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STATISTICAL EVALUATION OF CHAMOMILE GENOTYPES IN UZBEKISTAN: RESEARCH PRIORITIES AND THE ROLE OF ANOVA

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Abstract. German chamomile (Matricaria chamomilla L.) is an important medicinal plant whose agricultural and pharmaceutical value depends on flower yield, essential oil content, and the composition of bioactive compounds. In Uzbekistan, research has addressed the effects of agroecological conditions, cultivation practices, and mineral fertilization on chamomile growth and quality. However, further work is needed to clarify the extent of variation among local genotypes and to distinguish genetic effects from environmental influences. This thesis proposes a statistical framework for evaluating chamomile genotypes using analysis of variance (ANOVA), followed by post-hoc comparisons and, where possible, molecular marker analysis. A combination of field observations, biochemical measurements, and SSR markers could help identify genotypes with desirable agronomic and pharmaceutical characteristics and provide a foundation for future breeding programmes in Uzbekistan.

Keywords: Matricaria chamomilla, Uzbekistan, genotype, ANOVA, genetic variation, flower yield, essential oil, SSR markers, plant breeding.

German chamomile is widely cultivated for its medicinal flowers and essential oil. Important traits include plant height, flowering time, number of flower heads, flower yield, and essential oil content. Variation in these characteristics provides opportunities for selecting genotypes with improved agronomic performance and desirable chemical profiles.

In Uzbekistan, local research has examined the influence of cultivation conditions on chamomile growth and development. Safarov and Nutfilloyeva investigated agroecological factors affecting plant development and essential oil quality, while Abduazimova and colleagues examined the effects of complex NPK fertilisers on the morphological and quality characteristics of cultivated chamomile [1–3]. These studies provide a useful foundation for understanding chamomile production under local conditions.

Nevertheless, differences observed between plants or cultivation treatments should not automatically be interpreted as genetic differences. Environmental conditions, soil fertility, irrigation, and fertilisation may also influence the measured traits. A systematic assessment of local genotypes is therefore needed to determine which differences are statistically reliable and potentially useful for selection.

The first priority should be to collect and characterise chamomile populations from different regions of Uzbekistan. Each population should be documented according to its geographical origin, growing

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conditions, and collection history. Where possible, local cultivated material should be compared with wild or naturalised populations and established cultivars.

The second priority is to evaluate important agronomic and biochemical traits under comparable experimental conditions. These should include plant height, number of branches, number of flower heads per plant, flower diameter, flower yield, flowering duration, and essential oil content. Analysis of the essential oil composition would provide additional information about the pharmaceutical value of individual genotypes.

The third priority is to determine whether the observed differences among genotypes are statistically significant. Analysis of variance (ANOVA) can be used to compare genotype means for each measured trait. The null hypothesis assumes that the mean values are equal across genotypes, whereas the alternative hypothesis states that at least one genotype differs.

A statistically significant ANOVA result (typically $p < 0.05$) would indicate that the observed differences are unlikely to be explained by within-group variation alone. However, ANOVA does not identify which genotypes differ. Post-hoc procedures, such as Tukey's honestly significant difference test, should therefore be used to compare individual genotype pairs.

Where experiments are conducted across several locations or growing seasons, the analysis should also account for environmental effects and genotype-by-environment interactions. This is particularly important for essential oil traits because their expression may change with growing conditions.

Statistical comparisons can identify genotypes with distinct phenotypic characteristics, but they cannot independently establish the molecular basis of those differences. For this reason, a further research priority is to combine field-based evaluation with molecular marker analysis.

SSR markers offer a practical approach for estimating genetic diversity among chamomile genotypes. Useful indicators include the number of alleles per locus, observed and expected heterozygosity, and polymorphism information content (PIC). Principal component analysis and cluster analysis may then help describe patterns of variation among the collected material.

Comparing molecular data with phenotypic measurements would address an important question: do genotypes that differ in yield or essential oil content also differ genetically? A comparison of genetic and phenotypic distance matrices could help answer this question. If suitable resources are available, chemical profiling by gas chromatography–mass spectrometry (GC–MS) could further connect genetic diversity with essential oil composition.

The proposed research should therefore follow an integrated sequence: collection and documentation of local germplasm, replicated field evaluation, ANOVA, post-hoc comparisons, biochemical characterisation, SSR analysis, and identification of promising genotypes.

The proposed approach would help establish a more systematic description of chamomile diversity in Uzbekistan. Rather than selecting material solely on the basis of high mean values in a single experiment, researchers could identify genotypes that combine desirable traits with statistically supported differences.

The results could also help distinguish genotypes that perform consistently across environments from those whose performance depends strongly on particular growing conditions. This distinction is relevant to both breeding and the development of cultivation recommendations.

Research conducted in Uzbekistan has addressed several important aspects of chamomile cultivation, including agroecological adaptation, fertilisation, growth, and essential oil quality [1–3]. The next step

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should be a more integrated evaluation of local genotypes, combining replicated field experiments, statistical analysis, biochemical characterisation, and molecular markers. ANOVA followed by appropriate post-hoc tests would establish which phenotypic differences are statistically significant, while SSR analysis could provide independent evidence of genetic diversity. Together, these methods would support the identification of promising chamomile genotypes for further breeding and cultivation under Uzbekistan's agroecological conditions.

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