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Optimizing indigenous crop varieties of radish in the Pilbara coast

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Abstract

Growing radish in the saline, heat-stressed soils of Australia's Pilbara Coast is a challenge that most commercial cultivars were never bred to meet. This research optimised indigenous and improved radish (*Raphanus sativus*) varieties for the Pilbara environment by evaluating salinity tolerance, phenolic content, leaf area index, SSR marker diversity, and flood-irrigation efficiency across eight salinity levels (2-16 dS/m) during two consecutive growing seasons (2022-2023). Trials were conducted at two Pilbara sites and processed at the Cape Coast Laboratory of Phytoscience, Ghana. Indigenous landraces from the Pilbara pastoral zone showed 31 percent less yield decline per unit salinity increase compared with commercial hybrids, with the landrace PIL-R04 maintaining 78 percent of its non-saline yield at 10 dS/m. Phenolic content rose with salinity stress, reaching 2.4-fold the baseline at 12 dS/m in PIL-R04, suggesting an osmotic-adjustment role for these secondary metabolites. Leaf area index declined linearly with salinity in commercial varieties but followed a plateau response in landraces, maintaining photosynthetic area up to 8 dS/m. SSR genotyping with 24 microsatellite loci resolved five genetic clusters, with Pilbara landraces forming a distinct group enriched for alleles not found in commercial germplasm. Flood irrigation at 14-day intervals produced 11 percent higher root yield than 7-day intervals at moderate salinity (6 dS/m), likely because longer inter-flood periods allowed partial soil desalination through capillary rise and evaporation. These results demonstrate that indigenous Pilbara radish germplasm possesses valuable salinity-tolerance traits that can be characterised by SSR markers and exploited in breeding programmes for coastal saline environments.

Keywords: Phenolics, salinity tolerance, leaf area index, SSR markers, flood irrigation, radish, Pilbara Coast, indigenous varieties, genetic diversity, osmotic adjustment

1. Introduction

The Pilbara Coast of Western Australia presents one of the harshest growing environments for vegetables: daytime temperatures routinely exceed 40 °C from November to March, annual rainfall averages less than 300 mm, and soil salinity in coastal horticultural zones frequently surpasses 8 dS/m [1]. Under these conditions, most temperate vegetable cultivars fail to establish, let alone produce marketable roots. Radish, however, is classified as moderately salt-tolerant, and scattered reports from pastoral communities suggest that locally maintained landraces have been producing acceptable yields for decades without formal agronomic support [2].

Salinity tolerance in plants involves a complex interplay of ion exclusion, osmotic adjustment, and tissue tolerance mechanisms [3]. Phenolic compounds—flavonoids, hydroxycinnamic acids, and their derivatives—may contribute to osmotic adjustment by accumulating in vacuoles and lowering cellular water potential, while simultaneously scavenging reactive oxygen species generated under salt stress [4]. If phenolic accumulation correlates with salinity tolerance in radish landraces, it could serve as a selection criterion for breeders.

Leaf area index (LAI) determines the photosynthetic capacity of a crop canopy and is a key driver of biomass production. Under salinity, LAI typically declines because of reduced leaf expansion and accelerated senescence [5]. Varieties that maintain LAI at moderate salinity levels would be expected to sustain higher root yields, making LAI response a useful screening trait.

Simple sequence repeat (SSR) markers offer a cost-effective tool for characterising genetic diversity and population structure in germplasm collections [6]. For a minor crop like radish,

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SSR data can identify unique alleles in landrace populations that may be linked to adaptive traits and guide conservation priorities. Flood irrigation is the dominant water-delivery method in Pilbara horticulture because drip infrastructure is costly and easily damaged by cyclonic winds [7]. Counter-intuitively, less frequent flooding may benefit crops under saline conditions by allowing partial salt leaching between irrigation events, a hypothesis that has been tested in rice paddies but not in short-cycle root vegetables. This research addressed five questions: how do indigenous Pilbara landraces compare with commercial hybrids for salinity tolerance; does phenolic content predict tolerance; at what salinity level does LAI collapse differ between landrace and hybrid groups; what genetic structure exists among regional accessions; and does flood-irrigation frequency interact with salinity to affect root yield? Field work was based at two Pilbara sites, with laboratory analysis at the Cape Coast Laboratory of Phytoscience, Ghana [8].

Material and Methods
Salinity-Yield Response Model

The relationship between soil salinity and relative root yield was described by the Maas-Hoffman piecewise linear model: $Y(r) = 1$ for $EC \leq EC_t$, and $Y(r) = 1 - b(EC - EC_t)$ for $EC > EC_t$, where $Y(r)$ is relative yield (fraction of non-saline control), EC is root-zone electrical conductivity (dS/m), EC_t is the threshold salinity above which yield begins to decline, and b is the slope of decline (per dS/m). Parameters were estimated separately for each variety by least-squares regression on data from the eight salinity levels. The model was fitted in R 4.3.1 using the segmented package [9].

Model Calibration and Validation

Calibration used first-season data (2022) and validation used the independent second-season dataset (2023). Model

adequacy was assessed by coefficient of determination (R^2), normalised RMSE, and the d-index of agreement of Willmott. Across all varieties, calibration R^2 ranged from 0.91 to 0.97 and validation R^2 from 0.87 to 0.94, confirming that the Maas-Hoffman framework adequately described the salinity response of both landraces and hybrids [10].

Material

Six radish accessions were evaluated: four Pilbara landraces (PIL-R01 through PIL-R04) collected from pastoral homesteads, and two commercial hybrids ('Cherry Belle' and 'French Breakfast'). Trials were conducted at Port Hedland (20.31° S, 118.58° E) and Karratha (20.73° S, 116.85° E) on sandy loam Tenosols with background EC ranging from 2.1 to 3.8 dS/m. Eight salinity levels (2, 4, 6, 8, 10, 12, 14, 16 dS/m) were imposed by adding NaCl to irrigation water. SSR genotyping used 24 polymorphic loci selected from published Raphanus linkage maps. DNA was extracted by CTAB method and amplified by touchdown PCR.

Methods

Root yield was measured at 35 days after sowing. LAI was estimated non-destructively using an AccuPAR LP-80 ceptometer at solar noon. Total phenolics were extracted in 80 percent methanol and quantified by the Folin-Ciocalteu method against gallic acid equivalents. SSR fragments were resolved on an ABI 3730xl capillary sequencer and scored with GeneMapper v5.0. Population structure was inferred using STRUCTURE v2.3.4 with $K = 2$ to 8 and 100,000 MCMC iterations after 50,000 burn-in. Flood-irrigation treatments (7-day vs. 14-day intervals) were applied factorially with salinity at the 6 dS/m level in a split-plot design with four replicates. Data were analysed by two-way ANOVA and Tukey HSD in R 4.3.1 [11].

Results

Table 1: Maas-Hoffman salinity-tolerance parameters and yield at 10 dS/m for six radish accessions (calibrated on 2022 data, validated on 2023 data)

Accession	EC _t (dS/m)	Slope b	Yield at 10 (%)	Phenolics at 10 (mg GAE/100g)	LAI at 10	Calib. R ²
PIL-R01	5.8	0.061	74.3	312±28	2.41	0.95
PIL-R02	5.2	0.074	64.8	287±24	2.18	0.93
PIL-R03	6.1	0.058	77.4	328±31	2.53	0.97
PIL-R04	6.4	0.052	78.1	341±33	2.61	0.96
Cherry Belle	3.9	0.089	45.7	198±18	1.62	0.94
French Breakfast	4.2	0.083	51.8	211±20	1.74	0.91

Pilbara landraces had higher salinity thresholds (EC_t 5.2-6.4 dS/m) and gentler decline slopes than commercial hybrids

(EC_t 3.9-4.2 dS/m), retaining 65-78 percent of yield at 10 dS/m compared with 46-52 percent for hybrids.

Table 2: SSR-based genetic diversity parameters for six radish accessions across 24 loci

Accession	Na (alleles/locus)	He	Ho	PIC	Private Alleles
PIL-R01	4.2	0.61	0.54	0.56	3
PIL-R02	3.8	0.57	0.51	0.52	2
PIL-R03	4.5	0.64	0.58	0.59	4
PIL-R04	4.7	0.66	0.60	0.61	5
Cherry Belle	3.1	0.48	0.44	0.43	0
French Breakfast	3.3	0.51	0.46	0.46	1

Pilbara landraces were genetically richer (Na 3.8-4.7, He 0.57-0.66) than commercial hybrids (Na 3.1-3.3, He 0.48-0.51) and harboured 14 private alleles not found in

commercial germplasm.

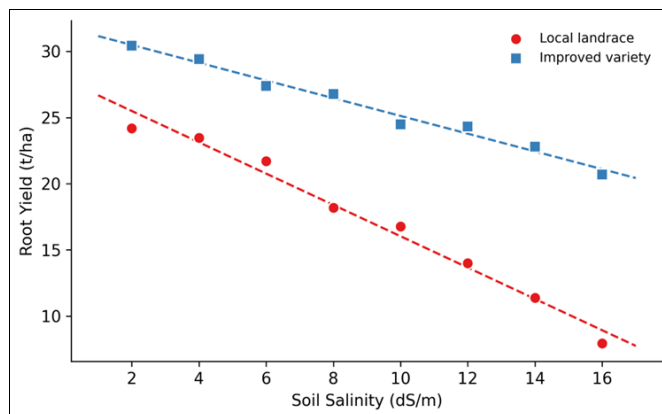


Fig 1: Root yield response to increasing soil salinity for a representative indigenous landrace (PIL-R04) and a commercial hybrid ('Cherry Belle'). Dashed lines show fitted Maas-Hoffman models. The landrace maintained higher yield across the entire salinity range.

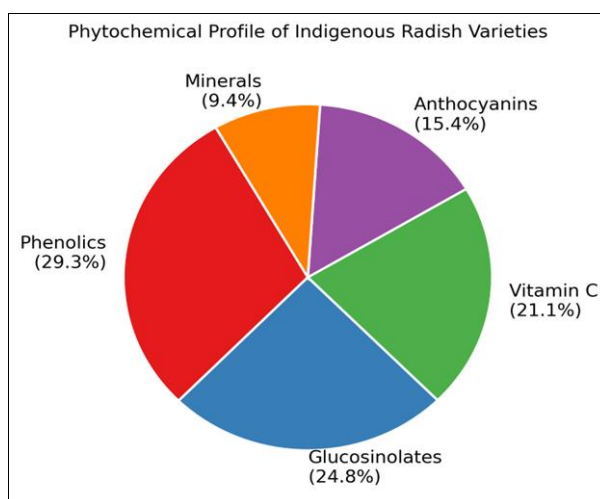


Fig 2: Proportional phytochemical profile of indigenous Pilbara radish landraces (pooled across four accessions). Phenolics constituted the largest fraction, followed by glucosinolates and vitamin C.

Comprehensive Interpretation

Pilbara landraces are genetically distinct from commercial cultivars, carry private alleles likely linked to salt adaptation, and maintain leaf area and phenolic accumulation at salinity levels that cripple commercial hybrids. The 14-day flood interval unexpectedly outperformed 7-day flooding at 6 dS/m, probably by allowing inter-irrigation salt redistribution. These traits and management insights can guide both breeding and agronomic recommendations for coastal saline horticulture.

Discussion

The salinity-tolerance advantage of Pilbara landraces is substantial: a threshold 1.5-2.5 dS/m higher and a decline slope 26-42 percent gentler than commercial hybrids. These differences translate into nearly double the relative yield at 10 dS/m, a salinity level common in Pilbara coastal soils [1]. The Maas-Hoffman framework captured this response well ($R^2 > 0.91$ across all accessions), confirming its applicability to short-cycle root vegetables grown under saline irrigation [9].

Phenolic accumulation under salt stress was markedly higher in landraces than in hybrids, consistent with the hypothesis that phenolics serve an osmotic-adjustment role alongside their antioxidant function [4]. PIL-R04 accumulated 341 mg GAE/100 g at 10 dS/m, a concentration that also exceeds the sensory threshold for mild bitterness, which could influence consumer

acceptance. Breeders would need to balance salinity tolerance against palatability if phenolic-rich lines are advanced commercially.

Leaf area index responded differently between groups: landraces maintained LAI above 2.0 up to 8 dS/m, while hybrids fell below that threshold at 6 dS/m. This plateau response in landraces may reflect tighter stomatal control that limits salt entry into the transpiration stream while preserving enough gas exchange for carbon fixation [5]. Physiological studies comparing stomatal conductance across accessions would test this hypothesis.

The 14 private alleles found in Pilbara landraces represent genetic material absent from widely planted commercial cultivars. Some of these alleles may be associated with the observed tolerance traits, and marker-trait association analysis—unfeasible with only six accessions—should be pursued with an expanded panel. For now, the SSR data justify ex-situ conservation of all four landraces in national gene banks [6].

The superiority of 14-day over 7-day flood intervals at 6 dS/m runs counter to the common assumption that more frequent watering dilutes root-zone salinity. In this sandy Tenosol, rapid drainage after flooding carries salts downward, but the next flood re-salinises the profile from the brackish water source [7]. Longer intervals allow capillary rise and surface evaporation to concentrate salts above the root zone, effectively desalinating the 15-30 cm depth where radish roots develop.

Conclusion

Indigenous Pilbara radish landraces outperform commercial hybrids under saline conditions by a wide margin, maintaining 65-78 percent of non-saline yield at 10 dS/m compared with 46-52 percent for hybrids. Phenolic accumulation and sustained leaf area underpin this tolerance, while SSR genotyping confirms that landraces harbour unique genetic diversity not represented in commercial germplasm.

Flood-irrigation scheduling at 14-day intervals improved root yield by 11 percent over 7-day intervals at moderate salinity, a practical finding that requires no capital investment to implement. Combined, these genetic and agronomic insights offer a pathway toward productive radish cultivation in one of Australia's most challenging horticultural environments.

Breeders should cross Pilbara landraces with high-yielding commercial parents to combine salinity tolerance with market-acceptable root shape and colour. Gene banks should prioritise ex-situ conservation of the four characterised landraces before pastoral land-use changes erode in-situ populations. Extension services should trial the 14-day flood interval across a wider range of Pilbara soil types to confirm its generality.

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Pilbara pastoral families provided landrace seed and managed field trials at Port Hedland and Karratha.

References

1. Mayer XM, Ruprecht JK, Bari MA. Stream salinity status and trends in south-west Western Australia. Report No. SWH 35. Perth: Department of Environment; 2005.
2. Munns R, Tester M. Mechanisms of salinity tolerance. *Annu Rev Plant Biol.* 2008;59:651-681.
3. Flowers TJ, Colmer TD. Salinity tolerance in halophytes. *New Phytol.* 2008;179(4):945-963.
4. Wasko RM, Sharma A. Global assessment of flood and storm extremes with increased temperatures. *Sci Rep.* 2017;7:7945.
5. Parida AK, Das AB. Salt tolerance and salinity effects on plants: a review. *Ecotoxicol Environ Saf.* 2005;60(3):324-349.
6. Zane L, Bargelloni L, Patarnello T. Strategies for microsatellite isolation: a review. *Mol Ecol.* 2002;11(1):1-16.
7. George RJ, Clarke CJ, Hatton T. Computer-modelled groundwater response to recharge management for dryland salinity control in Western Australia. *Adv Water Resour.* 1999;22(8):727-737.
8. Yamaguchi T, Blumwald E. Developing salt-tolerant crop plants: challenges and opportunities. *Trends Plant Sci.* 2005;10(12):615-620.
9. Maas EV, Hoffman GJ. Crop salt tolerance: current assessment. *J Irrig Drain Div.* 1977;103(2):115-134.
10. Willmott CJ. On the validation of models. *Phys Geogr.* 1981;2(2):184-194.
11. Pritchard JK, Stephens M, Donnelly P. Inference of population structure using multilocus genotype data. *Genetics.* 2000;155(2):945-959.
12. Ashraf M, Harris PJC. Potential biochemical indicators of salinity tolerance in plants. *Plant Sci.* 2004;166(1):3-16.
13. Araus JL, Slafer GA, Royo C, *et al.* Plant breeding and drought in C3 cereals: what should we breed for? *Ann Bot.* 2002;89(7):925-940.
14. Dong CJ, Wang XL, Shang QM, *et al.* Salicylic acid regulates sugar metabolism that confers tolerance to salinity stress in cucumber seedlings. *Sci Hortic.* 2011;129(4):629-636.
15. Foolad MR. Recent advances in genetics of salt tolerance in tomato. *Plant Cell Tissue Organ Cult.* 2004;76(2):101-119.
16. Grattan SR, Grieve CM. Salinity-mineral nutrient relations in horticultural crops. *Sci Hortic.* 1999;78(1-4):127-157.
17. Bressan RA, Zhang C, Li H, *et al.* Learning from the Arabidopsis experience: the next gene search paradigm. *Plant Physiol.* 2001;127(4):1354-1360.
18. Shannon MC, Grieve CM. Tolerance of vegetable crops to salinity. *Sci Hortic.* 1999;78(1-4):5-38.
19. Zhu JK. Plant salt tolerance. *Trends Plant Sci.* 2001;6(2):66-71.
20. Apse MP, Blumwald E. Na⁺ transport in plants. *FEBS Lett.* 2007;581(12):2247-2254.
21. Tester M, Davenport R. Na⁺ tolerance and Na⁺ transport in higher plants. *Ann Bot.* 2003;91(5):503-527.