

We have recently updated the information associated with each spot on our *S. enterica* sv. Typhimurium cDNA microarray upon which our 2003 Chan et al, *Journal of Bacteriology*, 185(2):553 paper was based. We have since re-analyzed the dataset and noted differences between this analysis and the published one. The vast majority of conclusions are not significantly impacted by the array updates. For example, the overall relationship of the serovars relative to one another does not change, the distinction of the human enteric fever associated serovars from the others is maintained, Arizona is still the most distinct of the serovars analyzed, and the behavior of SPI1, SPI2, and the virulence plasmid is consistent with what was published. We would nevertheless like to direct scientists to changes in the publicly available datasets and the Appendices referred to in the paper which are supported by our laboratory's website.

Listed below are some of the statements made within the text of the article that have changed upon reanalysis. A few changes are not significant (for example, the exact size of the final dataset is slightly smaller at 4,519 spots total) and therefore not mentioned. Again, we feel that the fact that the majority of results stated and the conclusions made do not change should be emphasized. However, the composition of the publicly available datasets does change which could ultimately influence some researchers' work. These Appendices and the raw datasets available for downloading from <http://genome-www5.stanford.edu/> have been updated.

List of Updated Changes to the Manuscript

Section in Manuscript	Original Result/Observation	Updated Information	Impact/Significance
M & M Data Analysis Pg. 555 Paragraph 2	410 false positive/negatives spots 250 false positive 160 false negative	91 fp/fn spots 71 fp 20 fn	Increased fidelity of array reflected in updated information
R & D Pg. 557 Paragraph 4	“... <i>sipA</i> , <i>sptP</i> , and <i>sipB</i> – gave microarray hybridization patterns the corresponded with that expected of the SARB set.”	<i>sipA</i> is absent in the updated dataset – can’t make conclusions about it	Uncertain about significance
R & D Pg. 557 Paragraph 5	In the core genes section, stated “Components of the <i>phs</i> operon... found to be present across the serovars.”	Is actually absent in Gallinarum, consistent with biochemical feature of this serovar	Better reflects biochemical information
R & D Pg. 559 Paragraph 1	In the core genes section, stated “... (<i>slrP</i> , <i>pagP</i> , <i>sopB</i> ... are shared across the serovars.”	<i>pagP</i> is absent in the updated dataset – can’t make conclusions about it	Uncertain about significance
R & D Pg. 559 Paragraph 3 Table 1		Estimates of % SL1344 genes shared is 1-2% lower for most non-Typhimurium serovars upon reanalysis. The order of the serovars with percentage values close to each other changes slightly.	Not significant as the percentages are still comparable to previously observed results and are within a reasonable level of variability.
R & D Pg. 559 Paragraph 5 Figure 2C	“... Tm2 appears to be genetically distinct from the other three strains of serovar Typhimurium.”	Upon reanalysis, all three strains are indistinguishable	Not significant
R & D Pg 560-561 Full Paragraph 2 Figure 4	There is a group B signature highlighted by the presence of <i>oafA</i> .	The group B signature, with <i>oafA</i> , is still present. However, the composition of this cluster does change.	Reflects the updated spot information. Significant for those that want to explore of group B serovars differ from the others.
R & D Pg. 560-561 Full Paragraph 4 Figure 3	There is a human disease and cold-blood associated cluster.	This cluster still exists and the <i>lpf</i> and <i>sodC</i> genes are still present. However, the composition of the other genes changes.	Significant for those that want to explore the human enteric disease serovars.