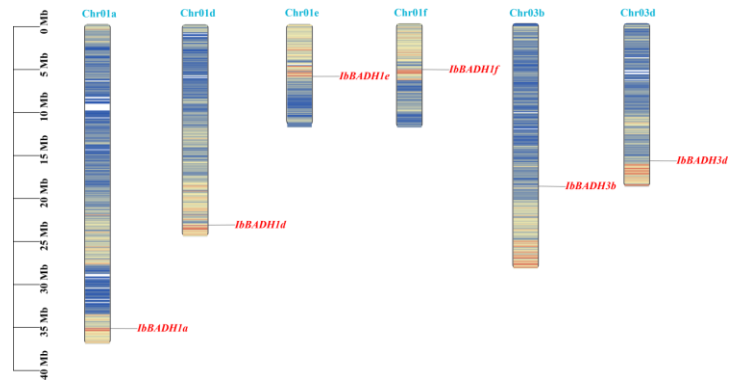


附图



Chr01a/01d/01e/01f 与 Chr03b/03d 为同源染色体

Chr01a/01d/01e/01f and Chr03b/03d are homologous chromosomes.

附图 1 甘薯 *IbBADH* 基因在同源染色体上的分布

Fig. S1 Distribution of *IbBADH* genes on sweetpotato homologous chromosomes

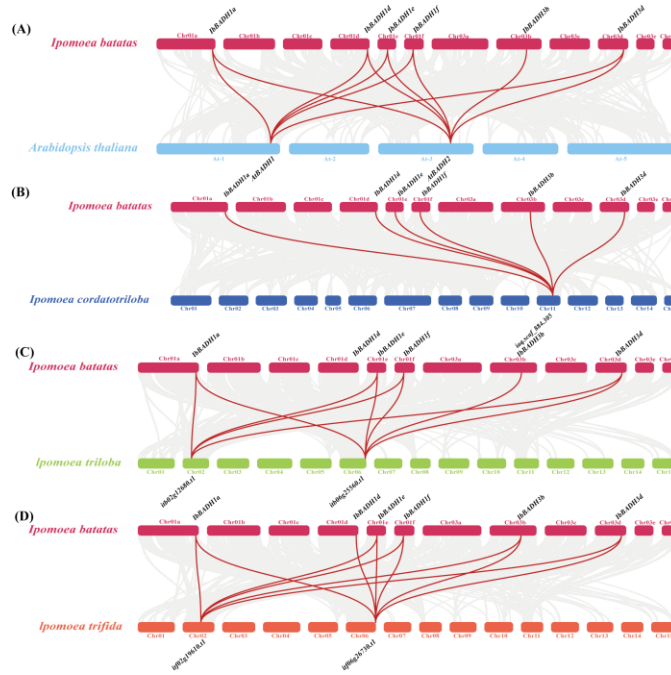


灰色用于表示一般共线区域；红色线条表示 *BADH* 基因对

Gray is used to indicate general co-localized regions; red lines indicate *BADH* gene pairs

附图 2 甘薯 *IbBADH* 基因在染色体间的共线性分析

Fig. S2 Synteny analysis of inter-chromosomal relationships of *IbBADH* genes



(A) 甘薯与拟南芥 *BADH* 基因的共线性关系；(B) 甘薯与小薯 *BADH* 基因的共线性关系；(C) 甘薯与三裂叶薯 *BADH* 基因的共线性关系；(D) 甘薯与三裂野牵牛 *BADH* 基因的共线性关系；

灰色用于表示一般共线区域；红色线条表示 *BADH* 基因对

Note: (A) Co-linearity of sweetpotato with the *BADH* gene of *Arabidopsis thaliana*; (B) Co-linearity of sweetpotato with the *BADH* gene of *Xiao shu*; (C) Co-linearity of sweetpotato with the *BADH* gene of *Ipomoea triloba*; (D) Co-linearity of sweetpotato covariance with the *BADH* gene of *Ipomoea trifida*;

Gray is used to indicate general co-localized regions; red lines indicate *BADH* gene pairs

附图 3 甘薯与拟南芥和旋花科近缘种 *BADH* 基因的共线性关系

Fig. S3 The collinearity of *BADH* gene in sweetpotato with *Arabidopsis* and species closely related to the Convolvulaceae family

>Pro-*BADH1a-A*

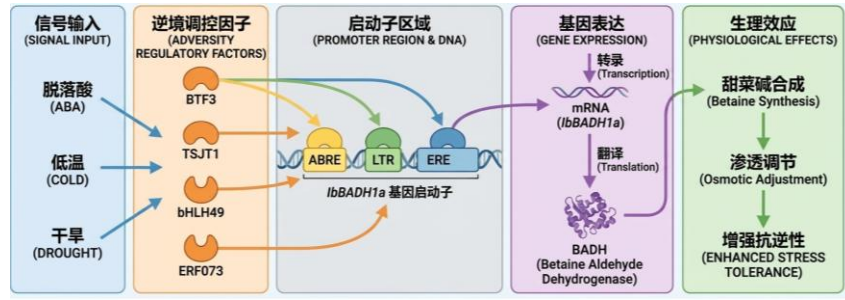
CTGCTAAGTTTCCTACTTGTACAGCAGCTTTGATAAATAGGACAGCACCTC
ACATTTGAAGTAGGGTGCAATGGTCAATGCCCAAATGACAGGAGCTATGT
 GCAAACACTCTCCCTCAAATTTGAAACTATTCTTACCAGTATAAACAAGA
 TGTTACCAACTTTGAGGCTCACTGCCATGAAATTGATCGGCA

蓝色下划线为引物结合区；Pro-*IbBADH1a-A* 长度 194 bp (-1609 bp 至 -1415 bp)；红色标注序列分别对应防御/胁迫响应 (TC-rich repeats 核心序列)、冷胁迫响应 (MYC 核心序列) 及光响应元件 (TCT-motif 核心序列)

Note: Blue underlines indicate primer-binding sites; Pro-*IbBADH1a-A* is 194bp (-1609 bp to -1415 bp); red-highlighted sequences correspond to core motifs related to defense/stress response, cold response, and light response

附图 4 Pro-*IbBADH1a-A* 片段序列

Fig. S4 *IbBADH1a* gene promoter segments and sequence of the Pro-*IbBADH1a-A* fragment



附图 5 *IbBADH1a* 的初步调控模型

Fig. S5 Preliminary regulatory model of *IbBADH1a*