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Research review paper

The thioredoxin *h* system: potential applications

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Abstract

The thioredoxin *h* system has the specific capability to reduce intramolecular disulfide bonds of proteins, thereby modifying their tertiary structure. It is involved in many processes: in the activation or deactivation of enzymes and enzyme inhibitors and in the germination process. This system can be used to improve the breadmaking quality of wheat by strengthening the dough. It can also decrease the epitope accessibility, then modifying the response of the IgE immune system. Transgenic barley and wheat have been created to confirm the functionality of the NADP-dependent thioredoxin *h* system.

Keywords: Thioredoxin; Seed germination; Food improvement; Allergenicity

Contents

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1. Introduction

Thioredoxins are small ubiquitous proteins characterized by a conserved dicysteine active site. They participate in dithiol/disulfide exchange reactions with a large range of substrates. In plants, two thioredoxin systems have been characterised, one localised in chloroplasts (*f* and *m* thioredoxins) involved in photosynthesis regulation and the other one in the cytosol (thioredoxin *h*). This latter system is analogous to the one present in animals and microorganisms. To operate, thioredoxin *h* needs to be reduced by the NADP thioredoxin reductase.

In this paper, we will review the different implications of the thioredoxin *h* system during seed germination, for improvement of dough for breadmaking quality and for modification of allergens or venoms properties.

1.1. Thioredoxin h and seed germination

Thioredoxin *h*, a 12-kDa protein with a catalytically active disulfide group, is ubiquitous in the plant kingdom and is localized in the cytosol, the endoplasmic reticulum and mitochondria.

Storage proteins, which are synthesized and stored within seeds, serve as the main source of nitrogen and as a primary source of carbon for the germination and growth of seedlings. When conditions are favourable for germination, these proteins are mobilized and proteolytically degraded. In most kind of seeds, the storage proteins are, even after maturity, enclosed within a membrane, thereby creating a structure known as a protein body. In several cereals, such as wheat, barley, rye, triticale, the protein body membrane is disrupted during maturation and drying of the grain, thereby exposing the storage proteins to endogenous proteases of the endosperm. However, in typically nonglutenous cereals such as corn, rice, sorghum and millet, storage proteins remain in protein bodies in the mature grains.

Several investigators have shown that, akin to the larger insoluble storage proteins, small cysteine-rich proteins of seeds are degraded during germination. Our laboratory has uncovered evidence that both protein groups undergo reduction in conjunction with their degradation This finding is consistent with the observation that these two groups of proteins are resistant to proteolysis in the oxidized (S-S) state. The NADP/thioredoxin *h* system (NTS) appears to play a role in the reduction of critical disulfide bonds of seed proteins (S-S→2SH) and, thereby, as seen below, triggers germination (Wong et al., 1995).

Thioredoxin *h* is reduced via NADPH by the flavin enzyme NADP–thioredoxin reductase (NTR) (Eq. (1)). The reduced thioredoxin *h* reduces disulfide bonds on target proteins (Eq. (2)).

$$\underset{\text{(-S-S-)}}{\textbf{Thioredoxin } \boldsymbol{h} \textbf{ ox}} + \textbf{NADPH} + \textbf{H+} \xrightarrow{\textbf{NADP-Thioredoxin Reductase}} \underset{\text{(-SH HS-)}}{\textbf{Thioredoxin } \boldsymbol{h} \textbf{ red}} + \textbf{NADP+} \quad (1)$$

$$\underset{\text{(-SH HS-)}}{\textbf{Thioredoxin } \boldsymbol{h} \textbf{ red}} + \underset{\text{(-S-S-)}}{\textbf{Protein ox}} \rightarrow \underset{\text{(-S-S-)}}{\textbf{Thioredoxin } \boldsymbol{h} \textbf{ ox}} + \underset{\text{(-SH HS-)}}{\textbf{Protein red}} \quad (2)$$