

# Correction

**EVOLUTION.** For the article “Adaptive evolution in the *Arabidopsis* MADS-box gene family inferred from its complete resolved phylogeny,” by León Patricio Martínez-Castilla and Elena R. Alvarez-Buylla, which appeared in issue 23, November 11, 2003,

of *Proc. Natl. Acad. Sci. USA* (**100**, 13407–13412; first published November 3, 2003; 10.1073/pnas.1835864100), due to a printer’s error in the footnote of Table 1, “\*,  $P < 0.05$ ” incorrectly appeared as “\*,  $P < 0.5$ .” The corrected table appears below.

**Table 1. Sites under PDS in the *A. thaliana* MADS-box gene family: “Site-specific analyses”**

Site-specific analyses (type I)	n	dN/dS ( $\omega$ ) under M0	$2\Delta\ell$ M3 vs. M0 (df LRT 3)	$2\Delta\ell$ M2 vs. M1 (df 2)	$2\Delta\ell$ M8 vs. M7 (df 2)	Parameter estimates under M8 $\beta$ (p,q)	Positively selected sites under M3	Positively selected sites under M2	Positively selected sites under M8
Node AG	7	0.22	28.76***	10.10*	10.57*	$P_1 = 0.98, \omega = 8.44$ $\beta (0.87, 3.82)$	<u>123</u>	No rate classes with dN/dS > 1	<u>123</u>
Node AH	7	0.26	59.09***	11.75**	7.36*	$P_1 = 0.81, \omega = 1.96$ $\beta (0.87, 3.48)$	<u>73</u> <u>74</u> <u>61</u> <u>72</u> <u>82</u> <u>107</u> <u>63</u>	<u>73</u> <u>74</u> <u>72</u> <u>61</u> <u>82</u> 63 107 107 <u>63</u> <u>48</u> <u>58</u> 81 110	<u>73</u> <u>72</u> <u>74</u> <u>61</u> <u>82</u>
Node AL	9	0.25	90.35***	18.39***	4.55	$P_1 = 0.93, \omega = 1.24$ $\beta (0.80, 2.28)$	<u>61</u> <u>72</u> <u>73</u> <u>82</u> <u>107</u> <u>110</u> <u>48</u> <u>74</u> <u>86</u> <u>58</u> <u>64</u> <u>66</u> <u>63</u> <u>65</u> <u>109</u>	<u>72</u> <u>73</u> <u>82</u> <u>74</u> <u>61</u> 107 48 110	<u>72</u> <u>73</u> <u>82</u> <u>48</u> <u>61</u> 74 107 110 58
Node AP	12	0.25	130.47***	21.26***	7.59*	$P_1 = 0.75, \omega = 1.18$ $\beta (0.56, 3.46)$	<u>58</u>	<u>58</u> <u>48</u> <u>57</u> <u>78</u> <u>89</u> 72 123 <u>73</u> <u>81</u>	<u>48</u> <u>57</u> <u>58</u> <u>72</u> <u>73</u> <u>78</u> <u>89</u> <u>123</u> <u>59</u> <u>65</u> <u>81</u> 47 60 <u>66</u> <u>92</u> <u>74</u> <u>100</u>
Node AQ	14	0.22	116.71***	14.97***	7.73*	$P_1 = 0.97, \omega = 4.67$ $\beta (0.47, 1.52)$	<u>58</u> <u>89</u>	<u>58</u>	<u>58</u>
Node AR	20	0.15	102.65***	30.18***	8.22*	$P_1 = 0.96, \omega = 1.12$ $\beta (1.64, 8.94)$	No rate classes with dN/dS > 1.	<u>73</u> <u>82</u> <u>72</u>	<u>82</u> <u>73</u>

Each comparison has  $n$  sequences, dN/dS is average ratio over sites under a codon model with one  $\omega$ . Proportion of the component of positively selected sites ( $P_1$ ) and parameters p and q of the beta distribution  $\beta(p,q)$  are given under M8. \*,  $P < 0.05$ ; \*\*,  $P < 0.005$ ; \*\*\*,  $P < 0.001$ ; bold underlined,  $PP \geq 0.99$  of being under positive selection; bold,  $0.99 > PP \geq 0.95$ ; italics,  $0.95 > PP \geq 0.90$ ; underlined,  $0.90 > PP \geq 0.70$ ; normal,  $0.70 > PP \geq 0.50$ .

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