Cybertaxonomy, phylogenomics, and other big words:
Can they really solve the challenges of hemiptera systematics?

**Colin Favret**

*University of Montreal, Biodiversity Centre, 4101 rue Sherbrooke est, Montreal (Quebec), H1X 2B2 Canada*

*ColinFavret@AphidNet.org: ORCID 0000-0001-6243-3184*

Today’s insect systematists are faced with unprecedented challenges and opportunities. On the one hand, the vast majority of the astounding diversity of insect life remains to be scientifically documented even as our world enters a new epoch of mass extinction. On the other hand, advances in biological and information technology have dramatically improved our capacity for data gathering and analysis as well as knowledge acquisition, integration, and diffusion. The latter progress is often touted as a solution to the former challenge. Cybertaxonomy is being implemented to automate routine tasks, improve taxon discrimination, democratize taxonomy, and facilitate the synergy of networked taxonomists. Phylogenomics is resolving some of the most vexing problems in phylogenetics and classification. Advances in biodiversity informatics, molecular species delimitation, automated character extraction, and machine vision pattern recognition, among others, are also playing important roles. Using recent research in Hemiptera systematics, and more particularly that of aphids, I will describe how modern methods are helping to advance the field and address its particular challenges. Yet, despite being one of the better-studied insect taxa, there is still a very long road ahead in aphid systematics, all the more so for other insect groups. I will discuss some of the major impediments and highlight the inability of modern methods to provide final resolution. The answer to the question in the title is obviously “no”, but significant progress is being made nonetheless.