

Fig. 1 Phenotypic appearance of *Hordeum vulgare*, *H. glaucum* and *H. marinum* plants grown under control hydroponic and salinity stress conditions. (a) Shoot phenotype; (b) Relative growth rate; (c) Plant water content; (d-e) Osmotic pressure of tissue sap from shoots (d) and roots (e). Data are mean \pm SD; n = 5, *t* significant at: ***, $P < 0.001$. (f-q) Root phenotypes as analyzed by Magnetic Resonance Imaging. (f-g) 2D projections of 3D images of salt-stressed roots of *H. vulgare* (f), *H. glaucum* (g) and *H. marinum* (h). The 3D images are shown in the Supplemental Movies S1 and S2. Red triangles point to root branches. (i-n) Virtual cross sections of control (i-k) and salt-stressed roots (l-n) of *H. vulgare* (i, l), *H. glaucum* (j, m) and *H. marinum* (k, n). (o-q) Virtual cross sections of individual control (left) and salt-stressed roots (right) of *H. vulgare* (o), *H. glaucum* (p) and *H. marinum* (q). Bars, 1 mm in (i-n), 500 μ m in (o-q).

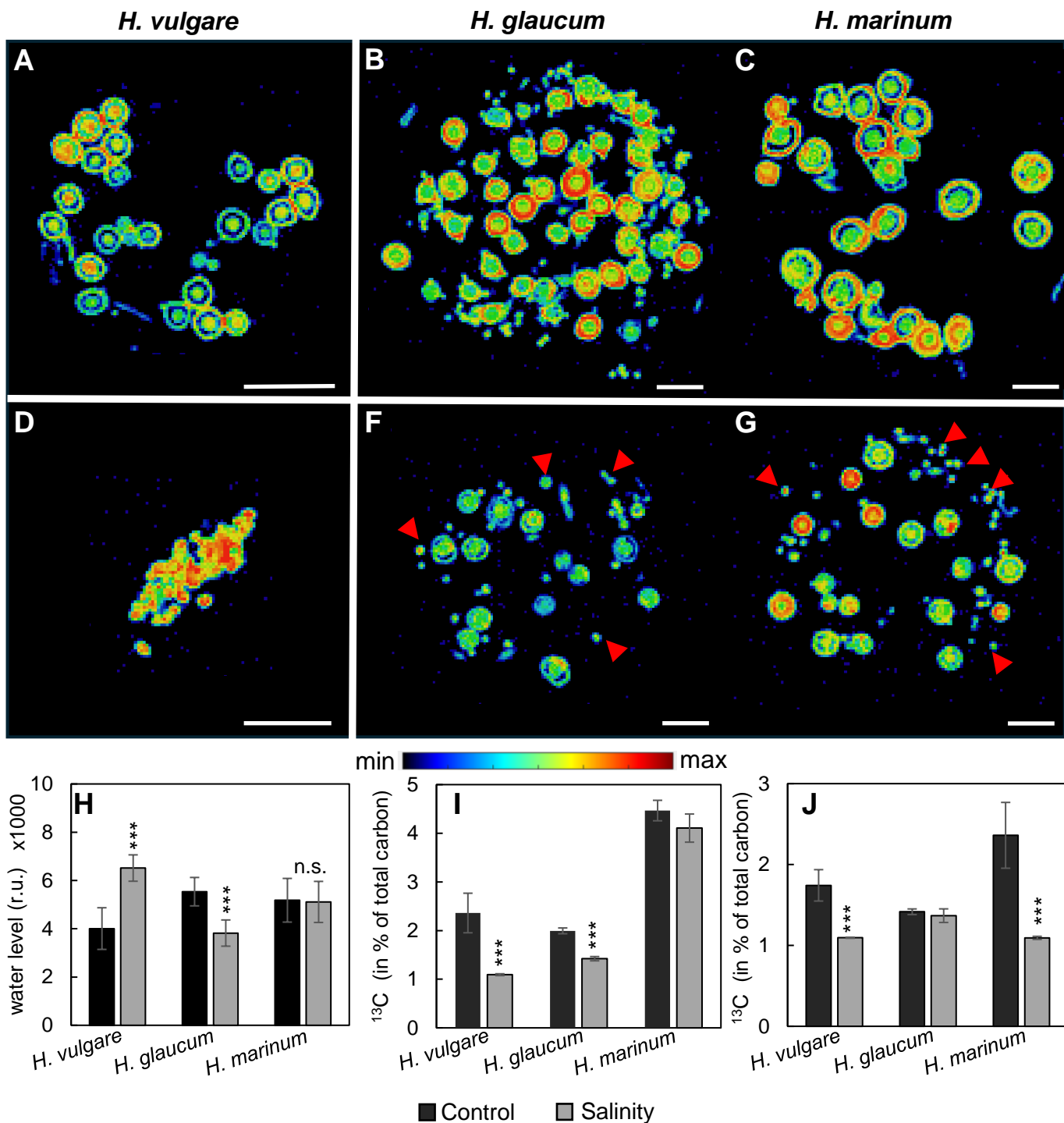


Fig. 2 Root water distribution, and ^{13}C -uptake and distribution in plants under hydroponic control and salt-stressed conditions. (a-g) Water distribution in virtual cross sections of control (a-c) and salt-stressed roots (d-g) of *H. vulgare* (a, d), *H. glaucum* (b, f) and *H. marinum* (c, g) as analyzed by Magnetic Resonance Imaging. Min/max values of the color bar represent the relative water concentrations. Red triangles indicate new formed roots under salinity stress. Bars, 1 mm in (a, d), 500 μm in (b, c, f, g). (h) Quantification of water content in roots of three barley species analyzed in (a-g). (i, j) ^{13}C -uptake and distribution in shoots (i) and roots (j) of three barley species under control and salinity stress conditions. Data are mean \pm SD; n = 7-25 in (h), = 3-5 in (i, j), *t* significant at: ***, $P < 0.001$, n.s., not significant.

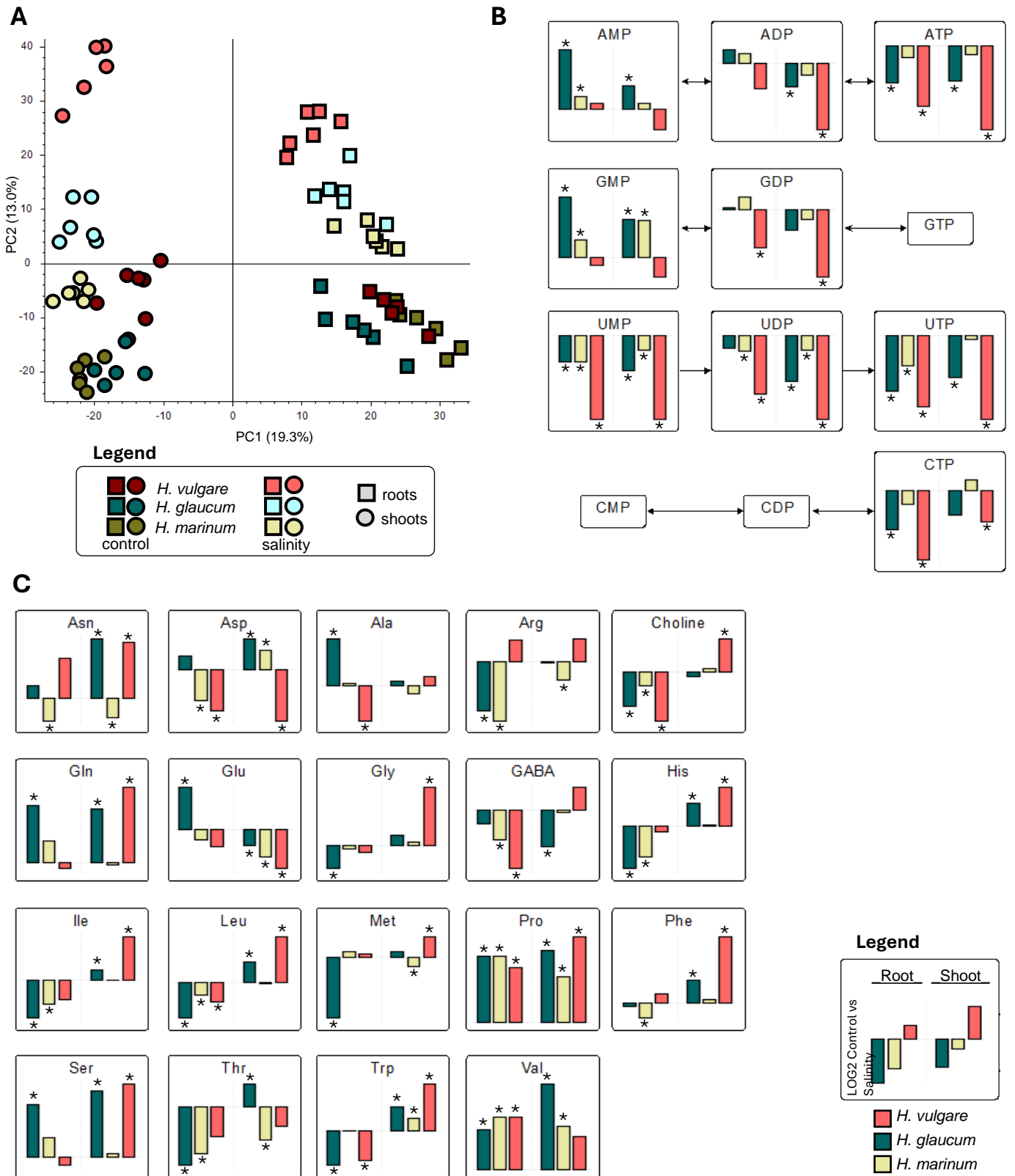


Fig. 3 The effect of salinity stress on metabolite content in three barley species. (a) Principal component analysis of metabolite distribution in roots and shoots of *H. vulgare*, *H. glaucum* and *H. marinum* plants grown under control and salinity stress conditions. (b, c) Changes in nucleotide (b) and amino acid content (c). Metabolomic data in (b, c) are shown as $\log_2(\text{fold-change})$ values of the relation salinity to control, negative values mean decreased metabolite content, positive values – increased metabolite content. Adjusted p -values were calculated using Benjamini-Hochberg correction method and significantly different values are indicated by *, $P < 0.05$ ($n = 6$).

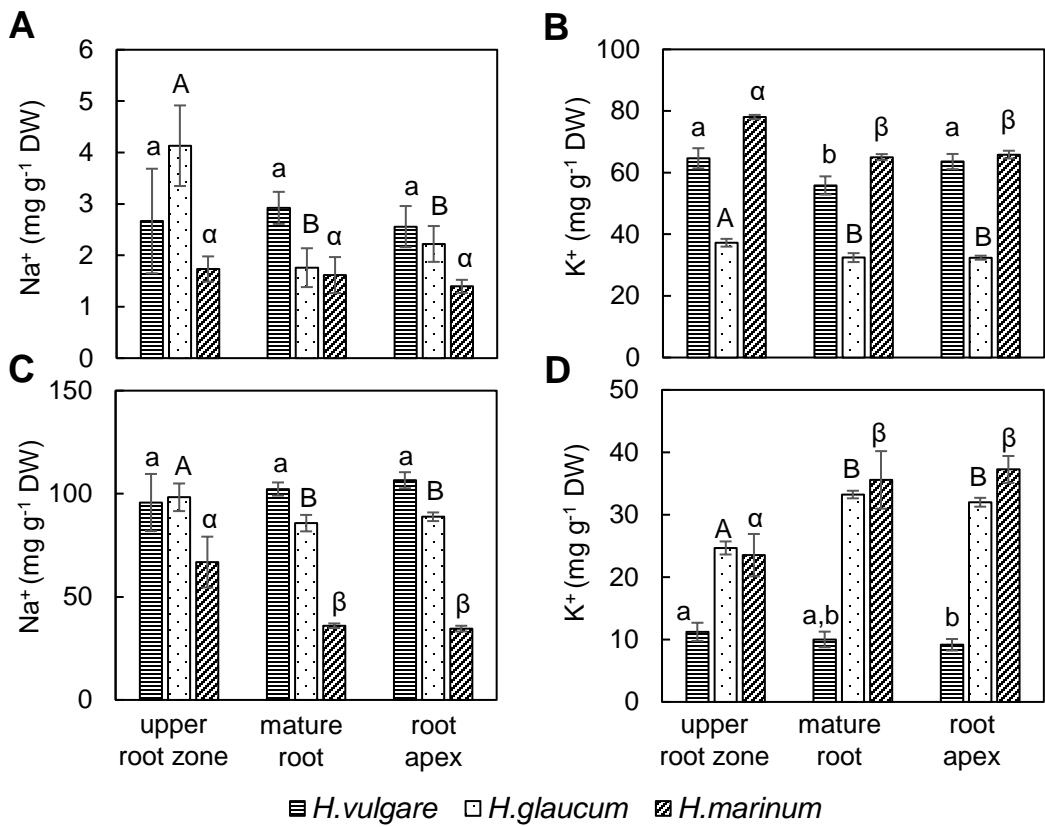


Fig. 4 Na⁺ (a, c) and K⁺ (b, d) accumulation in different root zones of *H. vulgare*, *H. glaucum* and *H. marinum* plants grown under control hydroponic (a, b) and salinity stress conditions (c, d). Data are mean \pm SD; n = 4, values followed by the same letter (Latin lowercase for *H. vulgare*, Latin uppercase for *H. glaucum* and Greek lowercase for *H. marinum*) do not differ significantly by ANOVA test at $p < 0.05$.

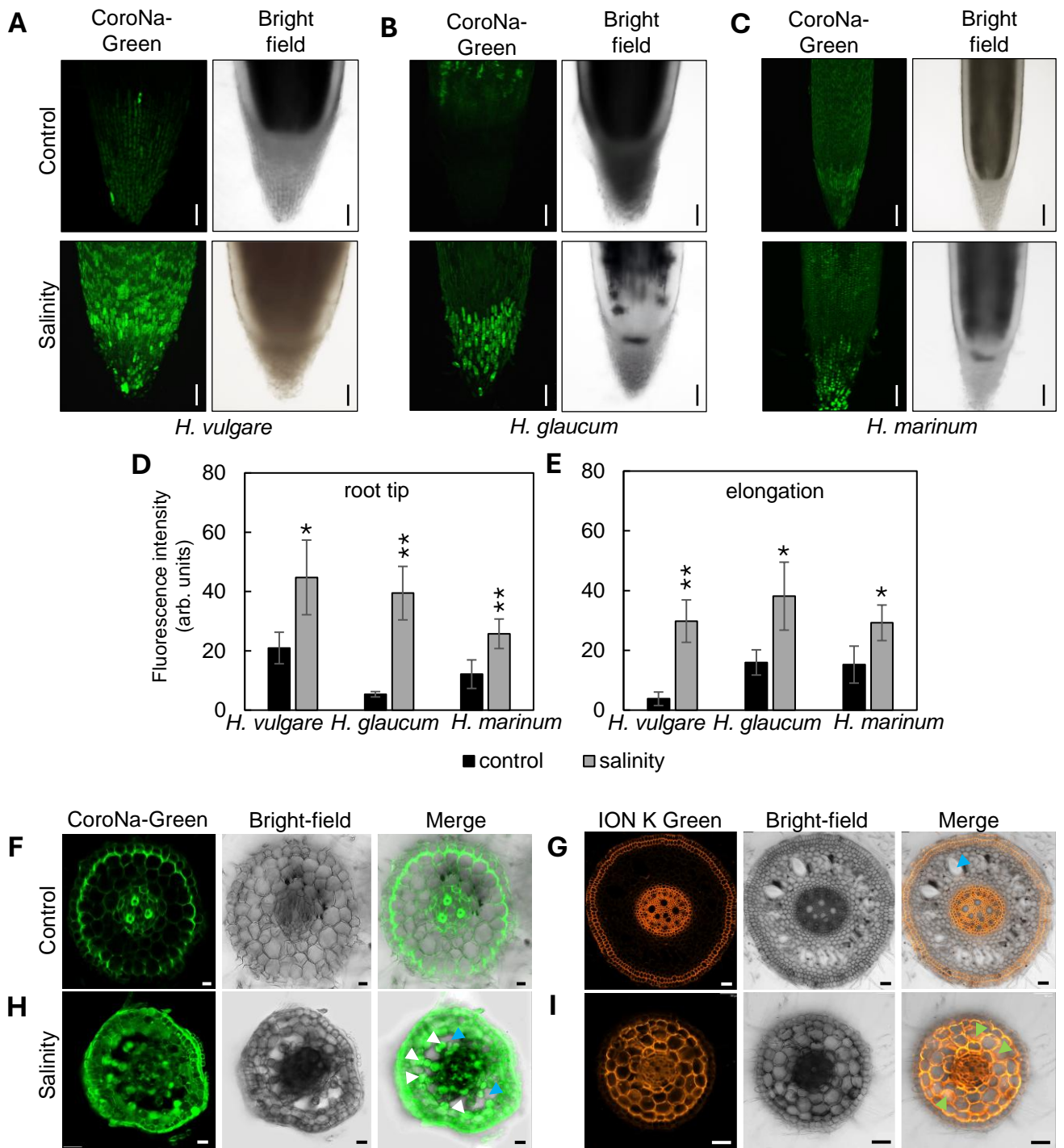


Fig. 5 Accumulation and patterning profiles of Na^+ and K^+ in roots of barley species grown under control and salinity stress conditions. (a-c) The representative images of Na^+ distribution within control (above left) and stressed roots (below left) of *H. vulgare* (a), *H. glaucum* (b) and *H. marinum* (c) as visualized by CoroNa Green (c). Panels next to fluorescence images represent respective bright field images. Bars, 100 μm . (d, e) Quantification of intensity of CoroNa Green fluorescence in root tips (d) and elongation zone (e). Data are mean \pm SD; $n = 3-4$, t significant at: *, $P < 0.05$; **, $P < 0.01$. (f-i) Na^+ (f, h) and K^+ distribution (g, i) in the upper parts of *H. marinum* roots grown under control (f, g) and salinity stress conditions (h, i) as analyzed by CoroNa Green and ION Potassium Green-2 AM staining, correspondingly. Vacuoles filled by Na^+ are indicated by white arrowheads, cytosolic K^+ - by green arrowheads and aerenchyma zone - by blue arrowheads. Bars, 50 μm .

