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Arabian Peninsula Date Palms: Genomic Advances, Phytochemical Controversies and the Translational Frontier

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ABSTRACT

The date palm (*Phoenix dactylifera* L.) has been cultivated in the Arabian Peninsula for some six millennia and is now the subject of rapid genomic and phytochemical reappraisal. This critical review asks three questions: what is robustly established in date palm genomics, agronomy and stress biology; which methodological artefacts distort the phytochemical and clinical literature; and which knowledge gaps are rate-limiting for translation. Structured searches (OpenAlex, PubMed, Europe PMC; October 2026) and verification of every cited record underpin the appraisal. Resequencing and a telomere-to-telomere Ajwa assembly have clarified domestication, population structure and the genetics of fruit colour and sugar type, but no candidate gene for sex, salinity or pest resistance has been validated in date palm itself. Folin–Ciocalteu assays overstate phenolics in sugar-rich fruit, small pilot studies have propagated through reviews, and *in vitro* anti-cancer effects at milligram-per-millilitre concentrations are unattainable through diet. Human trials establish safety but not therapeutic efficacy. Thirteen priority gaps are defined for 2026–2035.

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Introduction

The date palm (*Phoenix dactylifera* L., Arecaceae, 2n = 36) is among the oldest fruit crops, with archaeobotanical evidence of consumption and cultivation in eastern Arabia and Mesopotamia from the sixth to fourth millennia BCE (Tengberg 2012; Zohary et al. 2012). World production is approximately 10 million tonnes a year (FAO 2025), of which the Arabian Peninsula states supply roughly a quarter to a third (FAO 2025; GASTAT 2025). The crop also carries singular cultural weight: it anchors oasis landscapes inscribed as World Heritage (UNESCO 2006, 2018) and serves as a national emblem across the Gulf Cooperation Council (GCC).

Research on the species has expanded sharply since the first draft genome (Al-Dous et al. 2011). Whole-genome resequencing has reshaped domestication theory (Hazzouri et al. 2015; Mathew et al. 2015; Flowers et al. 2019), genome-wide association studies (GWAS) have mapped fruit colour, sugar composition and skin separation (Hazzouri et al. 2019; Malek et al. 2020; Younuskunju et al. 2023, 2024), and a telomere-to-telomere assembly of Ajwa has been released (Celii et al. 2025). Salinity tolerance has been dissected transcriptomically (Yaish et al. 2017; Al Kharusi et al. 2019), fruit phytochemistry profiled across cultivars and ripening stages (Al-Farsi et al. 2005; Eid et al. 2013; Alam et al. 2024), and clinical studies have examined glycaemic responses (Alkaabi et al. 2011; AlGeffari et al. 2016; Butler et al. 2022) and labour outcomes (Bagherzadeh Karimi et al. 2020).

This proliferation has generated controversies as well as clarifications. The Folin–Ciocalteu (F-C) assay, the method behind most reported total phenolic content (TPC) values, is biased upward by reducing sugars (Sánchez-Rangel et al. 2013; Pérez et al. 2023; Raposo et al. 2024). Small pilot studies are cited as if they were definitive, a pattern Greenberg (2009) termed citation distortion. In vitro cytotoxicity at milligram-per-millilitre concentrations (Khan et al. 2016, 2021) is repeated in the popular literature as evidence that dates "cure" cancer. Labour-induction trials carry a high risk of bias (Bagherzadeh Karimi et al. 2020; Salajegheh et al. 2024), and voucher specimens are rarely deposited in phytochemical studies.

This Review therefore addresses three research questions (RQ). RQ1: what is robustly established, and what remains contested, in the genomics, agronomy, pest biology and salinity physiology of Arabian Peninsula date palms? RQ2: which methodological artefacts—assay interference, citation amplification and translational overreach—distort the phytochemical and clinical literature, and how large are their effects? RQ3: which knowledge gaps are rate-limiting for climate-resilient breeding, evidence-based functional-food claims and biosecurity? Table 1 maps the sections of the Review to these questions and to the thirteen priority gaps synthesised in Section 10.

Table 1. Structure of the Review: research questions, sections, principal primary evidence and the priority gaps (Section 10) that each section informs.

Research question	Section	Principal primary evidence appraised	Gaps
RQ1 What is robustly established in genomics, agronomy, pest biology and salinity physiology?	3 Genomics	Al-Dous et al. 2011; Al-Mssallem et al. 2013; Hazzouri et al. 2015, 2019; Mathew et al. 2014, 2015; Torres et al. 2018; Celii et al. 2025	1, 4, 9
	4 Agronomy and climate	Wilkinson 1977; Al-Ghafri 2006; Al-Muaini et al. 2019; Dhaouadi and Haj-Amor 2026; Cohen et al. 2004; Mirani et al. 2020	8, 9
	5 Pests and disease	El-Sabea et al. 2009; Faleiro et al. 2011; Hoddle et al. 2015; Quenzar et al. 2001; Saleh et al. 2015; Khayi et al. 2023	3, 5, 13
	6 Salinity	Maas and Hoffman 1977; Al Kharusi et al. 2017, 2019; Yaish et al. 2017; Jana and Yaish 2020; Patankar et al. 2019	2

Research question	Section	Principal primary evidence appraised	Gaps
RQ2 Which methodological artefacts distort the phytochemical and clinical literature, and how large are they?	7 Composition and Folin–Ciocalteu	Singleton and Rossi 1965; Sánchez-Rangel et al. 2013; Lawag et al. 2023; Alam et al. 2021, 2024; Eid et al. 2013	7
	8 Glycaemic and clinical evidence	Alkaabi et al. 2011; AlGeffari et al. 2016; Butler et al. 2022; Alalwan et al. 2020; Rock et al. 2009; Khan et al. 2016, 2021; Al-Kuran et al. 2011; Kordi et al. 2013, 2017; Razali et al. 2017	7, 12
RQ3 Which gaps are rate-limiting for breeding, evidence-based claims and biosecurity?	9 Volatiles and tissues; 10 Synthesis	Flowers et al. 2022; Demirci et al. 2013; Hamed et al. 2017; Ben Thabet et al. 2009	6, 10, 11

2. Review approach

This is a critical narrative review reported against the SANRA criteria for narrative reviews (Baethge et al. 2019) and, for the search component, the PRISMA 2020 items that apply to non-systematic reviews (Page et al. 2021). The evidence base was assembled by the author from 2024 to 2026; to make the corpus reproducible, structured searches were run on 16 October 2026 in OpenAlex, PubMed and Europe PMC using the strings in Table 2, restricted to 2000–2026, with foundational earlier works (for example, the original F-C method and the crop salt-tolerance model) admitted through citation tracking. Grey literature was limited to statistical and normative sources from FAO, GASTAT, UNESCO, ICARDA and national ministries. Trial registries were searched on 16 October 2026 for "date fruit", "*Phoenix dactylifera*", "date palm" and "Ajwa": ClinicalTrials.gov (field-restricted queries on intervention and title, 97 raw records screened by hand to 31 date-related trials), the WHO ICTRP portal (26 unique records) and the Iranian Registry of Clinical Trials (13 records); the Saudi Clinical Trials Registry could not be reached on that date.

Table 2. Search strategy and records identified, 16 October 2026 (publication years 2000–2026). Every string was combined with ("*Phoenix dactylifera*" OR "date palm").

Domain	Additional search terms	OpenAlex	PubMed	Europe PMC
Baseline corpus	— (base string only)	15,424	2,022	7,704
Genomics and domestication	genome OR resequencing OR GWAS OR "sex determination" OR domestication	444	306	2,068
Salinity	salinity OR "salt tolerance" OR saline	634	97	1,422
Irrigation and climate	irrigation OR "water requirement" OR evapotranspiration OR "climate change"	928	75	1,386
Pests and disease	"*Rhynchophorus ferrugineus*" OR "red palm weevil" OR Bayoud OR "*Fusarium oxysporum*"	808	115	593

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Domain	Additional search terms	OpenAlex	PubMed	Europe PMC
Phenolics and antioxidants	phenolic OR polyphenol OR antioxidant OR Folin	1,976	555	2,878
Glycaemic and diabetes trials	"glycemic index" OR "glycaemic index" OR diabetes OR "randomized controlled trial" OR "randomised controlled trial"	184	80	851
Labour and pregnancy	labor OR labour OR pregnancy OR delivery	321	380	1,288
Cancer	cancer OR anticancer OR cytotoxic OR "MCF-7"	378	131	1,621
Volatiles, oils and other tissues	volatile OR "essential oil" OR "seed oil" OR pollen OR sap	1,309	272	2,667
Tissue culture	"tissue culture" OR "somatic embryogenesis" OR somaclonal	549	67	564
Human trials (sampling frame)	PubMed publication-type filter: clinical trial OR randomised controlled trial, all years	—	24	—

OpenAlex counts are title-and-abstract matches (filter title_and_abstract.search); PubMed counts use the date-of-publication limit 2000:2026[dp]; Europe PMC counts (PUB_YEAR 2000–2026) search full text where available and include preprints, so they exceed PubMed. Counts are records retrieved per database before de-duplication; selection for synthesis was purposive (Section 2). Of the 24 PubMed clinical-trial records, 15 were human trials of date fruit, seed or pollen as an intervention; the remainder concerned pollen allergy, animal nutrition or unrelated topics.

Studies were eligible if they reported primary data, a systematic review or meta-analysis, a genome resource, or an authoritative monograph on *P. dactylifera*, with priority given to Arabian Peninsula germplasm, sites or populations, and to work in English, French or Arabic. For the clinical sections the sampling frame was the 24 PubMed records carrying a clinical-trial publication type (Table 2), of which 15 were human trials of date fruit, seed or pollen, together with the trials included in the published meta-analyses; those bearing on the claims appraised here are summarised in Supplementary Table S1. In vitro and animal studies were included only as the object of appraisal, not as evidence of human effect. Titles and abstracts were screened by the author alone; selection for synthesis was purposive, aimed at identifying the primary study behind each widely repeated claim rather than at exhaustive coverage. The final evidence base comprises the references listed, each of which was checked against the publisher or indexer record in October 2026.

Human studies were appraised at the design level using the domains of the Cochrane RoB 2 tool (Sterne et al. 2019; Higgins et al. 2019), drawing on the published risk-of-bias judgements of the meta-analyses rather than re-grading trials *de novo*, and certainty is expressed in GRADE-style language. Citation profiles of seed studies were obtained from OpenAlex on 16 October 2026 (Supplementary Table S2). Statements that no study exists are scoped to this corpus and date. The limitations of the approach are those of any single-author narrative review: screening was not duplicated, selection was purposive, and database coverage of regional journals is incomplete.

3. Genomic architecture, sex determination and domestication history (RQ1)

3.1 Genome assemblies

The first assembly, for the Khalas cultivar, comprised roughly 380 Mb of a genome estimated at about 658 Mb and was highly fragmented (Al-Dous et al. 2011). Al-Mssallem et al. (2013) produced a 605 Mb assembly and estimated the genome at 671 Mb, and Hazzouri et al. (2019) released a 772 Mb PacBio assembly of the Barhee BC_4 male. The most recent advance is a telomere-to-telomere, haplotype-phased assembly of Ajwa with 19 further high-quality genomes (Celii et al. 2025):

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haplotype 1 spans 673.1 Mb with a single remaining gap in the chromosome 10 nucleolar organiser region. Under the new nomenclature the sex-determining region lies on chromosome 14, which corresponds to linkage group 12 of the Khalas genetic map (Mathew et al. 2014), and male-specific k-mers span approximately 14.7 Mb of the male haplotype. The change is one of numbering, not topology, but it complicates cross-reference to earlier maps; formal publication of the Ajwa resource and a community chromosome nomenclature anchored to it would remove the ambiguity.

3.2 Population structure and domestication

Resequencing of 62 cultivars from 12 countries at some seven million single-nucleotide polymorphisms revealed two subpopulations, North African versus Middle Eastern and South Asian, with admixture in Egypt and Sudan (Hazzouri et al. 2015). Genotyping-by-sequencing of 70 cultivars independently recovered the same bifurcation (Mathew et al. 2015). The discovery of apparently wild stands in Oman's Hajar Mountains (Gros-Balthazard et al. 2017) and the demonstration of extensive introgression from *Phoenix theophrasti* into North African cultivars (Flowers et al. 2019) imply a complex, multi-centred history (Gros-Balthazard and Flowers 2021); whether the Omani stands are relict wild populations or feral escapes remains open. Palaeogenomics is now feasible: a high-coverage genome was recovered from a 2,100-year-old Egyptian leaf (Pérez-Escobar et al. 2021), offering a template for archaeological material from Arabia. Taxonomic context for the genus is provided by the monograph of Barrow (1998).

3.3 Sex determination

Date palm has an XY system with heterogametic males (Cherif et al. 2013). The sex-determining region is telomeric on linkage group 12 and was estimated at roughly 5–13 Mb (Mathew et al. 2014). Genus-wide sequencing of 14 *Phoenix* species supports a two-locus model and identified four conserved male-specific candidates: a *CYP703*-like cytochrome P450, a *GPAT3*-like acyltransferase, a *LONELY GUY*-like gene and a cytidine deaminase (Torres et al. 2018); the Ajwa assembly places *CYP703*, *GPAT3* and *LOG3* within the 14.7 Mb male-specific region (Celii et al. 2025). None has been validated by knock-out or ectopic expression in *P. dactylifera*. Sex-linked markers already permit seedling sexing before the five-to-eight-year juvenile phase (Cherif et al. 2013). CRISPR/Cas9 mutagenesis of the candidates is feasible in principle (Ramesh et al. 2024), but routine transformation of date palm does not yet exist.

3.4 Genetic architecture of fruit traits

Hazzouri et al. (2015) identified *VIRESCENS* (*VIR*), an R2R3-MYB transcription factor, as the determinant of khalal-stage fruit colour: a copia-like retrotransposon inserted in exon 3 abolishes anthocyanin synthesis and yields yellow fruit, whereas the functional allele gives red to dark-brown fruit. A GWAS of 21 fruit traits in 145 female varieties and 12 males confirmed *VIR* and identified a second loss-of-function allele (Hazzouri et al. 2019). For sugar type, a tandem cluster of invertase genes segregates with the sucrose-retaining phenotype of cultivars such as Deglet Noor, whereas intact invertase activity gives the reducing-sugar fruit of Khalas, Sukkari, Ajwa and Barhee (Hazzouri et al. 2019; Malek et al. 2020). Subsequent GWAS mapped tamr-stage colour (Younuskunju et al. 2023) and fruit-skin separation (Younuskunju et al. 2024), the latter relevant to mechanical harvesting.

Major gaps remain. No GWAS for yield, bunch weight or fruit size has been published, reflecting the need for multi-year replicated phenotyping. Salinity tolerance, arguably the most valuable trait in the region (Al-Absi 2023), has no mapped quantitative trait locus (QTL). Bayoud resistance is tracked only by a correlative mitochondrial marker (Quenzar et al. 2001; Saleh et al. 2015) and the causal nuclear locus is unknown. Resistance to the red palm weevil has no genetic characterisation at all.

4. Agronomic systems, water and climate adaptation (RQ1)

4.1 Irrigation

Omani cultivation evolved around the aflaj, gravity-fed channels and tunnels whose social organisation Wilkinson (1977) documented and five of which are inscribed as World Heritage (UNESCO 2006). The national inventory recorded 4,112 aflaj, of which 3,017 were flowing, supplying some 680 million m³ a year of which about 410 million m³ is used (Al-Ghafri 2006). Reported crop water requirements across the Arab region span more than an order of magnitude, from about 2,500 to over 40,000 m³ ha⁻¹ yr⁻¹, because of differences in climate zone, cultivar, irrigation method and calculation protocol (Dhaouadi and Haj-Amor 2026); Penman–Monteith estimates for Saudi regions are far narrower (Al-Omran et al. 2019). Sap-flow measurements on commercial farms in the UAE show that actual palm water use is well below the volumes routinely applied, so that substantial savings are

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available without yield penalty (Al-Muaini et al. 2019). Dhaouadi and Haj-Amor (2026) project a 25% increase in irrigation demand by 2050, and temperature extremes in the Peninsula are projected to amplify under further warming (Vinodhkumar et al. 2024). Heat and drought responses have been characterised at the transcript and protein level, with induction of heat-shock proteins, antioxidant enzymes and osmoprotectant pathways (Rennenberg et al. 2025), but no breeding programme for thermotolerance or water-use efficiency exists. Genomic selection, which predicts breeding values from dense genotypes, has not been attempted in date palm.

4.2 Propagation and somaclonal variation

Offshoots give true-to-type plants but a palm produces only 10–30 in its lifetime (Zaid and Arias-Jiménez 2002). Somatic embryogenesis underpins commercial micropropagation (Fki et al. 2011; Al-Khayri et al. 2023), but tissue-culture plants show heritable off-types, including dwarfism and the "sheiss" fruit-set failure caused by floral abnormality (Cohen et al. 2004). Transposable-element-based markers detect variation in cultured material (Mirani et al. 2020), yet no diagnostic reliably predicts off-type phenotypes before field planting, and abnormalities may only appear at reproductive maturity five to eight years later. Reliable frequency estimates are scarce and laboratory-dependent, which is itself a gap.

5. Pest and disease biology (RQ1)

The red palm weevil, *Rhynchophorus ferrugineus*, is the gravest invertebrate threat to Gulf production (El-Shafie and Faleiro 2020; FAO 2020; Hoddle et al. 2024). El-Sabea et al. (2009) estimated losses from removing severely infested palms at US$5.18–25.92 million for the Gulf region at 1–5% infestation, and a recent ex-ante assessment put Saudi Arabia's control and treatment programme at about US$34.4 million a year (Eissa et al. 2023). Mass trapping with the aggregation pheromone ferrugineol is the mainstay of management (FAO 2020); recommended densities range from one trap per hectare where infestation is below 1% to four to ten per hectare in heavily infested area-wide programmes (Faleiro et al. 2011), and integrated guidance is now consolidated (El Bouhssini and Faleiro 2018; FAO 2020). Flight-mill studies show that a few individuals can fly more than 50 km in 24 h (Hoddle et al. 2015), although field dispersal appears predominantly local (Hoddle et al. 2024). Three genome assemblies have been published—a hybrid assembly of about 780 Mb (Hazzouri et al. 2020), a haplotype-resolved assembly of about 590 Mb per pseudo-haplotype from linked reads (Dias et al. 2021) and a 779 Mb near-chromosomal assembly from HiFi and Omni-C data (Sudalaimuthuasari et al. 2024)—and together they reveal expansions of chemoreceptor and detoxification gene families consistent with polyphagy. No date palm cultivar with documented weevil resistance has been reported.

Bayoud, caused by *Fusarium oxysporum f. sp. albedinis*, destroyed millions of palms in Morocco and Algeria but has not been reported from Arabian Peninsula plantations (Zaid and Arias-Jiménez 2002; El Hadrami et al. 2011). A mitochondrial plasmid-like marker associated with resistance in Moroccan cultivars (Quenzar et al. 2001) was found in 628 of 711 Saudi palms (Saleh et al. 2015), but it is correlative and the nuclear resistance gene has not been cloned despite the selection of resistant Moroccan varieties (Sedra 2011). A chromosome-scale pathogen genome (Khayi et al. 2023) now permits effector-guided resistance breeding. Given germplasm movement and warming, pre-emptive surveillance—soil DNA screening at quarantine points, sentinel plantings and harmonised diagnostics—is a low-cost biosecurity priority for the Gulf (gap 13).

6. Salinity tolerance (RQ1)

Date palm is classed as salt-tolerant: the threshold–slope model gives a soil saturation-extract threshold of 4 dS m^{-1} and a 50% yield reduction near 18 dS m^{-1} (Maas and Hoffman 1977; Ayers and Westcot 1985). Salt-affected land is nevertheless extensive—about 44% of Oman's land area is affected to some degree (Ahmed et al. 2013) and 35.5% of Abu Dhabi Emirate (Shahid et al. 2018)—and irrigation water quality is deteriorating (Alotaibi et al. 2023). Long-term trials at the International Center for Biosaline Agriculture in the UAE show cultivar-specific effects of saline irrigation on fruit minerals and quality (Dghaim et al. 2021; Hammami et al. 2024).

Mechanistic work has used the contrasting Omani cultivars Umsila (tolerant) and Zabad (sensitive) (Al Kharusi et al. 2017, 2019; Yaish et al. 2017). Tolerance involves Na^+ exclusion with maintained K^+/Na^+ ratios, compatible-solute accumulation, antioxidant enzyme induction and anatomical restriction of apoplastic Na^+ flux (Al Kharusi et al. 2019). Transcriptomics identified more than 2,000 salinity-responsive genes (Yaish et al. 2017), and candidate genes—the glyoxalase *PdGLX1* (Jana and Yaish 2020), the aquaporin *PdPIP1;2* (Patankar et al. 2019) and the kinase *PdVIK* (Al-Harrasi et al. 2020)—each confer tolerance when expressed in yeast or *Arabidopsis*. Validation in date palm itself is absent, no salinity QTL has been mapped, and whether seedling responses predict mature-palm performance is untested (Al-Absi 2023).

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7. Fruit composition and the Folin–Ciocalteu problem (RQ2)

7.1 Composition

At the tamr stage Arabian cultivars contain about 70–88 g carbohydrate, 2–5 g protein and 5–8 g dietary fibre per 100 g (Barreveld 1993; Ahmed et al. 2014; Assirey 2015). Sugar type divides cultivars sharply: reducing-sugar types (Khalas, Sukkari, Ajwa, Barhee) accumulate glucose and fructose with little sucrose, whereas sucrose-retaining types (Deglet Noor, Sellaj, Maktoomi) keep sucrose above 30% (AlGeffari et al. 2016), a dichotomy that maps to the invertase deletion described above (Malek et al. 2020). Fibre is predominantly insoluble (Kamal-Eldin et al. 2020), with pectic and xyloglucan soluble fractions recently characterised (Okonkwo et al. 2025). Potassium dominates the mineral profile and Ajwa tends to the highest mineral density among Saudi cultivars (Assirey 2015), a modest difference that the popular literature has inflated into exceptional health properties.

7.2 The Folin–Ciocalteu artefact

The F-C reagent measures reducing capacity, not phenolic structure (Singleton and Rossi 1965; Shahidi and Naczk 2004), and reducing sugars, ascorbate and amino acids react with it (Sánchez-Rangel et al. 2013; Pérez et al. 2023; Raposo et al. 2024). In honey, a comparably sugar-rich matrix, a sugar-corrected protocol lowered apparent TPC by 19.8–36.4% in four samples (Lawag et al. 2023); dates, with 50–80% reducing sugars by fresh weight, can be expected to show interference of at least this magnitude. Alam et al. (2021) showed directly, across 26 varieties, that F-C, ABTS, FRAP and DPPH values do not track HPLC-quantified phenolics. None of the TPC studies included in this Review reported a sugar-blank correction, and reviews continue to cite uncorrected values as phenolic concentrations. The consequence is visible in the spread of values for a single cultivar: reported Ajwa TPC differs more than threefold between studies (Saleh et al. 2011; Aldhafiri 2017), and the only meta-analysis of date TPC pools 22 uncorrected studies (AlFaris et al. 2021). HPLC or LC-MS/MS quantification should become the reference standard (Alam et al. 2024), with F-C reserved for screening and reported only with sugar blanks (Raposo et al. 2024).

7.3 Phenolic profiles and ripening

HPLC-based studies confirm ferulic, caffeic, p-coumaric, syringic and gallic acids and the flavonoids rutin, quercetin, luteolin and apigenin, with cultivar-specific patterns (Al-Farsi et al. 2005; Hong et al. 2006; Eid et al. 2013), and proanthocyanidins dominate the tannin fraction (Hammouda et al. 2013). Polyphenol content is highest at the unripe kimri stage and falls steeply through khalal and rutab to tamr, with Ajwa exceeding Barni and Khalas at khalal (Eid et al. 2013; Hammouda et al. 2013); anthocyanins are confined to fresh khalal and rutab fruit and antioxidant capacity falls markedly on sun-drying (Al-Farsi et al. 2005). Most published values therefore refer to tamr fruit and understate fresh-fruit composition. Alam et al. (2024) report that about half of date phenolics are ester-bound and missed by conventional extraction; this rests on one group and few cultivars and needs independent replication before it is treated as settled.

8. Glycaemic and clinical evidence (RQ2)

8.1 Glycaemic index

In a study of 13 healthy and 10 diabetic participants, the glycaemic index (GI) of five UAE cultivars ranged from 46.3 to 55.1 in the healthy group (Alkaabi et al. 2011), establishing the low-GI classification that the literature has repeated since. Across 17 Saudi cultivars GI ranged from 42.8 to 74.6, lowest for Shaqra, Sukkari and Sag'ai (42.8–44.6) and highest for the sucrose-retaining Sellaj and Maktoomi (71.0–74.6) (AlGeffari et al. 2016). Ripeness also matters: in 13 adults Khalas gave a mean GI of 71.1 at khalal and 53.0 at tamr, although variance was wide and the difference was not statistically significant (Alzahrani et al. 2023), so single-stage GI values should be generalised with caution. Glycaemic load depends on portion: three dates (about 30 g) give a low-to-moderate load, whereas the 100 g reference portion is high.

8.2 Diabetes trials

The largest trial randomised 79 Bahraini patients with type 2 diabetes to 60 g daily of Khalas dates or GI-matched raisins for 12 weeks and found no between-group difference in HbA1c, fasting glucose, lipids or body mass index (Butler et al. 2022). A 16-week trial of three dates a day in 100 adults with pre- or type 2 diabetes reported lower total cholesterol and higher HDL but no change in HbA1c or fasting glucose (Alalwan et al. 2020); three of its eleven authors are affiliated with Indena S.p.A., a manufacturer of botanical extracts, and the paper declares no conflict of interest—an affiliation that readers may reasonably expect to see discussed. A meta-analysis of six trials concluded that dates do not worsen glycaemic control (Mirghani 2021). Together these studies support safety at modest intakes but provide no evidence of therapeutic

benefit, and the popular claim that dates reverse diabetes has no clinical support.

8.3 Cardiovascular claims and citation amplification

The cardiovascular literature rests substantially on an uncontrolled four-week pilot study in ten healthy volunteers that reported reduced triglycerides (Rock et al. 2009). By 16 October 2026 OpenAlex recorded 97 citations of this pilot and 102 of the GI study of Alkaabi et al. (2011), both still accruing at 5–10 a year fifteen years on (Supplementary Table S2). The counts are modest; the amplification lies in the transfer of a ten-person, uncontrolled result into the conclusions of reviews as an established benefit, the mechanism Greenberg (2009) described, and even a measured review concedes that the vascular evidence is preliminary (Al-Dashti et al. 2021). No trial with hard cardiovascular endpoints exists. Mechanistic plausibility—inhibition of LDL oxidation *in vitro*, cholesterol binding by fibre—spans unvalidated steps, above all bioavailability: circulating polyphenols and their conjugates reach only nanomolar to low-micromolar concentrations after oral intake (Manach et al. 2005).

8.4 Anti-cancer claims

Methanolic Ajwa extract inhibits MCF-7 cells with IC_{50} values of 5–25 mg mL^{-1} (Khan et al. 2016), and pulp extract induces apoptosis in MDA-MB-231 cells via the AKT/mTOR pathway (Khan et al. 2021). These findings are repeated in reviews and popular literature as evidence that Ajwa treats cancer (Khalid et al. 2017), yet no registered trial of date fruit or extract in cancer patients was identified in ClinicalTrials.gov, the WHO ICTRP or the IRCT on 16 October 2026; the single registry record carrying a cancer term is a colon-health biomarker study in healthy volunteers. The gap is quantitative: an IC_{50} of 5–25 mg mL^{-1} is 5,000–25,000 µg mL^{-1}. Even if the roughly 250 mg of phenolics in 100 g of dates were absorbed completely and distributed instantly into 5 L of blood without metabolism—an impossible upper bound—the concentration would be about 50 µg mL^{-1}, 100–500-fold below the *in vitro* IC_{50}; realistic plasma concentrations are two to three orders of magnitude lower still (Manach et al. 2005). Unless metabolites prove far more active than parent compounds, anti-cancer effects of dietary dates are implausible.

8.5 Labour and delivery

Date consumption in late pregnancy is the most studied application. The first clinical report, a non-randomised comparison, found spontaneous labour in 96% of consumers versus 79% of non-consumers (Al-Kuran et al. 2011); randomised and quasi-randomised trials in Iran and Malaysia followed (Kordi et al. 2013, 2017; Razali et al. 2017). Meta-analyses consistently find shorter active-phase labour and less need for induction or augmentation (Bagherzadeh Karimi et al. 2020; Salajegheh et al. 2024). The evidence is weak, however: most trials were unblinded, with high risk of performance and detection bias (Bagherzadeh Karimi et al. 2020), heterogeneity is high, and the most recent review graded overall quality as unacceptable (Salajegheh et al. 2024). The putative oxytocin- or prostaglandin-like mechanism has not been characterised. The evidence supports safety but cannot establish efficacy with confidence (Supplementary Table S1).

9. Volatiles and underexplored tissues (RQ1, RQ3)

The fruit volatilome is dominated by aldehydes, alcohols, esters and ketones (Khalil et al. 2017); profiling of 148 palms from 135 varieties quantified 80 volatiles, identified discriminatory compounds such as β-ionone, and reported 2-methoxy-4-vinylphenol, a known red palm weevil attractant, in dates for the first time (Flowers et al. 2022), with implications for cultivar-specific pest risk and for authentication. Seed oil is oleic- and lauric-rich with β-sitosterol-dominated sterols (Nehdi et al. 2018) and shows antimicrobial activity relevant to food preservation (Alkhalidy et al. 2023). Spathe oil is dominated by 3,4-dimethoxytoluene and repels *Aedes aegypti* (Demirci et al. 2013). Two claims require independent confirmation: mammalian steroid hormones in pollen (Bentrad et al. 2017), which are biosynthetically implausible and may reflect contamination, and steroidal saponins in male flowers inferred from mass spectra without NMR (Hamed et al. 2017). Sap is characterised only for a Tunisian cultivar (Ben Thabet et al. 2009), bark and root chemistry are essentially undocumented (AbouZeid et al. 2024), and no *Phoenix* terpene synthase has, to the author's knowledge, been functionally characterised.

10. Thirteen priority gaps (RQ3)

Supplementary Table S3 summarises the molecular characterisation of regional germplasm underlying gaps 1 and 9.

1. **Yemeni cultivar fingerprinting.** Yemen holds a large and distinct cultivar assemblage (Ba-Angood

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2015), yet none of the published resequencing or genotyping panels identifies Yemeni accessions (Hazzouri et al. 2015, 2019; Mathew et al. 2015). Herbarium DNA and palaeogenomic approaches (Pérez-Escobar et al. 2021) offer a route while field access is constrained.

2. **Salinity QTL mapping.** GWAS on long-term saline-irrigation trial populations (Dghaim et al. 2021; Hammami et al. 2024) would convert candidate genes into selectable markers.

3. **Bayoud resistance-gene cloning.** Association mapping in Moroccan resistant selections (Sedra 2011), guided by effectors predicted from the pathogen genome (Khayi et al. 2023), would identify the nuclear locus.

4. **Sex-determining master regulator.** Functional tests of *CYP703*, *GPAT3* and *LOG3* (Torres et al. 2018; Celii et al. 2025) await routine transformation (Ramesh et al. 2024).

5. **Red palm weevil host-plant resistance.** No cultivar screening or resistance QTL exists; no-choice bioassays across diverse germplasm with metabolomic profiling are the first step.

6. **Terpene synthase functional genomics.** Genome mining, heterologous expression and enzyme assay of *Phoenix* terpene synthases would explain volatile biosynthesis and pest-relevant chemistry.

7. **Polyphenol pharmacokinetics.** No study identified in this Review has measured plasma or urine concentrations of date-derived phenolics after controlled dosing; stable-isotope dosing studies would establish bioavailability and half-life.

8. **Early detection of somaclonal variation.** Methylation or transcript classifiers predictive of off-types *in vitro* (Mirani et al. 2020).

9. **Climate-resilience breeding.** Multi-environment trials with dense genotyping would allow genomic selection for heat tolerance and water-use efficiency.

10. **Sap phytochemistry.** GC-MS and LC-MS profiling of sap from Arabian cultivars would fill a conspicuous gap for a traditional beverage and fermentation substrate.

11. **Bark and root metabolomics.** Untargeted profiling of these tissues may reveal metabolites of pharmaceutical or agrochemical interest.

12. **Definitive clinical trials.** Every health claim reviewed here requires adequately powered, pre-registered trials with objective endpoints and blinded assessment.

13. **Pre-emptive Bayoud surveillance.** Soil-DNA screening at quarantine points, sentinel plantings and harmonised diagnostics, coordinated across GCC plant-protection authorities, would insure against a disease that devastated North Africa (El Hadrami et al. 2011; Khayi et al. 2023).

Conclusions

Date palm research in the Arabian Peninsula has matured rapidly in genomics but not in translation. Resequencing and the Ajwa telomere-to-telomere assembly have settled population structure and the genetics of fruit colour and sugar type, yet no gene for sex, salinity or pest resistance has been validated in the species, and no QTL exists for the traits that matter most. The phytochemical and clinical literature is weakened by sugar interference in Folin–Ciocalteu assays, by reviews that amplify pilot studies, and by *in vitro* concentrations that diet cannot reach; human trials show safety, not efficacy. Closing the thirteen gaps identified here requires transformation protocols, field-based GWAS, HPLC-based phenolic standards, pharmacokinetic data and pre-registered trials—and a discipline of citing primary evidence.

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Author contributions

M. Alnuaimi conceived and designed the Review, conducted the literature searches and critical appraisal, prepared the supplementary material and wrote and approved the manuscript.

Ethics statement

This Review synthesises published literature and generated no new data from humans or animals. Ethical approval for the studies discussed was the responsibility of their original investigators.

Use of artificial intelligence

AI-assisted tools were used under the author's direction in preparing this revision for language editing, restructuring of the author's text, checking every reference against publisher and indexer records, and compiling the supplementary tables. All scientific content, interpretation and conclusions are the author's, and every AI-assisted change was checked by the author against the primary sources.

Data availability

No new primary data were generated. Search strings, record counts and dates are given in Table 2; trial-registry searches and the OpenAlex citation data are dated 16 October 2026 (Section 2). Supplementary Tables S1–S3 accompany the online article.

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