SUPPLEMENTARY MATERIAL

**Supplementary Figure 1.** SDS-PAGE and IgE Western Blot performed under reducing conditions with the following raw extracts: Lanes 1, *Dicologlossa spp.*; 2, *Sole spp.*; 3, *Lepidorhombus spp.*; 4, *Scophthalmus spp.*; 5, *Merluccius spp.*; 6, *Salmo spp.*; 7, *Gadus spp.*

Left, SDS-PAGE shows multiple bands of proteins in all of them, ranging from 10 kDa to more than 75 kDa. Right Western Blot shows a detection of protein bands, including:

1. **Low weight molecular bands (10-14kDa):** showing a weak recognition in Lanes 1, *Dicologlossa spp.*; 2, *Sole spp.*, but did not appear in the other lanes.

2. **High weight molecular bands (ranging from 37 to 50 kDa):** clearly recognized in all the lanes, but with a higher intensity in Lane 1 *Dicologlossa spp.*
Supplementary Figure 2. IgE Western Blot inhibition performed under reducing conditions with raw *Dicologlossa* spp. in solid phase and the patient serum was preincubated with the following fish extracts at 1 μg/ml before the IgE-immunodetection: Lanes 1, without inhibition (negative control); 2, *Dicologlossa* spp. (positive control); 3. *Solea* spp.; 4, *Lepidorhombus* spp.; 5, *Scophthalmus* spp.; 6. *Merluccius* spp.; 7. *Salmo* spp.; 8. *Gadus* spp.

It can be highlighted that in the IgE Western Blot inhibition, the patient serum recognized several protein bands, including the following:

1. **Low weight molecular bands (10-14kDa):** weak recognition in Lane 1, *Dicologlossa* spp. without inhibition (negative control); but it is completely inhibited in Lane 2 *Dicologlossa* spp (positive control) and Lane 3 *Solea*.

2. **High weight molecular bands (ranging from 37 to 50 kDa):** strong recognition in lane 1, *Dicologlossa* spp. without inhibition, partially inhibited in the rest.
**Supplementary Figure 3.** IgE Western Blot inhibition performed under reducing conditions with *Dicologlossa spp.* in solid phase and preincubating patient serum before IgE immunodetection with: Lane 1, without inhibition (negative control); 2, *Dicologlossa spp.* 1 mg/ml (positive control); 3, *Sole spp.* 0.032 mg/ml; 4, *Sole spp.* 0.125 mg/ml; 5, *Sole spp.* 0.5 mg/ml.

Patient serum recognized low weight molecular bands (10-14kDa) in Lane 1, without inhibition, which completely disappeared in Lane 2. This same band, was completely inhibited by *Sole spp.* at all concentrations tested, demonstrating that *Sole spp.* and *Dicologlossa spp.* share a protein with similar epitopes.
Supplementary Figure 4 Mass spectrometry sequencing revealed the identity of a parvalbumin beta-2-like, with a monoisotopic mass of 12185 Da, a calculated pI of 4.81, and a peptide sequence of 109 amino acids (Swissprot, NCBI database). This new protein has a protein sequence coverage of 28% with another parvalbumin beta-2-like of Hippoglossus stenolepis, a subspecies of Solea, included in the order pleuronectiformes.

MASCOT Search Results

Protein View: XP_035036110.1
parvalbumin beta-2-like [Hippoglossus stenolepis]

Database: NCBI-Pleuronectiformes
Score: 78
Expect: 0.0046
Monoisotopic mass (M_r): 12185 Da
Calculated pI: 4.81

Sequence similarity is available as an NCBI BLAST search of XP_035036110.1 against nr.

Search parameters
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)

Protein sequence coverage: 28%

Matched peptides shown in **bold red.**

1  MAFKNILEDAYIAAALVECKDAGTFCHKKEFTTGLALGKSTAVDIKKAFNI
51  IDQDRSCYIEDELKPLQNFDGSAALTDAETHAFLKQAGDTDNDGRIDG
101  DEFVVRNNA

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