all eukaryotes and among the largest families of eukaryotic transcription factors (Seetharam & Stuart, 2013). One identified plant-specific subfamily of this large protein family is the Indeterminate Domain (IDD) subfamily of TFs, which was first reported in *Zea mays* (Coelho et al., 2018; Prochetto & Reinheimer, 2020). Proteins belonging to the IDD subfamily can be distinguished from the remaining C2H2 members by the fact that they contain a highly conserved N-terminal IDD domain in addition to further C2H2 zinc finger domains (Prochetto & Reinheimer, 2020). Among previously identified functions controlled by C2H2-IDD proteins are metabolic and development processes like flowering time, root development, leaf differentiation and the regulation of the C4 Kranz anatomy (Coelho et al., 2018; Prochetto & Reinheimer, 2020).

**3. MYST**

Lysine acetyltransferases or histone acetyltransferases (HATs) together with histone deacetylases (HDACs), are responsible for reversible acetylation of histones and are found in eukaryotes in at least four TR families, namely MYST (MOZ, Ybf2/Sas3, Sas2 and TIP60), CBP (p300/CREB-binding protein), TAFII250 (TATA-binding protein associated factor) and GNAT (GCN5-related N-terminal acetyltransferase) (Boycheva et al., 2014; Pandey, 2002; Uhrig et al., 2017). HATs function as transcriptional regulators by having different regulatory effects on gene expression in plants, animals and fungi, indicating a high conservation of these proteins and their functions (Pandey, 2002). Especially in land plants, due to their sessile lifestyle, chromatin modifications provide an important mechanism in adapting to environmental stresses (Boycheva et al., 2014). The HAT subfamily MYST can be found with an average of two members in green algae, land plants, heterokonts and other photosynthetic eukaryotes involved for instances in transcriptional activation and silencing, apoptosis and in the process of the cell cycle (Latrasse et al., 2008; Uhrig et al., 2017).

**4. CBP**

Lysine acetyltransferases or histone acetyltransferases (HATs) together with histone deacetylases (HDACs), are responsible for reversible acetylation of histones and are found in eukaryotes in at least four TR families, namely MYST (MOZ, Ybf2/Sas3, Sas2 and TIP60), CBP (p300/CREB-binding protein), TAFII250 (TATA-binding protein associated factor) and GNAT (GCN5-related N-terminal acetyltransferase) (Boycheva et al., 2014; Pandey, 2002; Uhrig et al., 2017). HATs function as transcriptional regulators by having different regulatory effects on gene expression in plants, animals and fungi, indicating a high conservation of these proteins and their functions (Pandey, 2002). Especially in land plants, due to their sessile lifestyle, chromatin modifications provide an important mechanism in adapting to environmental stresses (Boycheva et al., 2014). CBP proteins belonging to the HAT subfamily CBP are transcriptional coactivators that play a role in tumor suppression, in further physiological events and in signal transduction (Uhrig et al., 2017; Yuan & Giordano, 2002). These TRs can be found in all photosynthetic eukaryotes with two to five members (Uhrig et al., 2017; Yuan & Giordano, 2002).

**5. TAFII250**

Lysine acetyltransferases or histone acetyltransferases (HATs) together with histone deacetylases (HDACs), are responsible for reversible acetylation of histones and are found in eukaryotes in at least four TR families, namely MYST (MOZ, Ybf2/Sas3, Sas2 and TIP60), CBP (p300/CREB-binding protein), TAFII250 (TATA-binding protein associated factor) and GNAT (GCN5-related N-terminal acetyltransferase) (Boycheva et al., 2014; Pandey, 2002; Uhrig et al., 2017). HATs function as transcriptional regulators by having different regulatory effects on gene expression in plants, animals and fungi, indicating a high conservation of these proteins and their functions (Pandey, 2002). Especially in land plants, due to their sessile lifestyle, chromatin modifications provide an important mechanism in adapting to environmental stresses (Boycheva et al., 2014). In non-photosynthetic eukaryotes, monocots, and dicots an average of one to two members of the HAT subfamily TAFII250 can be found (Uhrig et al., 2017). Furthermore, they are also present in early photosynthetic eukaryotes as red algae (Uhrig et al., 2017). Functions such as participation in light response and the phytochrome pathway could be observed (Boycheva et al., 2014).

**6. LOB1 & LOB2**

Previous text of AS2/LOB:

Conserved in a variety of evolutionarily divergent plant species, LOB DOMAIN (LBD) genes define a large, plant-specific family of largely unknown function. LBD genes have been implicated in a variety of developmental processes in plants, although to date, relatively few members have been assigned functions. LBD proteins have previously been predicted to be transcription factors, however supporting evidence has only been circumstantial. To address the biochemical function of LBD proteins, we identified a 6-bp consensus motif recognized by a wide cross-section of LBD proteins, and showed that LATERAL ORGAN BOUNDARIES (LOB), the founding member of the family, is a transcriptional activator in yeast. Thus, the LBD genes encode a novel class of DNA-binding transcription factors. Post-translational regulation of transcription factors is often crucial for control of gene expression. In our study, we demonstrate that members of the basic helix-loop-helix (bHLH) family of transcription factors are capable of interacting with LOB. The expression patterns of bHLH048 and LOB overlap at lateral organ boundaries. Interestingly, the interaction of bHLH048 with LOB results in reduced affinity of LOB for the consensus DNA motif. Thus, our studies suggest that bHLH048 post-translationally regulates the function of LOB at lateral organ boundaries. (Husbands et al., 2007)

To add:

According to (Huang et al., 2020) and (Zhang et al., 2020) the LBD family members can be classified into two subfamilies, namely class I and class II LBD proteins. These two classes are distinguished in their domain motifs. Compared to class I proteins, class II proteins lack an intact leucine-zipper-like domain (Zhang et al., 2020). In addition, zinc-finger motifs and GAS (Gly-Ala-Ser) blocks are present in both classes (Zhang et al., 2020).

**7. MYB-2R, MYB-3R and MYB-4R**

Previous text of MYB:

The cloning of the first transcription factor from plants, the C1 gene of maize, indicated that plants use transcription factors that are structurally related to those of animals in their control of gene expression, because C1 showed significant structural homology to the vertebrate cellular proto-oncogene c-MYB. Since 1987, the catalogue of MYB-related transcription factors has increased considerably in size due, primarily, to the ever-expanding number of MYB genes identified in higher plants (Arabidopsis thaliana is estimated to contain more than a hundred MYB genes). In vertebrates, the MYB-related proto-oncogenes comprise a small family with a central role in controlling cellular proliferation and commitment to development. However, while the functions of some plant MYB genes are relatively well understood they are, at present, quite distinct from their animal counterparts.

To add:

MYB TFs exhibit a highly conserved N-terminal MYB domain, which consists of one to four imperfect sequence repeats (Cao et al., 2020; Dubos et al., 2010). Based on the occurrence of these repeats, proteins belonging to the MYB family can be classified into four subfamilies, namely MYB-1R, MYB-2R, MYB-3R and MYB-4R (Cao et al., 2020).

**8. ADA2**

SWIRM domain proteins can be subdivided into 3 subfamilies, namely SWI3-type, LSD1-type (Lysine-specific demethylase 1), and Ada2-type (Adenosine deaminase isoenzymes 2), based on their domain architectures and sequence homology (Gao et al., 2012). ADA2-type proteins are known to be involved in lysine activation and transcriptional activation (Sterner et al., 2002).

**9. RKD**

According to (Chardin et al., 2014), the plant specific RWP-RK TF Family can be divided into the two subfamilies NLP (NIN-like proteins) and RKD (RWP-RK domain proteins). Proteins belonging to the subfamily NLP provide an additional PB1 (Phox and Bem 1) domain at their C-terminus (Chardin et al., 2014; Wu et al., 2020). RWP-RK proteins are involved in response to nitrate availability and in nodule interception (Wu et al., 2020).

**10. NLP**

According to (Chardin et al., 2014), the plant specific RWP-RK TF Family can be divided into the two subfamilies NLP (NIN-like proteins) and RKD (RWP-RK domain proteins). Proteins belonging to the subfamily NLP provide an additional PB1 (Phox and Bem 1) domain at their C-terminus (Chardin et al., 2014; Wu et al., 2020). RWP-RK proteins are involved in response to nitrate availability and in nodule interception (Wu et al., 2020).

**11. CRF**

(Rashotte & Goertzen, 2010) specify Cytokinin Response Factors (CRFs) as a subset of the AP2/ERF TF family. These proteins can be characterized by a N-terminal CRF domain relative to the AP2 DNA binding domain and by a CRF specific C-terminal region (Powell et al., 2019; Rashotte & Goertzen, 2010). CRF TFs are included in the cytokinin signal transduction pathway in the course of leaf development (Rashotte & Goertzen, 2010). (Rashotte & Goertzen, 2010) performed database searches, motif, and phylogenetic analyses to identify CRF genes in representatives of all major land plant lineages.

**12. ET**

Based on the study of (Raventós et al., 1998), the TF family HRT (Hordeum repressor of transcription) was previously integrated into TAPscan. The authors introduced this protein family as proteins containing a gibberellin phytohormone response element and are therefore involved in developmental and phytohormone-responsive regulations (Raventós et al., 1998). However, a more recent study by (Tedeschi et al., 2019) characterized this family as EFFECTORS OF TRANSCRIPTION (ET). ET proteins are plant-specific transcription factors specified by highly conserved ET repeats and a GIY-YIG domain, a DNA single-strand nuclease domain (Tedeschi et al., 2019). In line with (Raventós et al., 1998), also (Ivanov et al., 2012) were able to demonstrate an involvement in the regulation of gibberellin to ensure correct seed development. Moreover, it is suggested that ET proteins are involved in DNA repair (Tedeschi et al., 2019).

**13. HD-HDZ (C1HDZ, C2HDZ, C3HDZ, C4HDZ)**

The homeobox TF superfamily is defined by an occurrence of the characteristic homeodomain (HD) and can be defined as pan-eukaryotic since it is found in all eukaryotic organisms (Catarino et al., 2016; Romani et al., 2018). According to different references (e.g., (Catarino et al., 2016; Mukherjee et al., 2009; Que et al., 2018)), the HD superfamily is divided into 11 subfamilies, namely BEL, DDT, HDZ, KNOX, LD, NDX, PHD, PINTOX, PLINC, SAWADEE and WOX. Interestingly, all subfamilies evolved in the common ancestor, before terrestrialization and diversification of land plants (Catarino et al., 2016). Furthermore, the broad distribution and high conservation of domains induces a common highly conserved functional role in plants and whenever members are present, also in algae (Mukherjee et al., 2009). In general, homeobox TFs show diverse functions in developmental and physiological mechanisms (Romani et al., 2018). The HD-HDZ (HDZ) subfamily can be subdivided into four classes, namely classes C1HDZ, C2HDZ, C3HDZ and C4HDZ. The members of these classes exhibit a characteristic homeodomain and an additional leucine zipper (LZ) domain (Romani et al., 2018). Furthermore, in C2HDZ proteins an aromatic, large hydrophobic, acidic context (AHA)-like motif appears (Romani et al., 2018). Also, in C2HDZ proteins there are two additional exclusive motifs, in fact the C-terminal CPSCE sequence and the N-terminal ZIBEL-like motif (Romani et al., 2018). In addition, C3HDZ proteins exhibit a unique MEKHLA domain and 3HDZ and C4HDZ proteins show START/SAD domains (Romani et al., 2018).

**14. ZPR**

ZPR proteins are a group of transcriptional regulators that were derived by a duplication event of a C3HDZ protein in the common ancestor of ferns and seed plants and subsequent degenerative mutations. They are involved in the regulation of C3HDZ and in the regulation of plant form and growth (Floyd et al., 2014). Furthermore, ZPR regulators display the important role of gene duplications in the complexity of land plant developmental complexity (Floyd et al., 2014).

**15. HD-LD**

The homeobox TF superfamily is defined by an occurrence of the characteristic homeodomain (HD) and can be defined as pan-eukaryotic since it is found in all eukaryotic organisms (Catarino et al., 2016; Romani et al., 2018). According to different references (e.g., (Catarino et al., 2016; Mukherjee et al., 2009; Que et al., 2018)), the HD superfamily is divided into 11 subfamilies, namely BEL, DDT, HDZ, KNOX, LD, NDX, PHD, PINTOX, PLINC, SAWADEE and WOX. Interestingly, all subfamilies evolved in the common ancestor, before terrestrialization and diversification of land plants (Catarino et al., 2016). Furthermore, the broad distribution and high conservation of domains induces a common highly conserved functional role in plants and whenever members are present, also in algae (Mukherjee et al., 2009). In general, homeobox TFs show diverse functions in developmental and physiological mechanisms (Romani et al., 2018). In members of the LD subfamily, the conserved LUMI domain is expected in addition to the homeodomain (Mukherjee et al., 2009).

**16. HD-NDX**

The homeobox TF superfamily is defined by an occurrence of the characteristic homeodomain (HD) and can be defined as pan-eukaryotic since it is found in all eukaryotic organisms (Catarino et al., 2016; Romani et al., 2018). According to different references (e.g., (Catarino et al., 2016; Mukherjee et al., 2009; Que et al., 2018)), the HD superfamily is divided into 11 subfamilies, namely BEL, DDT, HDZ, KNOX, LD, NDX, PHD, PINTOX, PLINC, SAWADEE and WOX. Interestingly, all subfamilies evolved in the common ancestor, before terrestrialization and diversification of land plants (Catarino et al., 2016). Furthermore, the broad distribution and high conservation of domains induces a common highly conserved functional role in plants and whenever members are present, also in algae (Mukherjee et al., 2009). In general, homeobox TFs show diverse functions in developmental and physiological mechanisms (Romani et al., 2018). In members of the NDX subfamily, an NDX (Nodulin Homeobox genes) domain is expected in addition to the homeodomain (Mukherjee et al., 2009).

**17. HD-SAWADEE**

The homeobox TF superfamily is defined by an occurrence of the characteristic homeodomain (HD) and can be defined as pan-eukaryotic since it is found in all eukaryotic organisms (Catarino et al., 2016; Romani et al., 2018). According to different references (e.g., (Catarino et al., 2016; Mukherjee et al., 2009; Que et al., 2018)), the HD superfamily is divided into 11 subfamilies, namely BEL, DDT, HDZ, KNOX, LD, NDX, PHD, PINTOX, PLINC, SAWADEE and WOX. Interestingly, all subfamilies evolved in the common ancestor, before terrestrialization and diversification of land plants (Catarino et al., 2016). Furthermore, the broad distribution and high conservation of domains induces a common highly conserved functional role in plants and whenever members are present, also in algae (Mukherjee et al., 2009). In general, homeobox TFs show diverse functions in developmental and physiological mechanisms (Romani et al., 2018). In members of the SAWADEE subfamily, an SAWADEE domain is expected in addition to the homeodomain.

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