Abstract

Food allergy belongs among the most frequent disorders and its incidence is continuously rising over the last two decades in the developed world. Although the methods used in the diagnostics of food allergies are high sensitive, they have low specificity, which is affected by a purity of used extracts. Therefore, it is important to develop new proteomic procedures for isolation of food allergens in the pure and the biologically active forms, thereby improving the diagnostics of food allergies. Another approach for studying allergies is using an experimental model, which can help us to clarify the mechanisms of allergic response and the acquired findings employ in prophylaxis or allergy treatment.

In the first part, we have developed a new proteomic procedure for isolation of wheat allergens in the purified form. By this procedure, using Rotofor, HPLC and electrophoretic methods, we identified 27 potential wheat allergens, from which 7 were newly identified: endogenous α-amylase/subtilisin inhibitor, trypsin/α-amylase inhibitor CMX1/CMX3, TLP, XIP-1, β-glucosidase, class II chitinase, and 26 kDa endochitinase. Further, we showed that isolated allergens (α-amylase 0.19, LTP, TLP, and wheatwin) retained their biological activity and were capable to activate basophils (BAT).

In the second part, we isolated and identified rice allergens. For identification, we used raw and boiled forms of rice, which is the most common form for rice consumption. We identified 22 potential rice allergens, from which 6 were newly identified: glutelin C precursor, granule-bound starch synthase 1 protein, disulfide isomerase-like 1-1 protein, hypothetical protein OsI_13867, putative acid phosphatase precursor 1, and protein encoded by locus Os02g0453600. Moreover, for patients with food allergy (mainly wheat allergy), who were strongly positive in immunoblots and in BAT, we recommend to perform additional skin prick tests (SPT) with the boiled rice homogenate including both water-soluble and water-insoluble rice allergens.

In the third part, we introduced a mouse model of food allergy in which we showed that even small irreversible changes in the structure of ovalbumin after thermal processing and enzymatic digestion led to the formation of new epitopes shifting the immune system to Th1 response and reducing the allergic reaction. Furthermore, our preliminary experiments have shown that germ-free mice were not capable to develop the food allergy and even the colonization of germ-free mice by probiotic bacterium *Lactobacillus plantarum* was not sufficient to induce the food-allergy symptoms.