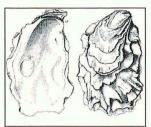
Crassostrea gigas or Magallana gigas: A Community-based Scientific Response

Recently, the oyster research, aquaculture, and trade communities were shaken up by the publication of two papers by Daniele Salvi et al. (2014, 2017) in which the genus *Crassostrea* was split into three different genera, such that the genus *Crassostrea* was shrunk to



include only the Atlantic species, while the Pacific species were assigned to the genera Talonostrea and Magallana. The consequence of this taxonomic action was that the well-known Crassostrea gigas was rebaptized to Magallana gigas. This nomenclatural change was almost immediately endorsed and "World the Register implemented by of Marine (WoRMS), which could give the erroneous Species" impression that from now of the name Crassostrea gigas should be abandoned in favour of Magallana gigas. Such a rash nomenclatural change for this well-known species worldwide is, however, not necessary and, in my opinion, even ill-advised for it would destabilize a long-term use of a commonly accepted, unequivocal name. Luckily, this point is also recognized by WoRMS itself, since it does recognize the Crassostrea gigas as an "accepted, alternate name representation" of Magallana gigas. In the same spirit, WoRMS does recognize Crassostrea talonata as an "accepted, alternate representation" of Talonostrea talonata. Hence, Crassostrea researchers, students, and the oyster stakeholders community in general, should not contribute to possible confusion or make life difficult by starting to implement the name Magallana gigas or by applying the names Magallana and Talonostrea to the former Pacific Crassostrea species. There is neither a nomenclatural obligation, nor a scientific need to do so! On the contrary, let us maintain nomenclatural stability and continue using the genus name Crassostrea in its former, well-accepted sense for both the Atlantic and Pacific cupped oysters. This use is perfectly supported by morphological, cytogenetic and DNA sequence evidence, showing that the former genus Crassostrea is a well-defined clade (monophyletic taxon), a point that was raised by Bayne and 25 co-authors (2017), who argued strongly against the split of Crassostrea into three genera. I'm far from alone with my concerns and I recommend reading the Bayne et al. (2017) paper for a compelling rationale to maintain the genus Crassostrea as it was.

Of course the preceding statement could easily be interpreted as the reaction of old-fashioned, grumpy, taxonomists, who want to stick to old habits and who do not want to accept scientific progress. Yet, this is not the case, for the co-authors in the rebuttal paper of Bayne et al. (2017) are all well-known oyster biologists, except for myself. In fact, as a Molluscan taxonomist, I personally do not reject the work by Salvi et al. (2014, 2017) as such, for on the basis of nuclear and mitochondrial DNA sequence data they do provide good evidence that the former Crassostrea clade indeed is split into an Atlantic (= Crassostrea sensu stricto) and a Pacific clade, both well-supported, and that this Pacific clade can be further divided into two well-supported clades that can be referred to as Magallana and Talonostrea. This Atlantic vs Pacific division of Crassostrea was, however, already observed long before the work of Salvi et al. (see e.g. O'Foighil et al. 1995; Wang et al. 2004), but it was never felt necessary to translate this division into a genus-level split. Now one can discuss how many and what sort of data are needed to delimit genera (since

there is no operational definition of a genus, except that it should be a monophyletic taxon) and one can question a number of specific issues in the work of Salvi et al. (as is done by Bayne et al. 2017), but the main point I wish to make here is that taxonomists should always try as much as possible to maintain nomenclatural stability and thus should wonder about the relevance and added value of introducing a new taxonomy and its concomitant nomenclatural changes. As such taxonomists should, by default, act conservatively. In the present case of Crassostrea, there simply is no added value to splitting this genus into three separate genera, since the former Crassostrea clade remains phylogenetically unaltered. On the contrary, by dividing Crassostrea into three genera one complicates nomenclature for the users since now three generic names have to be remembered and associated with the correct species. So, who gains from this? How does it help the users of *Crassostrea* taxonomy? Moreover, one will always be able to divide a "genus" into subclades (up to individual species), but is that a logical ground to give such subclades a genus-level rank? Of course not, for there is no general definition of what a genus really is (in fact it is just one of the, many, human hierarchical classificatory categories to delimit clades). As such, the former genus Crassostrea is just as well acceptable as a genus, as are the three "genera" into which it was split. All in all... the whole issue comes to a choice between splitting and lumping, and in that perspective I would always advocate to use nomenclatural stability as a decisive benchmark.

Against this background, there is no reason to drop the current use of *Crassostrea* for the Atlantic and Pacific cupped oysters jointly, and hence let us appreciate the work of Salvi et al. (2014, 2017) for its contribution to documenting the relationships among these two clades, without destabilizing a long-standing, commonly accepted nomenclatural framework. This is not only my opinion, but the opinion of a large community of oyster biologists, who expressed their concerns in the Bayne et al. (2017) rebuttal paper.

So, the name *Crassostrea gigas* should prevail, and the genus *Crassostrea* should be maintained as it was before its split into two or three genera.

Thierry Backeljau Royal Belgian Institute of Natural Sciences & University of Antwerp, Belgium

Bayne, B.L., Ahrens, M., Allen, S.K., Angl Es D Auriac, M., Backeljau, T., Beninger, P., Bohn, R., Boudry, P., Davis, J., Green, T., Guo, X., Hedgecock, D., Ibarra, A., Kingsley-Smith, P., Krause, M., Langdon, C., Lap Egue, S., Li, C., Manahan, D., Mann, R., Perez-Paralle, L., Powell, E.N., Rawson, P.D., Speiser, D., Sanchez, J.-L., Shumway, S. & Wang, H. 2017. The proposed dropping of the genus *Crassostrea* for all Pacific cupped oysters and its replacement by a new genus *Magallana*: A dissenting view. *Journal of Shellfish Research*, 36: 545-547.

O'Foighil, D., Gaffney, P.M. & Hilbish, T.J. 1995. Differences in mitochondrial 16S ribosomal gene sequences allow discrimination among American [*Crassostrea virginica* (Gmelin)] and Asian [*C. gigas* (Thunberg) *C. ariakensis* Wakiya] oyster species. Journal of Experimental Marine Biology and Ecology, 192: 211-220.

Salvi, D., Macali, A. & Mariottini, P. 2014. Molecular phylogenetics and systematics of the bivalve family ostreidae based on rRNA sequence-structure models and multilocus species tree. *PLoS ONE* 9: e108696.

Salvi, D. & Mariottini, P. 2017. Molecular taxonomy in 2D: a novel ITS2 rRNA sequence structure approach guides the description of the oysters subfamily Saccostreinae and the genus *Magallana* (Bivalvia: Ostreidae). *Zoological Journal of the Linnean Society*, 179: 263–276.

Wang, Y., Xu, Z. & Guo, X. 2004. Differences in the rDNA-bearing chromosome divide the Asian-Pacific and Atlantic species of *Crassostrea* (Bivalvia, Mollusca). *Biological Bulletin*, 206: 46–54.