

## Morphological and Genetic Differentiation among Subspecies of *Taeniatherum caput-medusae*: Disentangling Taxonomic Complexity in the Native Range

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### Abstract

Across its native range, *Taeniatherum caput-medusae* (L.) Nevski (medusahead) exhibits taxonomic complexity. Three subspecies have been recognized: *T. caput-medusae* ssp. *caput-medusae*, *T. caput-medusae* ssp. *asperum*, and *T. caput-medusae* ssp. *crinitum*. While subspecies *caput-medusae* is found in the western Mediterranean and subspecies *crinitum* occurs from eastern Europe to Central Asia, subspecies *asperum* is found throughout the entire geographic distribution of the species. Only subspecies *asperum* is believed to occur in the United States, where it is now invasive in portions of California, Idaho, Nevada, Oregon, Utah and Washington. As part of our ongoing research to better understand and manage this invasion, we are conducting genetic analyses of both native and invasive populations of medusahead. An important prerequisite to these analyses is the proper identification of the three subspecies. In the current study, plants from each native population were grown in a greenhouse common garden, harvested at maturity, and measured using previously described morphological characters. After Bonferroni correction, three characters: glume length, glume angle and palea length, were found to be statistically significant. Thus, these three characters were quite useful in assigning plants to each of the three subspecies. We found that two other characters, lemma hairs and conical cells, were less informative. Differentiation among native populations of medusahead was further assessed using a molecular genetic marker. The results of a UPGMA cluster diagram based on allozyme data, indicates that subspecies *crinitum* is genetically differentiated from the other two subspecies; some populations of subspecies *caput-medusae* and *asperum* co-occur within different clusters; and subspecies *asperum* is the most variable. Results of the analysis of multilocus genotypes are generally consistent with the UPGMA diagram (e.g., subspecies *caput-medusae* and *asperum* share six multilocus genotypes). Our findings confirm the need of such studies to disentangle the taxonomic complexity that can be found in the native range of invasive species.