Erratum to: Invasion of *Bromus tectorum* (L.) into California and the American Southwest: rapid, multi-directional and genetically diverse

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In Table 4 of the original publication, the final portion of the footnote was inadvertently deleted in the electronic PDF version of the article. The corrected version of Table 4, which has been edited to improve its clarity, is shown in this erratum:

The online version of the original article can be found under doi:[10.1007/s10530-014-0728-8](https://doi.org/10.1007/s10530-014-0728-8).

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Table 4 The likelihood that *B. tectorum* in regions in the study area was derived from specific geographic regions elsewhere in the United States

Region	Potential source of <i>B. tectorum</i>	Ln(likelihood)
Great Basin	Eastern USA	−147.57
	Mid-Continent USA	−241.97
	Central USA	−477.33
	Northwestern USA	<−500.00
Northern California	Northwestern USA	−267.68
	Mid-Continent USA	<−500.00
	Central USA	<−500.00
	Eastern USA	n/a
Southern California	Eastern USA	−17.22
	Mid-Continent USA	−39.17
	Central USA	−98.11
	Northwestern USA	−160.77
Southern Arizona	Northwestern USA	−104.29
	Central USA	−253.46
	Mid-Continent USA	−327.95
	Eastern USA	n/a

Populations in specific geographic regions are ranked according to their likelihood as a source; the least negative value indicates the most likely source region. Genotypes common to a region and all potential source populations were included in the analysis. The Eastern USA, which lacks populations with the *Got-4c* genotype, was excluded (n/a) as a source for Northern California and Southern Arizona populations. Ln(likelihood) values of <−500.00 indicate extremely negative values (e.g., 1.00×10^{-10})