**Results (Supplementary Data)**

**P2X7KO mice do not express native P2X7 receptors**

The experimental mice, either native or P2X7KO, used in the present work were generated from five matrix couples that were genotyped prior each new litter, supporting the genetic background of the new generated animals (Supplementary Figure 1). For this, the genomic DNA from the tail of five wild type and five P2X7KO knockouts matrix mice couples were extracted and submitted to PCR reaction using specific set of primers (native for wild type and neomycin for P2X7KO). DNA samples corresponding to each animal was subjected to two PCR reactions, one with primers to amplify a fragment corresponding to the P2X7 native sequence and one with primers for amplification of a region containing part of the P2X7neomycin chimera sequence, obtained by the replacement of the region of the gene encoding Cys506 to Pro532 with the neomycin resistance gene [1]. The amplification of a unique fragment of 418 bp corresponding to the native sequence was observed only when genomic DNA from males and females wild type was used as template (Fig S1, WT panels A and C). None of the ten samples of genomic DNA originated from P2X7KO knockout mice, male and female, showed PCR product amplification using these native primers (Fig. S1, Neo panels B and D). Contrarily, these latter samples showed amplification bands of 510 bp at agarose gels, only in reactions were the 3´neomycin primer was used for amplification (Fig. S1, Neo panels B and C) confirming that animals, that forming matrix couples, carry the mutant allele.

**Material Methods (Supplementary Data)**

**PCR analysis**

Pieces of tail, approximately 5 mm long and weighing 5 mg, were digested overnight at 55° C, with rotation in 500 ml of lysis buffer (100 mM Tris-HCl pH 8.5, 20 mM NaCl, 5 mM EDTA, 0.2% SDS and 20 mg/ml) and 1 ml of proteinase K (10 mg/ml - Sigma-Aldrich). The enzyme was inactivated for 5 minutes at 95° C. The sample was centrifugated 2500 g for 5 minutes, 1 ml of isopropanol was added at the supernant and centrifugated again 7000 g for 10 minutes. The pellet was washed by isopropanol 70% and ressuspended at 200 ml of water. The DNA extract was quantified by absorbance at 260 nm at NanoVue Spectrophotometer (Ge Healthcare).

The PCR mix (25 μl) contained 0.2 mM dNTP, 1 μM of primer and 1.25 units GoTaq DNA polymerase (Promega). Two microliter of the DNA extract (about 250 ng DNA) was added to both PCR mixtures containing the primer combinations for amplification of wild-type and neomycin alleles, respectively. The PCR conditions were: 94°C for 5 min, followed by 26 cycles at 94°C for 30 s, 68°C for 30 s, 72°C for 60 s. Cycling was followed by a final extension step at 72°C for 5 min. PCR primers (Nat) used for wild type sequence mice were P2X7 native forward (GCA GCC CAG CCC TGA TAC AGA CAT T) and P2X7 native reverse (TCG GGA CAG CAC GAG CTT ATG GA); for P2X7KO knockout mice carrying the P2X7 chimera neomycin (Neo) the following primers were used the P2X7 5´ forward (GAC AGC CCG AGT TGG TGC CAG TGT G) and the 3´ neomycin reverse (GGT GGG GGT GGG GGT GGG ATT AGA T) [1].

Sequências P2X7nat:

Senso: 5´gca gcc cag ccc tga TAC aga cat t3´

Antisenso: 5´tcg gga cag cac gag ctt atg ga3´

Sequências P2X7neo

Senso: 5´gac agc ccg agt tgg tgc cag tgt g3´

Antisenso: 5´ggt ggg ggt ggg ggt ggg att aga t3´

Reaction products were run on 1.5% agarose gels (10 μl/lane) in TAE buffer (40 mM Tris–acetate; 1 mM EDTA; pH 8.0) at 136 V and visualized using ethidium bromide staining.

[1] Le Freuve RA, Brough D, Iwakura Y., Takeda K and Rothwell J. Priming of macrophages with lipopolysaccharide potentiates P2X7-mediated cell death via caspase-1-dependent mechanism, independently of cytokine production. J Biol Chem 2002; 277:3210-3218.