Genetic control of biosynthesis of soluble isoforms of lipoxygenase in bread wheat grain

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INTRODUCTION

Lipoxygenases (linoleat:oxygen oxidoreductase, EC 1.13.12, Lpx) occur in plants as groups of enzymes catalyzing dioxidation of non-saturated fatty acids with forming superoxide radicals. Structural genes of Lpx are known to be differently expressed in the plant ontogenesis and, apparently, its different isoforms may initiate the synthesis of signaling molecules, be involved in inducing structural or metabolic changes in the cell or may participate in the fine regulation of developmental processes[1]. Lpx expression is regulated by jasmine and abscisic acids and also by different forms of stress, such as wounding, water deficiency, or pathogen attack[2]. The structural genes for Lpx biosynthesis are known to be located in the chromosomes of 4 and 5 homoeological groups[3].

MATERIALS AND METHODS

A full set of bread wheat intervarietal substitution lines, Saratovskaya 29/Janetzkis Probat (S29/JP), with the recipient and the donor having the contrasting levels of LOX activity and 63 recombinant inbred lines of ITMI population were used in this work. Lpx activity was assayed spectrophotometrically according to Doderer[4]. Specific activity was expressed by ratio of activity units to 1 mg of protein in 1 ml of incubation media. Protein concentration was determined by the Lowry method[5]. Results are submitted in % concerning the recipient.

RESULTS AND DISCUSSION

It has been shown, that chromosomes of different homoelogous groups participate in the control of this character. It may be concluded, that the regulator genes affect the functional LOX activity along with the structural genes. During three-years of investigating soluble lipoxygenase activity in grain of substitution lines S29/JP involving chromosomes of 4 and 5 homeologous groups it was found that the donor JP has Lpx activity 2,5 times higher compared to the recipient S29. The most significant influence of substitution for chromosomes 4A and 4D on the trait was detected (1,7 and 1,25 times higher comparing to S29).

Using the recombinant inbred lines of ITMI population the QTL was identified on the short arm of 4B chromosome, near the marker *Xbcd1262* responsible for polymorphism on specific LOX activity[6]. This result corresponds to the data obtained using recombinant inbred lines of durum wheat[7]. In a similar position of 4B chromosome, one of the clusters for defence response was found earlier[8]. It may point to a linked inheritance of the LOX gene with this cluster in 4B chromosome.

In the same material a minor QTL for LOX activity was detected for the first time on 7B chromosome near the marker *Xksud2a*[6]. In a comparable position the QTL was localized and associated with yellow pigment in durum wheat[9]. One of the LOX functions is the degradation of this pigment. In the largest cluster of defence response genes on the long arm of 7B chromosome, two genes of traumatin, *Tha1* and *Tha2*[8] were mapped. This protein is a product of LOX pathway. It is possible that the coincidence of the QTLs positions being close to several physiologically linked characters is not mere chance but may serve as the indirect confirmation of LOX gene existence on the long arm of 7B chromosome in wheat as well as its linking with the genes for defence response.

The mapped positions of LOX genes of barley on 4H and 7H chromosomes[9] coincides with that found in our work, with QTLs on 4B and 7B chromosomes. The gene *LOXC* on 7H chromosome of barley is structural; possibly, there is the structural gene of LOX in 7B chromosome of wheat. It is possible this gene expresses only under certain conditions or (and) the coding isoforms are so scanty that they still need to be identified.

By comparing the positions of newly found and early mapped Lpx genes and loci it may be assumed a similar positioning of loci for soluble forms of lipoxygenase on 4B and 7B chromosomes in bread and durum wheat and barley. Possibly, they are localised in linkage groups with different defence response genes forming big functional units for adaptation of plants to different kinds of stresses. Probably, the soluble isoenzymes coded by these genes, are identical in wheat and barley and are introduced from the one common ancestor.

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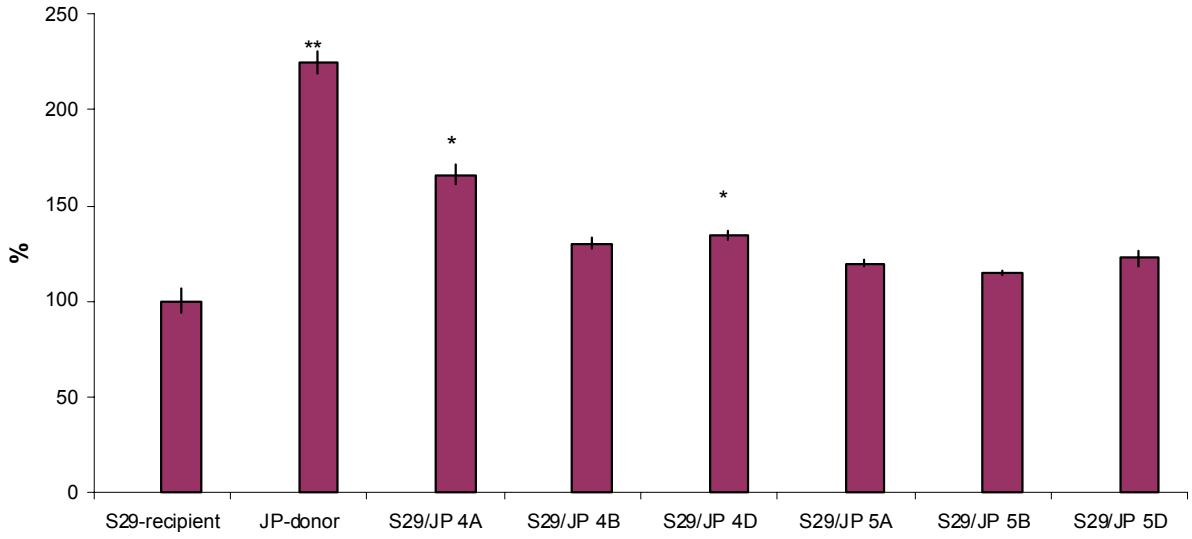

Fig.1. Specific Lpx activity in the intervarietal substitution lines Saratovskaya 29/Janetzkis Probat (S29/JP) on chromosomes of 4 and 5 homoeological groups. *, ** - significantly different from S29 at $P<0.05$, $P<0.01$, accordingly

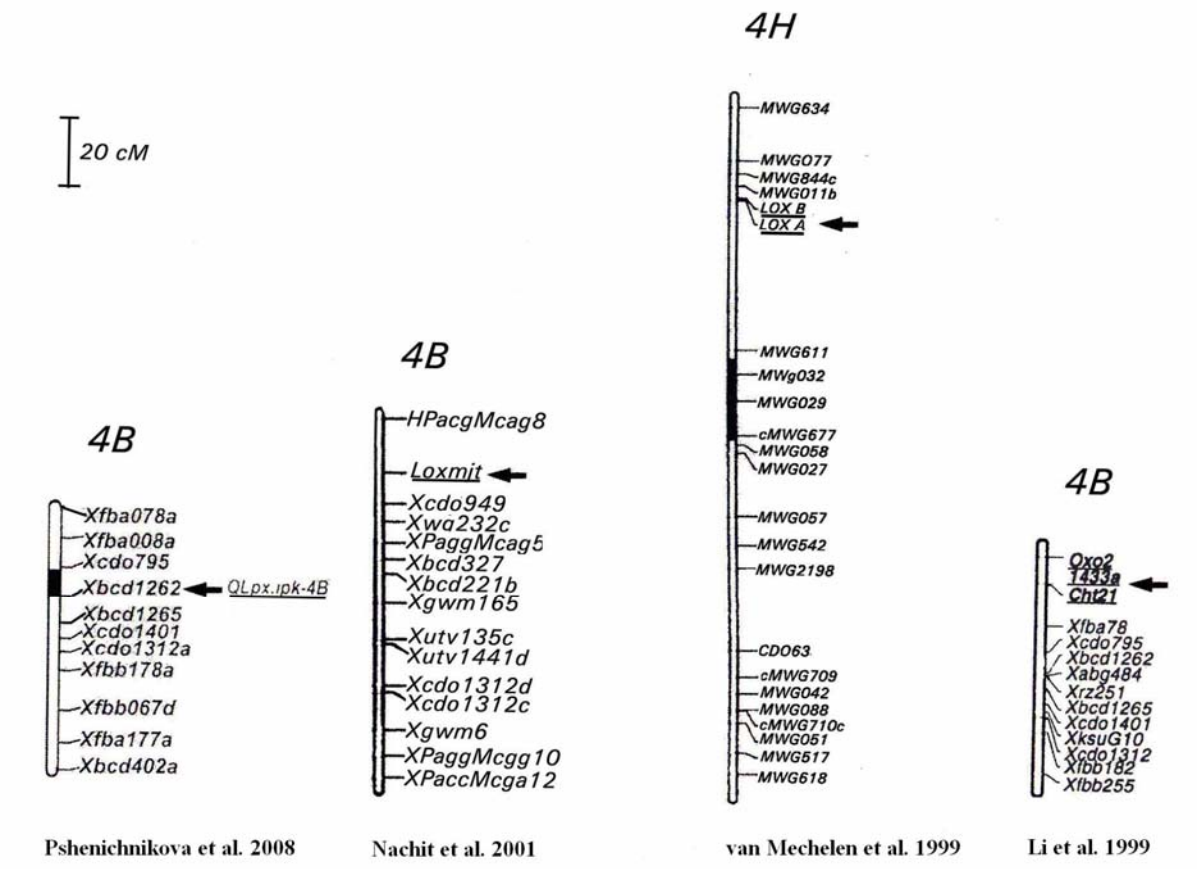

Figure 2. Comparing maps of 4B chromosome of bread and durum wheat and 4H chromosome of barley