Dynamic expression of a glutamate decarboxylase gene in multiple non-neural tissues during mouse development

ABSTRACT
Gad1 expression can occur in some sites where tissues that need signals for patterning and differentiation (AER, vibrissal placodes) or in other sites of proliferating stem cell populations that produce multiple differentiated tissues (tail bud mesenchyme, pharyngeal endoderm and mesie) as well. The dynamism of Gad1 expression in tissues suggests that GABA signaling has a more significant role in development than previously thought.

INTRODUCTION
Recombinant TATA-binding protein (TBP) and a family of TBP-associated factors (TAFIIs) make up the background RNA polymerase II (pol II) transcription factor TFIID [, with at least 12 TAFINII being identified], and their conservation has been demonstrated by studying their cDNAs for evolutionary survival from yeast to mammals. The TFIID complex comprises several TAFIIs, including SAGA and PCAF complexes that lack TBP. In comparison, TS lesions in TAFII145, ITU-L, and TDII90 have a less significant impact on the expression of specialized genes involved in the cell cycle than other proteins. Genetic studies have shown that TAFII30 is required for viability of mouse F9 embryonal carcinoma cells and for their differentiation into parietal endoderm, while without it undifferentiated F9.cells die from apoptosis; however not the retinoic acid-deficient F9) cells survive but hardly any other type of regulatory protein, and there are also several studies on taFI1305. TAFI I135 contains 1083 amino acids and several functional domains, four of them have been described: TAFIII136 interacts with different glutamine-rich domain (i.e., catalyzed by Sp1 and CREB) and acts as a coactivator in vitro for these activators; in cells transfected with CAT II knockout cells can secrete subdomains of TFUII135, namely, TLJ378 which act as dominant negative repressors It has also been suggested that some neurodegenerative diseases may result from the sequestration of TAFII135 by expanded polyglutamine domains and consequent interference with CREB activity. Two conserved regions, CR-I and corresponding to a histone fold domain (which is required for heterodimerisation of hTAFII20/yTAFINII) are found in TAFiI135 and shared with the Drosophila homologue dTAFFI110 and the mammalian RAFI I105. TAFII135's potentiation of ligand-dependent transactivation by the receptor for all-trans retinoic acid (RAR) in transfected mammalian cells is dependent on the CR-II domain. Despite these investigations, there is little information about its physiological functions beyond those described in these studies. It is increasingly clear that the targeted 26S proteasome-mediated proteolysis of transcription factors plays a crucial role in the transactivation process. The stability of activation domains is closely linked to their potency. Deficiency-related mutations in the VP16 activation domain, which overlap with other cleavage domains and sequences required for degradation, lead to increased stability of proteins. Additionally, several nuclear receptors have been observed to undergo targeted proteolysis based on ligands. Proteolysis and transactivation are intimately connected, as demonstrated by deletion of the -helix H12 of their ligand binding domain that stabilizes the estrogen receptor, RAR, and RXR proteins. A mechanism for attenuating the physiological response to ligands in the presence of nuclear receptors may involve targeted proteolysis. Targeted proteostasis has also been suggested as a means of controlling other physiological

responses, such as STAT factors and heat shock regulation. Whether or not components of the basal transcription apparatus are subjected to targeted proteolysis of transcriptional activators in response to physiological stimuli remains unclear. Here, TBP and TAFII135 are selectively depleted in extracts from T-RA differentiated F9 cells and from differentiatent C2C12 cells. TBP and TAFII135 are selectively targeted for proteolytic degradation, leading to depletion as they are blocked by proteasome inhibitors. This process occurs simultaneously with the degradation of RAR2 during differentiation in F9 cells, which is a critical activator in primitive endoderm differentiation. These results demonstrate a new pathway that regulates the intracellular levels of two TFIID components and indicate that RA not only induces targeted proteolysis of RAR2 but also basal transcription factors that mediate transcriptional activation in F9 cells. Furthermore, we show that stable ectopic expression of TAFII135 (tafitous endoderm) of the class F9 cells delayed targeted degradation of their endogenous fatty acid TAFII1, TBP and RAR2 in response to T-RA, thus the cell has an increased growth rate and its ability to differentiate into primitive endotherm is impaired at an early stage, but it readily differentiates into parietal endorm. Upon treatment with T-RA, the cells exhibit an atypical elongated structure that differs from the primitive endodermal cells and is resistant to bt2cAMP differentiation.

CONCLUSION

Results showed that intracellular calcium level ([Ca2+]i) measured in mouse NIH-3T3 and human HeLa and SaOS-2 cells were significantly upregulated by ethylene, which is produced by the same plant, after being exposed to ethylene gas. The data supports earlier research that revealed an upregulation of [Ca2+]i and a marked increase in the expression of an ethylene-responsive gene, SDERR, in invertebrate cells (primmorphs of the marine sponge S. domuncula). These findings suggest that ethylene may play a role in both plant biological processes and animal one by modulating intracellular signaling pathways.