

Differentially expressions of pivotal genes involved in pigment, nitrogen and sugar starch pathway and climatic responses in varieties planted in Bijie and Baofeng, China

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Abstract

Genes involved in the pigment, nitrogen, starch and sugar metabolism pathway were examined at expression level between Bina 1 and JiUCAIPING 2 cultivar planted in Bijie, Guizhou and Baofeng, Henan.

Seven genes which included *ZDS*, *Chl*, *GS1-3*, *Nir-3*, *Hex*, *SPP2*, *TPP* were identified as differently expressed between two cultivars and all of them expressed at higher level in JiUCAIPING 2 compared with that in Bina 1.

Compared with the plants grew under Baofeng environment both *Nir-3* gene in Bina1 and *Hex* gene in JiUCAIPING 2 expressed at a lower level as well as *CSIE* gene expressed at a higher level in both cultivars.

Results showed that some pivotal genes expressed at lower level in Bina 1 indicating that the responding metabolism pathway activities were much weaker compared with that in JiUCAIPING2. The nitrogen pathway in Bina 1 and sugar pathway in JiUCAIPING 2 were affected mostly by environment.

Key words

Carbon and Nitrogen Metabolism, Gene Expression, Climatic Response

Introduction

China is a very large country and the climatic conditions are markedly different across the whole land. A lot of places can grow tobacco which has a very strong suitability to local climatic and ecological conditions. Bijie locates in the southwest area of China and is a subtropical humid monsoon climate with abundant rainfall and average temperature around 10~15 °C. Baofeng locates in the central of China which is semi-humid continental monsoon climate with four distinct seasons and average temperature about 14 °C. These two places are all typical tobacco planting areas in China with tobaccos in Bijie having moderate aroma style and that in Baofeng having strong aroma style. This research mainly focused on the gene expression differences in pivotal metabolism pathways between the tobacco planted in Bijie and Baofeng. The genes examined involved in pigment, nitrogen, starch and sugar metabolism pathway.

Materials and Methods

- ◆ Tobacco Varieties: Bina 1, JiUCAIPING 2, K326
- ◆ Sample: Leaf sample on the 11 or 12 stalk position.
- ◆ Cultivation Methods: Grew in matrix with nutrient solution supplying every 3 days.
- ◆ Solution Content: 10 mM/LKNO₃, 2 mM/L(NH₄)₂SO₄, 1 mM/LKH₂PO₄, 1.5mM/L K₂SO₄, 2 mM/LCaCl₂, 2.5 ×10⁻¹mM/LMgSO₄, 2.5×10⁻²mM/LKCl, 1.25×10⁻²mM/LH₃BO₃, 1×10⁻³mM/LMnSO₄, 1×10⁻³mM/LZnSO₄, 2.5×10⁻²mM/LCuSO₄, 2.5× 10⁻²mM/L(NH₄)₆Mo₇O₂₄, 1 ×10⁻¹mM/L Fe-EDTA
- ◆ Gene Examination: Reverse Transcription PCR

Table 1. Genes description and abbreviations as well as the primers used in the research

Pathway	Gene Name	Abbreviation	
Control Gene	Ribosomal protein L25	<i>L25</i>	
Starch and Sucrose Metabolism	Extracellular invertase	<i>Inv</i>	
	UDP-glucose dehydrogenase	<i>UGDD</i>	
	Cellulose synthase-like protein	<i>CSIE</i>	
	Granule-bound starch synthase I	<i>GBSSI</i>	
	UDP-Glucose Pyrophosphorylase	<i>UGPase</i>	
	Starch branching enzyme	<i>SBE</i>	
	Sucrose synthase	<i>SuSy</i>	
	Hexokinase	<i>Hex</i>	
	ADP-glucose pyrophosphorylase small subunit	<i>AGP</i>	
	Pectin methylesterase	<i>PME</i>	
	Sucrose-6-phosphate phosphatase	<i>SPP2</i>	
	Trehalose-phosphate phosphatase	<i>TPP</i>	
	Nitrogen Metabolism	Glutamine synthetase	<i>GS1-3</i>
		Glutamine synthetase	<i>GS1-5</i>
Glutamate dehydrogenase		<i>Gdh1</i>	
Nitrate reductase		<i>Nit</i>	
Nitrite reductase 1		<i>Nir-1</i>	
Nitrite reductase 2		<i>Nir-2</i>	
Nitrite reductase 3		<i>Nir-3</i>	
Pigment Metabolism	Phytoene synthase	<i>PSY</i>	
	Carotenoid cleavage dioxygenase,	<i>CCD</i>	
	Zeta-carotene desaturase	<i>ZDS</i>	
	Chlorophyllase	<i>Chl</i>	
	9-cis-Epoxy-carotenoid dioxygenase	<i>NCED</i>	

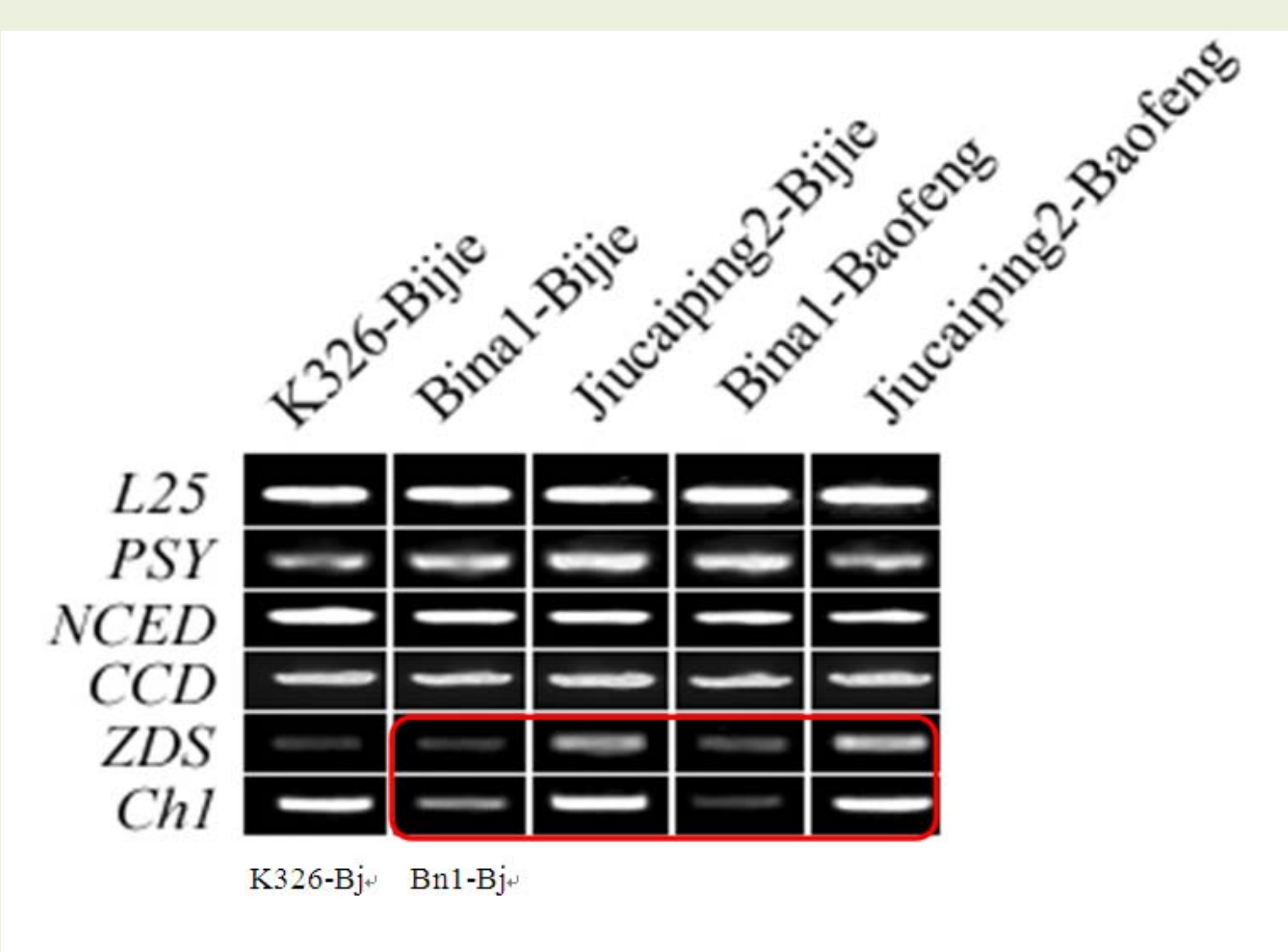


Fig.1

Expression pattern of pivotal genes involved in pigment pathway in tobacco leaf grown in Bijie and Baofeng

Notes:

- K326-Bijie : K326 tobacco variety planted in Bijie (Control)
- Bina1-Bijie : Bina 1 tobacco variety planted in Bijie
- JiUCAIPING2-Bijie : JiUCAIPING 2 tobacco variety planted in Bijie
- Bina1-Baofeng : Bina 1 tobacco variety planted in Baofeng
- JiUCAIPING2-Baofeng : JiUCAIPING 2 tobacco variety planted in Baofeng

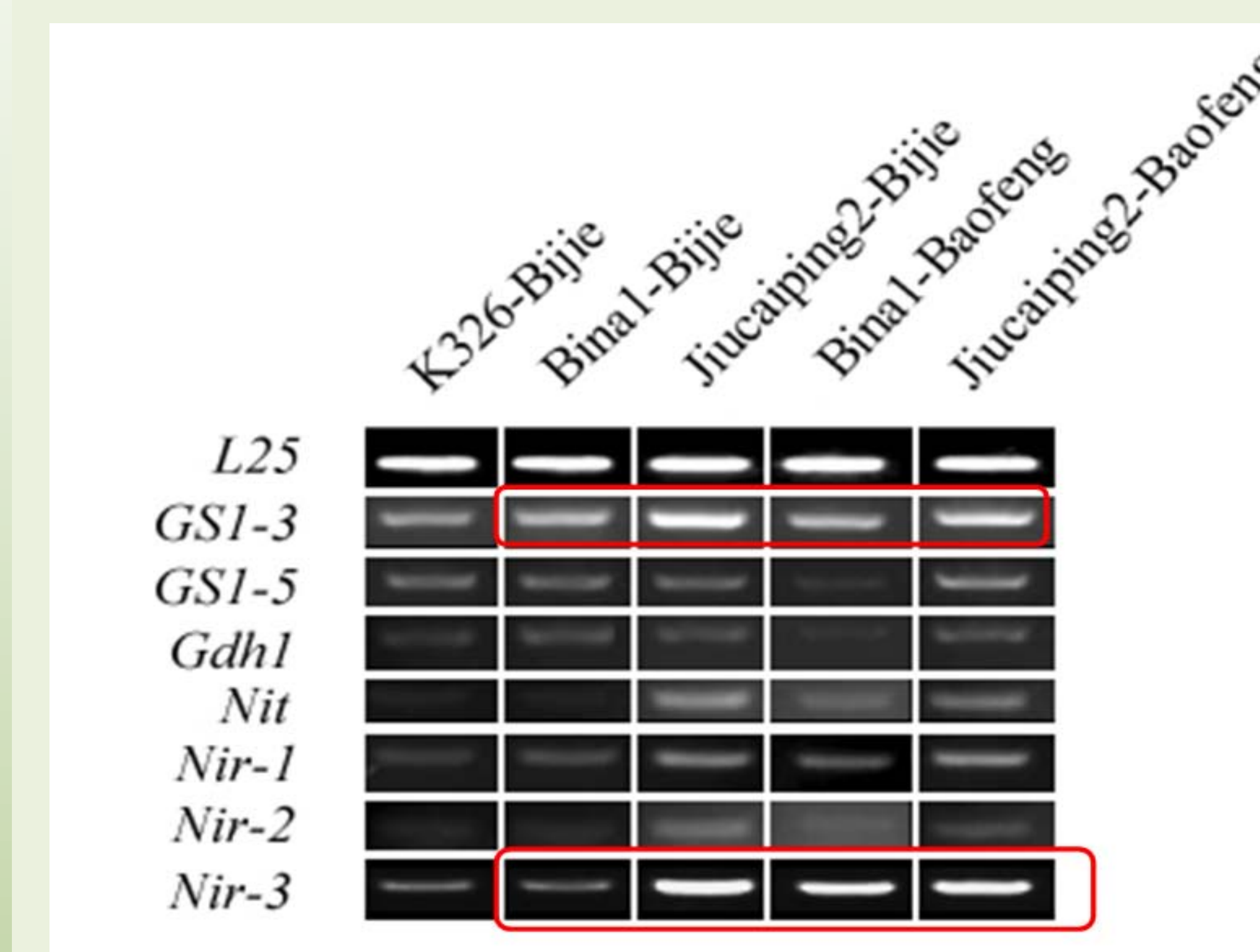


Fig.2

Expression pattern of pivotal genes involved in nitrogen pathway in tobacco leaf grown in Bijie and Baofeng

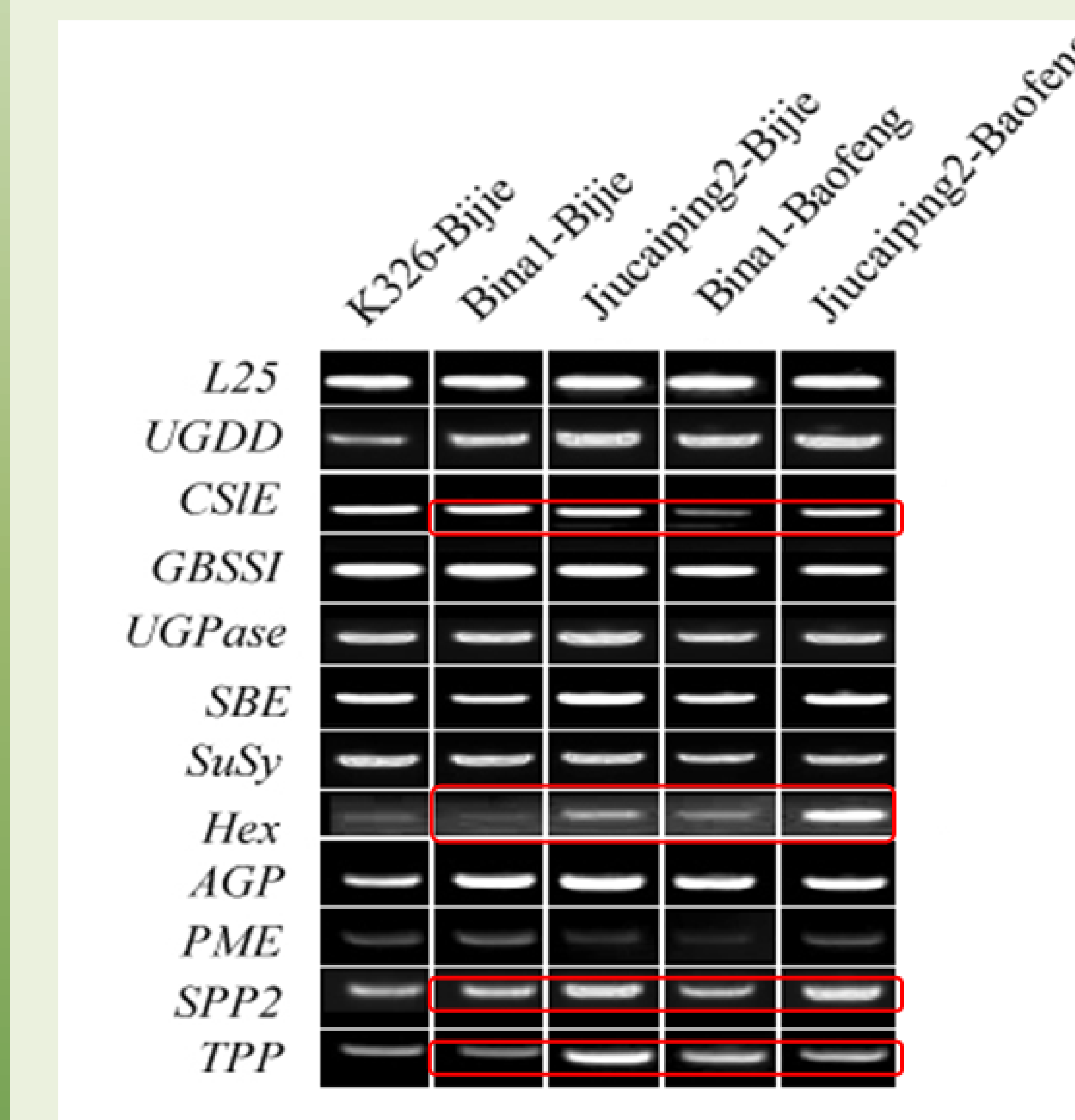


Fig.3

Expression pattern of pivotal genes involved in starch and sugar pathway in tobacco leaf grown in Bijie and Baofeng

Results and Discussion

◆ Although most of the expression of the pivotal genes involved in the pigment, nitrogen, sugar and starch pathways are unchanged between the tobacco varieties Bina 1 and JiUCAIPING 2 or between the leaf sample from Bijie and Baofeng, still few genes were changed dramatically on the level of gene expression. These genes were considered as the key differentially expressed genes among the varieties and climate-response genes.

◆ Differentially expressed genes between Bina 1 and JiUCAIPING 2 are *ZDS*, *Chl*, *GS-1*, *Nir-3*, *Hex*, *SPP2*, *TPP* and all genes expressed at a higher level in JiUCAIPING 2 variety while at a lower in Bina 1 Variety.

◆ Differentially expressed genes between the leaf sample from Bijie and Baofeng are *Nir-3*, *Hex* and *CSIE* gene which are involved in nitrogen and sugar metabolism pathway.

Conclusion

◆ Differentially expressed genes all expressed at a higher level in JiUCAIPING 2 tobacco variety.

◆ Nitrogen and sugar pathway were probably affected mostly by climatic conditions between Bijie and Baofeng.