

Novel Malaria Vaccine Candidates

Malaria remains one of the world's most deadly diseases, killing a child under five years of age every 30 seconds. Our Branch aims to produce and characterize recombinant protein vaccines for Phase I and II human trials. We use Wyatt instruments coupled to a Waters HPLC to characterize these recombinant proteins. Wyatt instruments facilitate our understanding of purity, identity and aggregation states of recombinant protein vaccine candidates.

The solution profile of a candidate antigen was analyzed using analytical size exclusion chromatography with on-line multi-angle light scattering (SEC-MALS-HPLC), refractive index (RI) and ultraviolet (UV) detection. A Waters 2695 HPLC and 2996 PDA detector was connected in series to a Wyatt EOS and an Optilab RI detector run by the ASTRA V software suite. An isocratic elution at 0.5 mL/min was performed using a Tosoh Biosciences TSK gel G3000PWxl column (Part#:08021) and TSK gel Guard PWxl column (Part#:08033) with 0.04mM KH_2PO_4 , 2.97mM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 308mM NaCl, 0.5M urea, pH 7.4, 0.02% sodium azide for mobile phase.

The SEC-MALS trace in Figure 1 suggests the solution state of our vaccine candidate was comprised of three populations. Using the supportive resources at Wyatt Tech. Inc., we concluded that we did not have complete separation of monomer and dimer on the leading edge of the monomer peak. In addition, and perhaps more importantly, there appears to be a large M_w species (whose peak max shows up early—at 12.5 min) that is bleeding onto everything afterward, as seen in Figure 2.

The Wyatt SEC-MALS results clearly indicated the presence of three populations, monomer, dimer and tetramer, which was later verified by boundary sedimentation equilibrium studies.

This note graciously submitted Richard L. Shimp, Jr., David L. Narum, and Peter F. Duggan, Malaria Vaccine Development Branch (NIAID/NIH) Rockville, MD. Full details published in *Protein Expression and Purification* (in press) doi:10.1016/j.pep.2006.06.018.

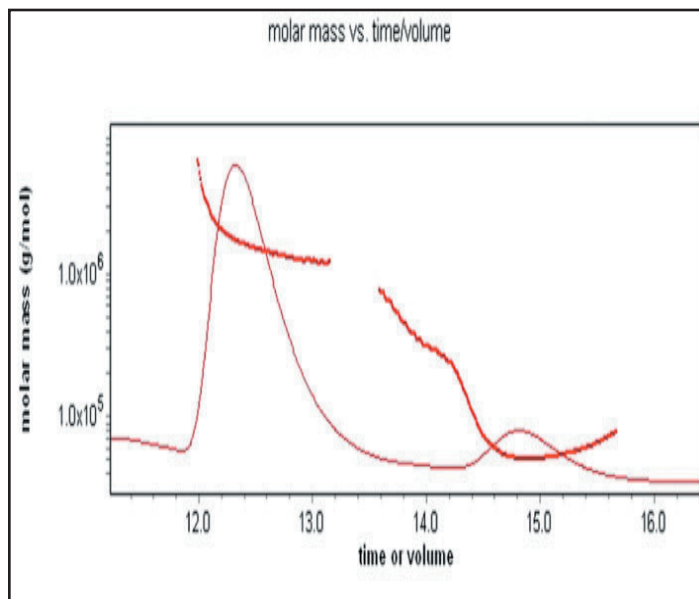


Figure 1. MALS results of the sample showing tetramers and dimers mixed in with monomer populations. The expected mass should be about 43kDa.

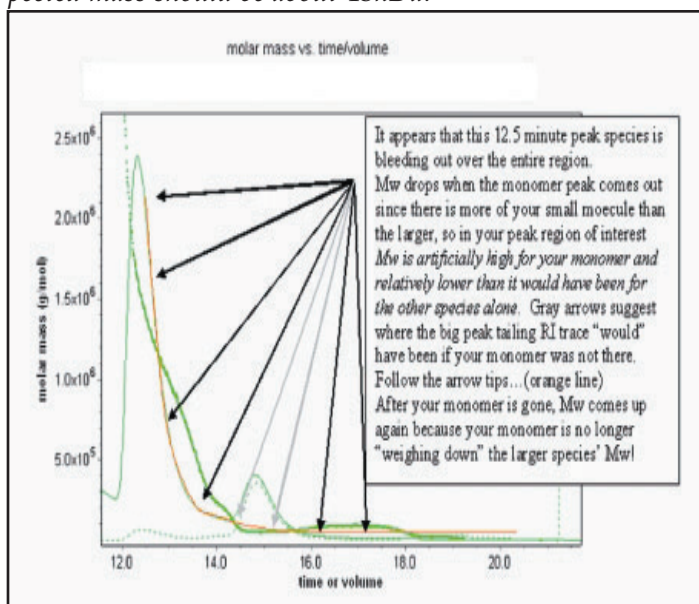


Figure 2. Interpretation of the results which suggest there is a mixture of monomer and aggregate forms of the vaccine.