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**Figure S1. Upstream Regulator Analysis of MSG.** L-glutamic acid (MSG) induced gene expression in cardiac tissue at 2 hours post-exposure (A) and hepatic tissue 3 hours post-exposure (B). Down regulated genes are shown in green and upregulated genes are in red. The p value and fold change, respectively, of significantly altered genes are shown adjacent to the affected genes. This analysis predicts a modulatory role of monosodium glutamate in the activation of gene expression pathways in cardiac and hepatic tissue following exposure to 1080.

**Table S1. Comprehensive Metabolic Panel.** ALT = Alanine Aminotransferase, AST = Aspartate Transaminase, BUN = Blood Urea Nitrogen. *n* = 4-10, \* *p <* 0.05 one-way ANOVA followed by Dunnett’s multiple comparison test vs. Sham Control.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|   | **Treatment Time** | **ALT (U/L)** | **AST (U/L)** | **BUN (mg/dL)** |
| **Control Sham** | 0.5 h | 65.0 ± 14.3 | 147.3 ± 68.7 | 13.8 ± 5.5 |
| **Control TX** | 0.5 h | 68.5 ± 20.8 | 237.9 ± 172.2 | 29.8 ± 25.1 |
| **Exposed Sham** | 0.5 h | 106.5 ± 64.1 | 247.3 ± 2.00 | 45.2 ± 36.5\* |
| **Exposed TX** | 0.5 h | 64.1 ± 20.3 | 216.8 ± 110.2 | 28.8 ± 18.4 |

**Table S2. Predicted Activation of the Acute Phase Response Pathway.** Predicated activation of the acute phase response pathway in multiple organs following exposure to 1080. The heart, liver, lungs, and kidneys were collected from control and 1080-exposed rats (n=4) at 2 or 3 hours post-exposure, snap frozen, and processed for transcriptomic analysis as described in Materials and Methods. Z scores ≥2.0 indicate the predicted activation of a signaling pathway.

|  |  |  |
| --- | --- | --- |
| **Tissue** | **Z score at 2 Hours** | **Z score at 3 Hours** |
| Heart | 2.31 | 1.79 |
| Liver | 1.89 | 2.14 |
| Lung | 1.13 | 1.51 |
| Kidney | 1.63 | 2.45 |

**Table S3. Predicated Activation of the IL-8 Signaling Pathway in Multiple Organs following Exposure to 1080.** The heart, liver, lungs, and kidneys were collected from control and 1080-exposed rats (n=4) at 2 or 3 hours post-exposure, snap frozen, and processed for transcriptomic analysis as described in Materials and Methods. Z scores ≥2.0 indicate the predicted activation of a signaling pathway.

|  |  |  |
| --- | --- | --- |
| **Tissue** | **Z score at 2 Hours** | **Z score at 3 Hours** |
| Heart | 2.89 | 3.00 |
| Liver | 1.41 | 2.71 |
| Lung | 2.12 | 1.81 |
| Kidney | No change | 1.34 |

**Table S4. Predicated Activation of the IL-6 Signaling Pathway in Multiple Organs following Exposure to 1080.** The heart, liver, lungs, and kidneys were collected from control and 1080-exposed rats (n=4) at 2 or 3 hours post-exposure, snap frozen, and processed for transcriptomic analysis as described in Materials and Methods. Z scores ≥2.0 indicate the predicted activation of a signaling pathway.

|  |  |  |
| --- | --- | --- |
| **Tissue** | **Z score at 2 Hours** | **Z score at 3 Hours** |
| Heart | 2.31 | 2.24 |
| Liver | 2.12 | 2.32 |
| Lung | 1.63 | 2.50 |
| Kidney | 1.63 | 2.24 |

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**Figure S2. IL-10 Concentration.** Animals were exposed to 0.5 x LD50 of 1080. Treated animals were given MB (5mg/kg, SC) and MSG (250 mg/kg, IP). Injections were administered 0.5 h after exposure and BALF was collected 24 h after exposure. Error bars indicate standard deviation with average marked, n = 6, no significance found with one-way ANOVA followed by Dunnett’s multiple comparison test vs. Sham Control.

**Table S5. White Blood Cell Counts.** WBCs = Total white blood cells, *n* = 4-10.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|   | **Treatment Time** | **WBCs (103/µl)** | **Neutrophils (103/µl)** | **Lymphocytes (103/µl)** | **Monocytes (103/µl)** |
| **Control Sham** | 0.5 h | 6.67 ± 1.53 | 1.46 ± 0.92 | 4.90 ± 2.08 | 0.47 ± 0.37 |
| **Control TX** | 0.5 h | 7.14 ± 1.67 | 1.76 ± 0.74 | 4.98 ± 1.94 | 0.75 ± 0.97 |
| **Exposed Sham** | 0.5 h | 6.66 ± 0.95 | 2.78 ± 2.19 | 3.17 ± 2.00 | 0.52 ± 0.15 |
| **Exposed TX** | 0.5 h | 4.58 ± 1.87 | 1.52 ± 0.27 | 3.61 ± 3.84 | 0.37 ± 0.15 |