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Research Article

ENHANCING CANCER TREATMENT BY COMBINING TRADITIONAL KNOWLEDGE FROM KORAPUT DISTRICT WILD MEDICINAL TUBERS WITH STRUCTURE-BASED VIRTUAL SCREENING OF ANAPLASTIC LYMPHOMA KINASE INHIBITORS

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ABSTRACT

Objective: This study aimed to document the ethnobotanical uses of wild edible medicinal tubers and rhizomes consumed by tribal communities in Koraput district, Odisha, India, to evaluate their nutritional composition, and to identify potential phytochemicals as anaplastic lymphoma kinase (ALK) inhibitors for cancer therapy through structure-based virtual screening (SBVS).

Methods: Ethnobotanical data were collected through semi-structured interviews, focus group discussions, and participant observation with tribal communities in the Koraput district over 18 months (January 2023–June 2024). Twenty-seven wild edible medicinal plant species with underground storage organs were identified and authenticated with herbarium voucher specimens. Nutritional analysis was performed using standard Association of Official Analytical Chemists methods to determine protein, carbohydrate, fat, fiber, mineral, and vitamin content. For computational drug discovery, 793 phytomolecules from these 27 plants were retrieved from the : Indian Medicinal Plants, Phytochemistry and Therapeutics (IMPPAT) database and subjected to SBVS against the ALK protein (PDB ID: 4FOB) using AutoDock Vina. Compounds with favorable binding affinities were further evaluated for drug-likeness, Absorption, Distribution, Metabolism, Excretion, and Toxicity (ADMET) properties using SwissADME and ProTox-III, and molecular dynamics (MD) stability using iMODS and CABSflex servers.

Results: The study documented 27 species across 13 plant families, with Zingiberaceae being the most represented (11 species, 40.7%). Tubers (15 species) and rhizomes (12 species) were the primary plant parts used, traditionally employed to treat 23 different ailments, predominantly gastrointestinal disorders. Nutritional analysis revealed significant levels of essential nutrients: proteins (8.5–15.2%), carbohydrates (45.8–72.3%), dietary fiber (12.4–28.7%), and various minerals and vitamins. Virtual screening of 793 phytomolecules identified eight compounds with binding energies better than −7 kcal/mol against ALK. After toxicity profiling, three compounds in toxicity class 6 (non-toxic, LD50 > 5000 mg/kg) were identified as safe candidates. Gibberellic acid (IMPHY011559) from *Datura stramonium* exhibited the highest binding affinity (−8.6 kcal/mol) and favorable ADMET properties. MD simulations confirmed the stability of the ALK-gibberellic acid complex.

Conclusion: Wild medicinal tubers and rhizomes represent underutilized resources that bridge traditional knowledge and modern nutritional science, offering solutions for malnutrition and health challenges in tribal populations. The integration of ethnobotanical knowledge with computational drug discovery identified gibberellic acid as a promising ALK inhibitor candidate. These findings support the incorporation of indigenous knowledge systems into nutrition and healthcare practices while highlighting the potential of culturally relevant phytochemicals for cancer treatment. However, these *in silico* predictions require validation through *in vitro* and *in vivo* experimental studies.

Keywords: Anaplastic lymphoma kinase inhibitor, Anticancer, Ethnobotany, Tribal communities, Nutritional analysis, Virtual Screening.

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INTRODUCTION

Traditional indigenous communities across the world have, over millennia, evolved sophisticated knowledge systems in the use of wild plants as a source of food and medicinal purposes. Tribal communities in India represent 8.6% of India's population and are custodians of very valuable traditional ecological knowledge about the local biodiversity. The Koraput district of Odisha, within the Eastern Ghats biodiversity hotspot, harbors several tribal groups such as the Kondh, Paraja, Gadaba, and Bonda tribes, which have preserved strong relationships with their natural environment [1]. Wild edible plants (WEPs) are a lifeline for these communities, feeding families and supplying remedies when gardens run bare and cupboards echo in the lean months. Among WEPs, underground storage organs such as crisp tubers and knobby rhizomes stand out for their dense nutrients, long shelf life, and year-round availability. These parts of the plant serve a double purpose: People eat them as food and use them as medicine, blending nourishment and healing in a way long valued by traditional systems. India's tribal communities face a serious nutritional crisis, with malnutrition striking far more often than it does in the general population, leaving too many children with thin arms and tired eyes. According to the latest National Family Health Survey of India, children in tribal regions still face higher rates of stunting, wasting, and being underweight than the national average, with many barely reaching their parents' shoulders by age five [2].

Many tribal populations continue to use traditional indoor heating and cooking methods that burn fossil fuels such as coal, wood, or manure; lung cancer is a major concern. Fine particulate matter (PM2.5), one of the carcinogenic particles found in the harmful smoke released by this, can enter the lungs deeply. Even among non-smokers, studies reveal that prolonged exposure to this indoor air pollution dramatically raises the risk of lung cancer. Rural and tribal communities frequently use these fuels on a daily basis and have poor ventilation, increasing their lifetime exposure. Poor ventilation and daily use of these fuels increase lifetime exposure to indoor air pollution, putting even non-smokers in these communities at greater risk. Lung cancer risk is also increased by smoking practices that are prevalent among some tribal groups, such as using tobacco, charas, and ganja. Poverty, limited access to healthcare, and environmental factors all increase this risk, making lung cancer a serious health issue for these populations that use fossil fuels [3].

Wild, edible, and medicinal plants remain largely untapped, yet they hold real promise for boosting nutrition in these communities. Think of a handful of tart, vitamin-rich berries gathered at the edge of a forest. Recent studies highlight how WEPs can fill gaps in traditional diets, offering essential nutrients, bioactive compounds, and trace minerals you will not find in a plain bowl of rice. Still, there's a significant gap in thorough documentation and solid scientific evidence of these plants' nutritional value, especially when it comes to their traditional medicinal uses, such as the bitter leaves brewed into village remedies. Blending traditional knowledge with modern nutritional science can open the door to solutions that fit a community's culture and last over time, such as crafting meal plans rooted in familiar local grains to address health and nutrition challenges in tribal communities [4]. This approach, called "nutrition-sensitive ethnobotany," recognizes that in many Indigenous traditions, food and medicine grow side by side, and studying those ties can lead to more effective interventions. This study aims to bridge the gap between indigenous wisdom and modern science by collecting detailed ethnobotanical data on wild edible and medicinal tubers and rhizomes used by tribal communities in the Koraput district, along with insights into their nutritional value, such as the earthy, nutty taste of freshly dug yams. This research expands the body of work exploring how indigenous knowledge and mainstream nutritional science intersect, shaping food security, health, and sustainable development for indigenous communities, such as the way a traditional maize harvest can inform modern diet planning.

The study also looks for natural substances that might block the anaplastic lymphoma kinase (ALK) protein, which is crucial in cancer, using computer-based techniques known as structure-based virtual screening (SBVS). This technique predicts how well a compound will fit and bind to the ALK protein, allowing for the rapid testing of numerous compounds [5]. Following the selection of the best compounds, the study uses absorption, distribution, metabolism, excretion, and toxicity (ADMET) analysis to examine the compounds' safety as well as potential absorption and breakdown by the body. The study intends to support nutrition and health in tribal communities while simultaneously discovering new possible cancer-fighting molecules by fusing traditional knowledge of medicinal plants with contemporary computer techniques. In general, it aims to create workable and sustainable solutions that link drug discovery, medicine, and food.

LITERATURE REVIEW

Indigenous knowledge systems and WEPs

Indigenous peoples have built rich, flexible systems of knowledge over generations, learning how to read the land, track the seasons, and care for the places they call home. When it comes to wild foods, they cover everything from spotting the right plant in the field to knowing when it's in season, how to prepare it, what nutrients it offers, and how it can heal [6]. Studies show that indigenous knowledge systems are alive, constantly evolving through hands-on experimentation, careful observation, and the passing of wisdom from one generation to the next, like a grandmother teaching her grandson which plants heal and which ones harm. Researchers across India have found that tribal communities make wide use of WEPs, everything from tangy tamarind pods to forest yams. A study has indicated that indigenous people in the Himalayas utilize more than 200 WEP species, several of which possess medicinal uses [7]. Parallel to these developments, studies in the Western Ghats have located several wild food plants with dual nutritional and medicinal purposes. The notion of "medicine as food" is strongly rooted in traditional knowledge systems, an acknowledgement of a relationship between nutrition and health. This is in contrast to modern systems that tend to isolate nutrition and healthcare as distinct fields. Most contemporary research has commenced validating this classic knowledge, revealing that most WEPs possess bioactive compounds with medicinal properties [8].

Nutritional value of WEPs

WEPs have been acknowledged as key sources of macro and micronutrients, commonly possessing greater levels of vitamins, minerals, and phytochemicals than crops raised under cultivation. WEPs have been demonstrated to significantly contribute to diet diversity and nutritional adequacy within rural and indigenous populations [9]. Among these plants are underground storage organs, such as tubers and rhizomes, which contribute to the high carbohydrate content, dietary fiber presence, and storage of bioactive compounds. Research has reported on the nutritional content of some of the wild tubers and rhizomes, highlighting their use as sources of energy, protein, minerals, and vitamins. Beyond their simple nutritional value lies the nutritional significance of WEPs, which includes their contribution to dietary variety and micronutrients that will be absent in monotonous staple food-based diets. This is especially true for tribal communities, where finding a basket of fresh vegetables or other varied foods can be a rare challenge [10].

Therapeutic properties of edible underground plant parts

People around the world have long relied on edible roots and tubers in traditional medicine, brewing them into teas or tonics for their healing qualities. These parts of the plant often store high levels of bioactive compounds, alkaloids, glycosides, phenolics, and fragrant essential oils that give them their healing power [11]. Studies have confirmed that some traditional remedies, such as those made from plant roots, work effectively, as seen in the use of ginger to settle a queasy stomach. For example, studies show turmeric rhizomes ease inflammation, ginger rhizomes soothe the stomach after a heavy meal, and certain wild tubers help regulate the immune system. The way these plants serve as both food and medicine demonstrates the profound understanding Indigenous people have of the connection between nutrition and health, as seen in the use of a bitter root to calm a fever [12]. Many people see this view as relevant to today's functional foods and nutraceuticals, from probiotic yogurts to omega-3 supplements.

Koraput district ethnobotanical studies

The Koraput district, within the Eastern Ghats of Odisha, is identified as a hotspot of biodiversity with dense flora and fauna. The district is inhabited by many tribal populations who have retained traditional ways of life and have excellent knowledge of plant resources within the area. Past ethnobotanical research in Koraput has reported the utilization of some medicinal plants among tribal groups [13]. In contrast, there has been little attention given to WEPs with underground storage organs. This is a serious loophole in recording traditional knowledge in the area. The Koraput tribal groups, such as the Kondh, Paraja, Gadaba, and Bonda tribes, possess unique culture and knowledge systems concerning the use of plants. Knowledge of the differences and similarities in plant use in these groups is essential for adequate documentation of traditional knowledge [14].

ALK protein of non-small cell lung cancer (NSCLC)

About 80–85% of all cases of lung cancer are NSCLC. It all starts with the epithelial cells that line the lungs' airways [15]. ALK-positive lung cancer is a subtype of NSCLC that is primarily linked to the ALK protein through genetic changes involving the *ALK* gene [16]. ALK is a protein (PDB ID: 4FOB) produced by the *ALK* gene that resides on the cell surface and functions as an antenna to take in signals from the environment. Upon activation, it transmits these signals within the cell to regulate critical functions such as cell division and growth. During development, this signaling is crucial, particularly in the nervous system. The *ALK* gene becomes overactive due to alterations or mutations in certain cancer-causing cells to grow out of control and develop into tumors [17]. ALK is a good target for cancer medications because it can block this overactivity and slow or even stop the growth of tumors [18].

STUDY AREA AND COMMUNITIES

Geographic description

Koraput district is situated in southwestern Odisha, India, at 18°20'–19°57' N latitude and 82°18' to 83°52' E longitude. The district area is 8534 square kilometers and has hilly tracts, dense forests, and many rivers and streams. It falls within the Eastern Ghats biodiversity hotspot and has a tropical monsoon climate with clear wet and dry periods. The topography of the district is characterized by hills, plateaus, and valleys, with altitudes between 300 and 1000 m above sea level [19]. The region enjoys an average annual rainfall of 1500–2000 mm during the southwest monsoon season (June–September). It is mostly warm and humid with temperatures varying from 15°C to 40°C during the year. The natural cover in the Koraput district is mainly of tropical moist deciduous forests, with pockets of semi-evergreen forests in more rainfall-affected areas. The forests are highly biodiverse and support various plant and animal species. The district holds many protected areas, from quiet wildlife sanctuaries where hornbills call at dawn to dense reserved forests that stretch for miles [20].

Tribal communities

In the Koraput district, tribals make up almost 52% of the people, according to the 2011 India Census, a figure that means more than every other face in the market belongs to a tribal community. The Kondh, Bhuyan, Gadaba, Bonda, and Poroja stand out as the region's most prominent tribal communities, each with its own distinct traditions and stories. Every community carries its own culture, language, and a body of traditional knowledge like stories told around a fire on cold nights [21]. The Kondh tribe is the district's largest tribal community, living mainly in the rugged hill country where mist hangs low in the mornings. They have long lived off the land, farming small plots and gathering in the shade of thick forest canopies, with a deep, practiced knowledge of every useful plant. The Kondh people possess a deep cultural heritage, shaped by centuries of caring for the forest and utilizing its resources wisely, such as gathering wild honey without harming the hives. The Paraja are another influential group in Koraput, known for their expertise in traditional medicine and their skill in utilizing local plants, such as crushing fresh neem leaves to create a healing paste [22]. They have preserved precise knowledge about the healing properties of many plants, such as the cool, bitter leaves used for fevers, and still blend age-old remedies with today's medical practices. In the district's southern hills, the Gadaba tribe preserves rare customs and knows how to use wild plants, such as simmering forest herbs into a rich, earthy tea. They have learned how to spot and use all kinds of wild plants, from the sharp-scented mint by the stream to roots that can soothe a cough. Although few in number, the Bonda tribe remains one of the oldest communities of the area, their traditions as weathered as the hills they call home. They have held on to their traditional way of life and know the forest like the back of their hand, from the taste of fresh honey to the roots that heal fevers [22].

Traditional livelihood systems

The Koraput tribes have traditionally depended upon a combination of agriculture, forest products, and animal husbandry as their means of livelihood. Agriculture is predominantly rain-fed, and rice, millets, pulses, and vegetables are crops grown. Settled agriculture and shifting cultivation (jhum) coexist in some areas, as done by the populations. Forest resources form a central component of the indigenous livelihood systems, providing food, medicine, building materials, and income from gathering and selling non-timber forest products [23]. WEPs contribute significantly to the traditional food systems, especially during the lean season when agricultural production is not sufficient. The indigenous knowledge of wild plant use is normally transmitted through generations through oral tradition, field demonstrations, and communal practices. This knowledge consists of elaborate information on the identification of plants, how to collect them, processing procedures, and their utilization as food and medicine.

METHODS

Study design

This study utilized mixed methods involving ethnobotanical questionnaires, nutritional content analysis, and recording of traditional knowledge. The fieldwork took 18 months (January 2023–June 2024) to allow for seasonal trends in the availability and usage of plants.

Site selection and sampling

The study was conducted in selected villages across the Koraput district, representing different geographical zones and tribal communities. A total of 15 villages were selected using stratified random sampling to ensure representation of different tribal groups and ecological zones. The villages were divided into three zones depending on their geographical position and altitude: Highland zones (above 600 m), mid-altitude zones (300–600 m), and lowland zones (below 300 m). This division was crucial for determining differences in plant supply and use patterns among different ecological zones.

Data collection methods

Ethnobotanical surveys

Data collection at the primary level was carried out using semi-structured interviews with key informants such as traditional healers, old community members, and women possessing specialized knowledge regarding the use of wild plants. Collective knowledge regarding the wild edible medicinal plants was collected using focus group discussions in each village. Participant observation was utilized to record actual practices regarding plant collection, processing, and usage. This involved accompanying the community members on visits to the forest and observing conventional preparation processes.

Plant collection and identification

Plant samples were gathered with the assistance of native informants at various seasons to obtain the widest possible range of available species. Harvesting was undertaken by following standard ethnobotanical procedure, with due documentation of indigenous names, utilization, and processing procedures. Identification was accomplished through standard taxonomic keys and regional flora. Voucher specimens were prepared and maintained in the herbarium of the Department of Botany, Centurion University, for later reference.

Nutritional analysis

Fresh plant samples were drawn at the seasons of peak availability for nutritional analysis. The samples were processed or stored by suitable procedures for maintaining nutritional quality. Nutritional composition was determined following standard Association of Official Analytical Chemists (AOAC) methods. Moisture content was determined by the oven-drying method (AOAC 925.10). Crude protein content was estimated using the Kjeldahl method (AOAC 984.13) with a nitrogen-to-protein conversion factor of 6.25. Crude fat was extracted using the Soxhlet extraction method (AOAC 920.39). Crude fiber was determined by acid-base digestion (AOAC 978.10). Total carbohydrate content was calculated by the difference method. Ash content was determined by dry ashing at 550°C (AOAC 923.03). Mineral analysis was performed using atomic absorption spectrophotometry (AAS, PerkinElmer PinAAcle 900T) for calcium, iron, magnesium, and zinc, whereas phosphorus was determined by the vanadomolybdate colorimetric method (AOAC 965.17) using a ultraviolet (UV)-Visible spectrophotometer (Shimadzu UV-1800). Potassium and sodium were analyzed using flame photometry (Systronics Flame Photometer 128). Vitamin C was determined by the 2,6-dichlorophenolindophenol titrimetric method (AOAC 967.21), whereas beta-carotene (Vitamin A precursor) was extracted and quantified using high-performance liquid chromatography (Waters Alliance e2695) with UV detection at 450 nm.

SBVS

Target protein and ligand database

SBVS [24] is a computer-based technique used to find potential drug compounds by testing how small molecules fit into the 3D structure of a target protein. This specific structure was chosen based on several critical factors: (1) it represents the kinase domain in complex with a small molecule inhibitor, providing a well-defined binding pocket suitable for SBVS; (2) the structure has high resolution (2.10 Å), ensuring accurate representation of the active site geometry and amino acid residue positions; (3) the co-crystallized ligand occupies the Adenosine Triphosphate (ATP)-binding site, which is the primary target for kinase inhibitors; and (4) this structure has been extensively validated and utilized in previous computational drug discovery studies targeting ALK. While other ALK structures exist, including phosphorylated forms and complexes with different inhibitors, 4FOB was selected as it provides an optimal balance of structural quality, active site accessibility, and relevance to drug design for ALK inhibition [25]. The crystal structure of the ALK protein (PDB ID: 4FOB) was selected for this study from the RCSB Protein Data Bank [26]. The protein structure was prepared using Discovery Studio software [27] by removing water molecules, heteroatoms, extra chains, and bound ligands to clean the structure [28]. The prepared protein was then saved in the Protein Data Bank, partial charge (Q), and atom type (T) (PDBQT) format because AutoDock Vina [29], the docking software used, only accepts PDBQT files. The protein was then opened in AutoDock Vina [30], where the active site residues were identified and selected. The grid box dimensions and center coordinates were determined through a systematic analysis of the ALK protein's active site. First, the ATP-binding pocket was identified by analyzing the co-crystallized ligand position and the location of known catalytic residues (Leu1122, Gly1123, His1124, Gly1125, Val1130, Ala1148, Val1180, Leu1196, Leu1198, Met1199, Ala1200, Gly1202, Leu1256, Pro1260, and Gly1269) [31]. The grid box center coordinates (X: 21, Y: 9, Z: 8) were positioned at the geometric center of these active site residues to ensure complete coverage of the binding pocket. The grid box dimensions (13 Å × 16 Å × 9 Å) were selected to encompass the entire active site with sufficient margin (approximately 5 Å beyond the farthest active site residue) to allow flexible docking of ligands of varying sizes while maintaining computational efficiency [32]. These parameters were validated by successfully re-docking the native co-crystallized ligand, which reproduced the experimental binding pose with an Root Mean Square Deviation (RMSD) < 2.0 Å.

Before molecular docking, an initial filtering step was applied to the 793 phytochemicals retrieved from the IMPPAT database [33]. All compounds were screened for basic drug-likeness properties to exclude molecules with unfavorable pharmaceutical characteristics. This preliminary filtering included removal of compounds that violated Lipinski's Rule of Five (molecular weight>500 Da, logP>5, hydrogen bond donors>5, hydrogen bond acceptors>10), contained reactive or toxic functional groups, or exhibited poor structural quality in the database. This initial screening ensured that only potentially drug-like compounds proceeded to the computationally intensive docking step, thereby improving the efficiency of the virtual screening workflow and focusing subsequent analysis on molecules with realistic therapeutic potential. These ligand structures were then converted into the PDBQT format using Open Babel software [34], making them compatible for docking in AutoDock Vina. This comprehensive preparation of both protein and ligand libraries enabled efficient and accurate SBVS of natural compounds against the ALK protein [35].

ADMET profiling

ADMET profiling was conducted on the natural compounds identified through SBVS (Structure-Based Virtual Screening) to predict their safety and efficacy as potential medications. ADMET profiling was performed using SwissADME [36] and ProTox-III. SwissADME was used to predict physicochemical properties, lipophilicity, water solubility, pharmacokinetic parameters (including gastrointestinal absorption and blood–brain barrier permeation), and drug-likeness according to multiple rules (Lipinski, Ghose, Veber, Egan, and Muegge) [37]. ProTox-III was employed to assess toxicity endpoints, including acute toxicity (LD50), hepatotoxicity, carcinogenicity, mutagenicity, cytotoxicity, and immunotoxicity using machine learning models trained on experimental toxicity data [38].

Molecular dynamics simulation studies

Molecular dynamics (MD) simulations were performed using two complementary online platforms: iMODS [39] and CABSflex 3.0 [40]. The iMODS server employs normal mode analysis (NMA) in internal coordinates to study the collective motions and structural flexibility of protein-ligand complexes. Simulations were conducted using default parameters: the elastic network model with a 10 Å cutoff distance, calculation of the first 20 non-trivial normal modes, and analysis over the entire protein structure. CABSflex 3.0 utilizes coarse-grained MD with the CABS force field to simulate protein flexibility. Although these are web-based servers with preset parameters, the simulations effectively model protein dynamics at room temperature in an implicit solvent environment. Each simulation was run in triplicate to ensure reproducibility of results. The output provided insights into flexibility (root mean square fluctuation [RMSF]), atomic displacement (B-factor), structural deformability, eigenvalues, variance, residue correlations (covariance), and elastic network connectivity of the ALK-IMPHY011559 complex formed between the ALK protein (4FOB) [41] and the top molecule. The simulations helped validate that the compound binds stably within the active site of the protein, supporting its potential as an effective anticancer agent.

Statistical analysis

Every analysis was carried out in triplicate, and the mean±standard deviation was used to express the findings. Software called SPSS (version 26.0) was used to perform statistical analysis. Significant differences ($p<0.05$) between plant species were identified using a one-way analysis of variance test, followed by Tukey's honest significant difference *post hoc* test for multiple comparisons to determine which specific species differed significantly from one another.

RESULTS

Ethnobotanical diversity and herbarium authentication

To ensure accurate species identification, every plant specimen collected for this study was carefully authenticated following the Flora of Odisha taxonomic rules. The authenticated specimens were systematically cataloged and deposited at the Department of Botany, Centurion University of Technology and Management, Odisha, India, as permanent reference material for future research. Each specimen was assigned a unique herbarium voucher number ranging from CUTM/BOT/2023/03 to CUTM/BOT/2024/27. The research reported 27 wild edible medicinal plants with underground storage organs consumed by tribal communities in the Koraput district (Table 1). These species are represented by 18 different botanical families, with Zingiberaceae being the most diverse family with 11 species (40.7%), followed by Liliaceae with 4 species (15%), and Euphorbiaceae with 2 species (7%). Diversity in family representation reflects the wide range of plant resources consumed by tribal communities. The predominance of Zingiberaceae mirrors the centrality of rhizomatous species in medicine systems based on traditional practices for digestive and inflammatory diseases.

Parts of the plant

Among the 27 reported species, the most frequent uses were of tubers (15 species, 55%) and then rhizomes (12 species, 44%). This trend is due to the availability of underground storage organs throughout the year with concentrated nutrients and bioactive substances. Tubers are also highly appreciated for their elevated carbohydrate value and capacity to offer energy during periods of food shortages. Rhizomes are more used therapeutically because they have more bioactive compounds, although most are sources of food as well.

Growth forms

The species that were documented showed varied growth habits, with herbs being the dominant growth form (19 species, 70%), followed by

Table 1: Ethnobotanical inventory of wild edible medicinal tubers and rhizomes used by tribal communities in Koraput district, Odisha

S. No.	Local name	Botanical name	Family	Habit	Part used	Traditional uses	Voucher No
1	Torani	*Alpinia calcarata* Rosc.	Zingiberaceae	Herb	Rhizome	Rheumatism, Weakness	CUTM/BOT/2023/03
2	Bana Haladi	*Curcuma montana* Roxb.	Zingiberaceae	Herb	Rhizome	Malnutrition, Gout	CUTM/BOT/2023/04
3	Tulsi	*Ocimum tenuiflorum* L.	Lamiaceae	Herb	Rhizome	Cough, Cold, Fever, Respiratory disorders	CUTM/BOT/2023/05
4	Satabari	*Asparagus racemosus* Willd.	Liliaceae	Climber	Tuber	Headache, Inflammation, Otorrhea	CUTM/BOT/2023/11
5	Saphed-Musli	*Chlorophytum borivilianum* Sant and Fernandez	Liliaceae	Herb	Tuber	Impotency, Sexual power	CUTM/BOT/2023/12
6	Nilakantha-Kedar	*Hedychium spicatum* Buch-Ham.	Zingiberaceae	Herb	Rhizome	Rheumatism, Loose motion	CUTM/BOT/2023/13
7	Aambakashiaada	*Curcuma amada* Roxb.	Zingiberaceae	Herb	Rhizome	Stomachache, Sprain	CUTM/BOT/2023/17
8	BhuinKokharu	*Ipomoea mauritiana* Jacq.	Convolvulaceae	Climber	Tuber	Diabetes, Epilepsy, Snake bite	CUTM/BOT/2023/18
9	Simili	*Bombax ceiba* L.	Bombacaceae	Tree	Tuber	Acne, Boils, Menstrual disorder, Vertigo	CUTM/BOT/2023/22
10	Sunthi	*Curcuma aromatica* Salisb.	Zingiberaceae	Herb	Rhizome	Abdominal discomfort	CUTM/BOT/2023/23
11	Rama Kedara	*Kaempferia galanga* Linn.	Zingiberaceae	Shrub	Rhizome	Malaria, Leprosy	CUTM/BOT/2023/24
12	Ahira	*Putranjiva roxburghii* Wall.	Euphorbiaceae	Tree	Tuber	Diabetes, Rheumatism	CUTM/BOT/2023/35
13	Kala Haladi	*Curcuma caesia* Roxb.	Zingiberaceae	Herb	Rhizome	Stomach disorder	CUTM/BOT/2023/36
14	Bana Piaja	*Urginea indica* (Roxb.) Kunth.	Liliaceae	Herb	Tuber	Hypertension, Menstrual disorder	CUTM/BOT/2023/37
15	Katha Aalu	*Manihot esculenta* Crantz.	Euphorbiaceae	Herb	Rhizome	Indigestion	CUTM/BOT/2023/38
16	Bana aalu	*Dioscorea pentaphylla* Linn.	Dioscoreaceae	Climber	Tuber	Swellings, Joint pain	CUTM/BOT/2024/20
17	Haladi	*Curcuma longa* L.	Zingiberaceae	Herb	Rhizome	Worm infection, Skin disease	CUTM/BOT/2024/21
18	Phiriki	*Benkara malabarica* [Lam] Tirveng.	Rubiaceae	Shrub	Tuber	Abdominal pain, Throat infection	CUTM/BOT/2024/22
19	Palua	*Curcuma angustifolia* Roxb.	Zingiberaceae	Herb	Rhizome	Diarrhoea, Indigestion, Stomach problems	CUTM/BOT/2024/23
20	Rakta Kayeen	*Nymphaea pubescens* Willd.	Nymphaeaceae	Herb	Tuber	Blood dysentery, Excess menstrual bleeding	CUTM/BOT/2024/26
21	Dhutura	*Datura stramonium* L.	Solanaceae	Herb	Tuber	Asthma, Joint pain, Skin disorders	CUTM/BOT/2024/27
22	Dina	*Leea indica* (Burm.f.) Merr.	Vitaceae	Shrub	Tuber	Diarrhea, Anxiety	CUTM/BOT/2024/31
23	Gandha shunthi	*Curcuma zedoaria* (Christm) Rosc.	Zingiberaceae	Herb	Rhizome	Stomach problems, Stimulant	CUTM/BOT/2024/32
24	Deo-Shandha	*Chionanthusmala-elengi* [Dennst.] Green	Oleaceae	Tree	Tuber	Blood pressure, Snake bite	CUTM/BOT/2024/33
25	Kangada	*Momordica dioica* Roxb. ex Willd.	Cucurbitaceae	Climber	Tuber	Abortion, Poison, Rheumatism	CUTM/BOT/2024/34
26	Keokanda	*Costus speciosus* (Koenig) Sm.	Zingiberaceae	Herb	Tuber	Constipation, Vertigo, Bilious vomiting	CUTM/BOT/2024/35
27	Pancha angulia	*Gloriosa superba* L.	Liliaceae	Herb	Tuber	Bubo, Gout, Otalgia	CUTM/BOT/2024/36

Voucher specimens are deposited at the Herbarium of the Department of Botany, Centurion University of Technology and Management, Odisha, India

climbers (3 species, 11%), trees (3 species, 11%), and shrubs (2 species, 8%) (Table 2). This diversity comes from how tribal communities have adapted to use the resources in many different ecological niches, from dense forests rich with wild berries to riverbanks teeming with fish. Herbaceous plants are usually easier to spot and gather, think of soft stems brushing your boots while climbing, species can reach right up into the forest canopy for hidden resources. Tree species often produce more underground storage organs, think thick, starchy roots, but they can take a lot more work to dig up.

Traditional uses and applications

Medicinal applications

People have long used the reported plants to treat 23 different ailments, from stubborn coughs to aching joints. Gastrointestinal problems topped the list, with 12 species (about 48%) used to treat stomach aches, diarrhea, indigestion, and similar issues. It shows just how central the gastrointestinal system is in traditional medicine, much like the way healers focus on soothing a patient's stomach after a heavy, spicy meal. Six species (about 24%) were used to treat inflammatory diseases such as rheumatism and aching joints, whereas four species (or 16%) helped heal skin problems and close small wounds. People also turned to it for diabetes, menstrual problems, and lung ailments, from labored breathing to stubborn coughs.

Preparation methods

They used time-honored methods, adjusting them for each plant's species and the reason it was needed, boiling tough roots for medicine, for example. Raw eating was practiced for species that had low flavors and no toxic substances. Boiling was the prevalent processing technique (60% of species), followed by milling to paste form (40%), and fermentation (20%). Multistep, timed complex preparation techniques were used. For instance, some tubers needed extended boiling to eliminate toxic substances, whereas others were fermented to make them easy to digest and nutritious.

Seasonal availability and patterns of use

Availability and utilization of wild food medicinal plants demonstrated clear-cut seasonality. The maximum collection seasons were during the post-monsoon months (October–December) when plants had stored maximum reserves in underground parts. Some species were available throughout the year, ensuring food availability even in times

Table 2: Family-wise distribution and habit analysis of documented species

Family	No. of species	Percentage	Dominant habit	Plant parts used
Zingiberaceae	11	40	Herb	Rhizome [11]
Liliaceae	4	15	Herb	Tuber [4]
Euphorbiaceae	2	8	Herb/Tree	Tuber [1], Rhizome [1]
Lamiaceae	1	4	Herb	Rhizome [1]
Solanaceae	1	4	Herb	Tuber [1]
Bombacaceae	1	4	Tree	Tuber [1]
Convolvulaceae	1	4	Climber	Tuber [1]
Cucurbitaceae	1	4	Climber	Tuber [1]
Dioscoreaceae	1	3	Climber	Tuber [1]
Nymphaeaceae	1	4	Herb	Tuber [1]
Oleaceae	1	3	Tree	Tuber [1]
Rubiaceae	1	4	Shrub	Tuber [1]
Vitaceae	1	3	Shrub	Tuber [1]
Total	27	100	Herb (56%)	Tuber [15], Rhizome [12]

Percentages calculated based on the total of 27 documented species. Data are presented as mean±standard deviation of triplicate measurements for quantitative assessments

of scarcity. Others were seasonally specific, necessitating a very specific timing of collection and processing. Traditional knowledge is known to contain extensive information on optimal harvest timing for various species.

Results of nutritional analysis

Macronutrient content

Nutritional content showed great variation in macronutrient content among the species recorded. Carbohydrate content varied from 45.8% of dry weight to 72.3%, averaging 58.7%. *Dioscorea pentaphylla* tubers had the highest content of carbohydrates (72.3%), whereas *Curcuma longa* rhizomes had the lowest carbohydrate content (45.8%) (Table 3). Protein content ranged from 8.5% to 15.2%, averaging 11.8%. *Asparagus racemosus* tubers packed the most protein 15.2% making them a prized source of nourishment in tribal diets, much like the hearty root slices simmering in a clay pot over the fire. Crude fat ranged from 0.8% to 4.2%, and most species carried a moderate amount of lipids, enough to leave a faint sheen on the surface. All species were rich in dietary fiber, ranging from 12.4% to 28.7%, with an average of 18.9%. A high fiber content plays a key role in keeping the digestive system healthy and may explain why ancient people turned to these plants to ease stomach troubles, much like chewing gritty plant stems for relief.

Micronutrient content

The mineral analysis revealed key elements calcium, iron, phosphorus, potassium, and magnesium, such as the faint metallic tang you catch when tasting well water. Calcium levels ranged from 45 to 280 mg/100 g, with *Chlorophytum borivilianum* tubers topping the list, their dense, pale flesh packed with the most (Table 4). Iron levels ranged from 3.2 to 12.8 mg/100 g, and a few species packed a hefty dose enough to tint the flesh a faint rust-red. In nearly every species, potassium levels stayed high, falling somewhere between 280 and 890 mg/100 g, about the amount you would find in a ripe banana. Potassium plays a key role in keeping your heart working smoothly and your body's fluids in balance, making it an essential part of good nutrition. Phosphorus levels ran from 32 to 156 mg/100 g, enough to help keep bones strong and fuel the body's energy use like the steady burn of a small campfire. Tests measured the vitamins in *Curcuma alismatifolia* tubers, detecting Vitamin C, Vitamin A precursors, and several B-complex vitamins. Vitamin C levels ranged from 8.5 to 45.2 mg/100g, with fresh tubers containing more than the rhizomes, similar to the crisp snap of a just-dug root.

Nutritional importance in tribal diets

Role in dietary diversity

The recorded wild medicinal food plants are making a valuable contribution to the diversity of diets among tribal communities. In the lean season, the plants may contribute as much as 25% of the total caloric intake and high levels of essential nutrients. The species richness and the nutritional value of these plants assist in overcoming micronutrient malnutrition that is prevalent in simple diets of staple foods. The mineral richness of most species is most useful in overcoming iron and calcium deficiencies.

Seasonal food security

Wild food plants contribute importantly to seasonal food security, supplying nutrition when agricultural yields are inadequate. The underground storage organs are especially useful since they can still be accessed during times of drought when other foods are not available. The traditional knowledge regarding the best timing for collection and processing provides full nutritional utilization from these crops. This knowledge is a higher-order understanding of seasonal nutrition management.

Virtual screening of small molecules with drug likeness filters

During the virtual screening process, drug-likeness filters were very important in reducing the number of small molecules and helping focus only on the most promising candidates. After initial docking of all 793 phytochemicals from the wild tuber and rhizome database, various drug-likeness rules were applied to remove compounds that were likely to have poor pharmaceutical properties. These filters included Veber's and Egan's criteria, which take into account aspects such as polar surface area and the number of rotatable bonds for good oral bioavailability; Ghose's rules, which assess molecular properties such as logP, molar refractivity, and total number of atoms; and Lipinski's Rule of Five, which looks for attributes like molecular weight and hydrogen bond donors and acceptors. The GSK 4/400 rule, which limits logP to 4 and molecular weight to 400, and Pfizer's 3/75 rule, which limits logP to 3 and the number of aromatic rings to 7.5, are two examples of industry-specific guidelines that were also used because they have been linked to lower attrition in drug development pipelines.

By systematically applying all these drug-likeness filters, the virtual screening process successfully narrowed down the initial set of 793 phytomolecules to just 21 small molecules that exhibited strong drug-like properties. These selected compounds proceeded to further ADMET evaluation and toxicity screening, improving the likelihood that the final candidates are both effective and safe for use as potential ALK inhibitors against cancer.

Best binding affinity with toxicity profiling

Following virtual screening and drug-likeness filtering, compounds with docking scores better than −7 kcal/mol against the ALK protein were selected for further toxicity profiling, resulting in eight top-ranked compounds (Table 5). These eight were then checked for toxicity and their LD50 values. After this step, three compounds were found to be safe (in toxicity class 6, which means very low toxicity). Among them, the compound ID IMPHY011559 had the best results overall, so it was chosen as the top candidate to block ALK and act as a possible anticancer agent. Using Discovery Studio software, the interaction between 4FOB and IMPHY011559 was displayed in 3D, 2D, and surface visualization. This made it easier to see how the chosen substance fits and binds within the protein (Figs. 1-3). Following virtual screening and drug-likeness filtering, compounds with docking scores better than −7 kcal/mol against the ALK protein were selected for further toxicity profiling, resulting in eight top-ranked compounds (Table 5).

Simulation studies and their outcome

The molecular dynamic simulation studies of the complex formed between the ALK protein (4FOB) and the selected compound

Table 3: Nutritional composition of selected wild edible medicinal tubers and rhizomes (per 100 g dry weight)

Species	Moisture (%)	Carbohydrates (%)	Protein (%)	Fat (%)	Crude Fiber (%)	Ash (%)	Energy (kcal)
Alpinia calcarata	12.4	58.2	10.8	2.1	16.5	8.2	295
Asparagus racemosus	8.9	52.3	15.2	1.8	22.7	9.8	287
Benkara malabarica	10.7	61.4	9.8	1.6	17.2	8.6	305
Bombax ceiba	15.2	64.7	9.5	1.4	14.3	6.8	310
Chionanthus mala elengi	11.3	55.8	12.4	2.5	19.8	9.5	291
Chlorophytum borivilianum	11.8	56.4	12.6	2.3	18.9	10.2	298
Costus speciosus	13.7	61.2	10.4	1.7	15.8	7.9	302
Curcuma angustifolia	10.5	68.3	8.9	1.2	12.4	5.8	320
Curcuma caesia	9.8	59.7	11.2	2.8	16.2	8.5	305
Curcuma amada	9.2	62.1	10.6	2.4	15.8	7.9	308
Curcuma aromatica	8.8	57.4	11.8	2.9	17.6	8.3	300
Curcuma longa	8.2	45.8	12.4	4.2	20.6	11.8	267
Curcuma montana	9.6	58.9	11.5	2.7	16.9	8.1	303
Curcuma zedoaria	9.1	56.2	12.1	3.1	18.4	8.7	296
Dioscorea pentaphylla	14.6	72.3	8.5	0.8	13.1	5.2	335
Gloriosa superba	10.3	54.7	13.8	2.6	21.4	9.9	295
Hedychium spicatum	11.9	55.3	11.7	2.2	19.6	8.8	289
Ipomoea mauritiana	16.8	66.2	9.8	1.3	14.7	6.9	315
Kaempferia galanga	9.4	48.6	12.8	3.4	22.3	12.9	274
Leea indica	12.6	62.4	10.2	1.8	17.5	7.1	307
Manihot esculenta	18.2	70.4	8.7	1.1	12.8	5.6	327
Momordica dioica	13.5	59.6	11.3	1.9	16.4	8.2	301
Nymphaea pubescens	13.4	57.9	11.5	2.4	18.3	8.9	298
Putranjiva roxburghii	11.7	59.8	10.9	2	16.4	8.3	304
Urginea indica	8.6	51.2	13.4	2.9	28.7	11.6	285
Ocimum tenuiflorum	9.2	53.8	14.6	2.7	19.4	10.5	292
Datura stramonium	11.3	56.9	12.1	2.4	17.8	9.7	301
Mean±SD	11.8±2.8	58.8±6.4	11.4±1.8	2.2±0.7	17.8±3.6	8.6±1.9	300±15

Data are presented as mean±standard deviation (SD) of triplicate determinations (n=3). All values are expressed per 100 g dry weight basis. kcal: Kilocalories

Table 4: Mineral content of selected wild edible medicinal tubers and rhizomes (mg/100 g dry weight)

Species	Ca (mg/100g)	Fe (mg/100g)	P (mg/100g)	K (mg/100g)	Mg (mg/100g)	Na (mg/100g)	Zn (mg/100g)
Alpinia calcarata	158	8.4	89	520	84	28	2.8
Asparagus racemosus	245	12.8	156	780	126	32	4.2
Benkara malabarica	120	7.2	82	480	68	24	2.5
Bombax ceiba	92	6.2	67	420	58	18	1.9
Chionanthus mala elengi	165	9.6	98	590	88	26	3.1
Chlorophytum borivilianum	280	9.8	142	690	112	29	3.8
Costus speciosus	134	7.6	78	540	76	22	2.4
Curcuma angustifolia	86	5.4	45	380	48	15	1.6
Curcuma caesia	124	8.8	96	620	89	25	3.2
Curcuma amada	136	8.2	88	580	82	24	2.9
Curcuma aromatica	148	9.1	102	640	91	27	3.3
Curcuma longa	168	11.2	134	710	105	31	3.9
Curcuma montana	142	8.6	94	600	86	26	3
Curcuma zedoaria	155	9.4	106	660	94	28	3.4
Dioscorea pentaphylla	68	4.8	32	290	42	12	1.4
Gloriosa superba	198	10.6	118	650	98	27	3.6
Hedychium spicatum	145	8.2	86	580	82	24	2.9
Ipomoea mauritiana	78	5.8	52	340	51	16	1.8
Kaempferia galanga	186	9.4	108	640	94	28	3.4
Leea indica	112	6.8	74	480	67	21	2.2
Manihot esculenta	45	3.2	28	280	35	8	1.2
Momordica dioica	128	7.8	84	520	74	23	2.6
Nymphaea pubescens	156	8.6	92	560	78	26	2.8
Putranjiva roxburghii	128	7.4	84	510	72	23	2.6
Urginea indica	218	11.6	128	740	108	34	4.1
Ocimum tenuiflorum	175	9.2	105	680	91	29	3.3
Datura stramonium	142	8.1	88	570	79	25	2.7
Mean±SD	144±55	8.2±2.3	88±32	554±138	80±24	24±6	2.9±0.8

Mineral contents are expressed as mg per 100 g of dry weight. Data are presented as mean±standard deviation (SD) of triplicate determinations (n=3)

IMPHY011559 were conducted using the iMODS and CABSflex 3.0 servers. These advanced computational tools allowed detailed analysis of the dynamic behavior and stability of the protein-ligand complex. Key parameters studied included the RMSF to assess residue-level flexibility (Fig. 4), B-factor analysis to measure atomic displacement and thermal motion (Fig. 5), and deformability plots to identify regions of the protein susceptible to structural changes (Fig. 6). The eigenvalue calculations provided look into the stiffness of the protein motions, with lower eigenvalues indicating regions easier to deform (Fig. 7). Variance analysis was employed to understand

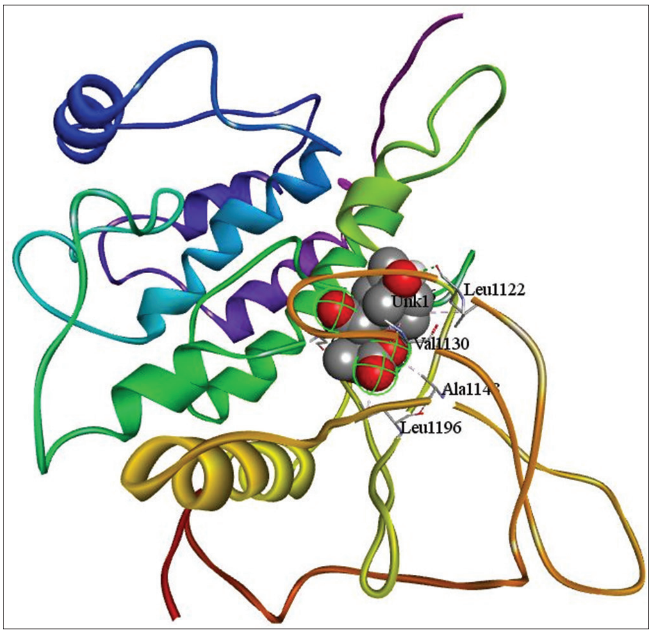

Fig. 1: Three-dimensional visualization of the docked complex between the anaplastic lymphoma kinase (ALK) protein (PDB ID: 4FOB) and gibberellic acid (IMPHY011559). The ALK protein structure is displayed in cartoon representation (ribbons) showing the secondary structural elements, with the binding pocket highlighted. Gibberellic acid is shown in stick model representation within the active site. Hydrogen bonds between the ligand and protein residues are indicated by yellow dashed lines, demonstrating key stabilizing interactions. The visualization was generated using Discovery Studio software and illustrates the favorable binding orientation of gibberellic acid within the ATP-binding pocket of ALK, which is critical for its predicted inhibitory activity

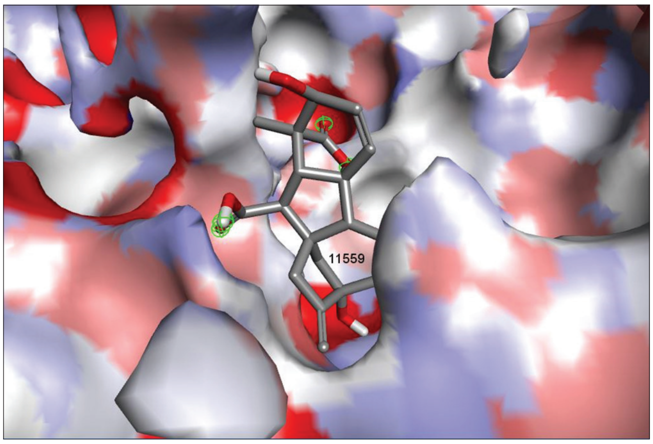

Fig. 2: Molecular surface representation of the anaplastic lymphoma kinase protein (4FOB) active site with gibberellic acid (IMPHY011559) bound. The protein surface is rendered to show the shape and electrostatic properties of the binding pocket, with different colors indicating hydrophobic (green/gray), hydrophilic (blue), and negatively charged (red) regions. Gibberellic acid is displayed in stick representation, demonstrating how the compound fits snugly within the binding cavity. This surface visualization reveals the complementarity between the ligand structure and the active site topology, indicating favorable shape and chemical compatibility that contribute to the strong binding affinity (−8.6 kcal/mol)

collective motions contributing to the complex's dynamics (Fig. 8), while covariance maps detailed the correlated, uncorrelated, and anti-

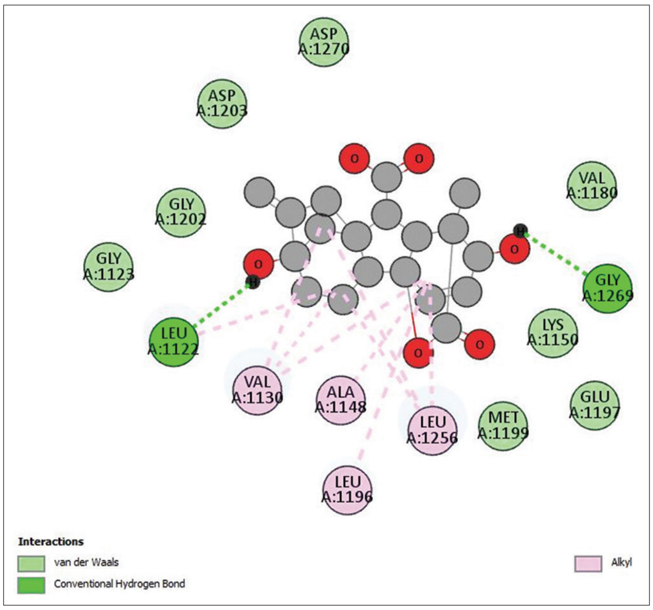

Fig. 3: Two-dimensional interaction diagram of gibberellic acid (IMPHY011559) with anaplastic lymphoma kinase protein (4FOB) active site residues. The diagram displays all molecular interactions between the ligand and surrounding amino acid residues within the binding pocket. Green dashed lines represent conventional hydrogen bonds with specific residues (with bond distances indicated), whereas other interactions, such as π-π stacking, hydrophobic contacts, and van der Waals forces, are color-coded according to interaction type. Key active site residues, including Leu1122, Gly1123, His1124, Gly1125, Val1130, Ala1148, Val1180, Leu1196, Leu1198, Met1199, Ala1200, Gly1202, Leu1256, Pro1260, and Gly1269, are labeled, showing the extensive network of stabilizing interactions. This detailed interaction map explains the molecular basis for the strong binding affinity observed in docking studies

correlated movements of amino acid residues (Fig. 9). In addition, elastic network models illustrated the interconnectedness and rigidity of the protein by showing spring-like connections between atom pairs (Fig. 10). All of these studies supported the 4FOB-IMPHY011559 complex's potential as an efficient ALK inhibitor for anticancer treatment by confirming its stability and advantageous dynamic characteristics. The comprehensive simulation data thus validated the docking results and provided a strong foundation for further experimental and clinical exploration of this promising molecule (Table 6).

DISCUSSION

Integration of traditional knowledge and nutritional science

This research highlights the strong potential of combining traditional knowledge with modern nutritional science. Wild tubers and rhizomes used by tribal communities are rich in fiber and bioactive compounds, helping address nutritional gaps, especially during dry seasons when fresh greens are scarce. Their high dietary fiber content (12.4–28.7%) explains their widespread traditional use for digestive disorders. Soluble fiber regulates digestion and reduces diarrhea, whereas insoluble fiber improves bowel movement and relieves constipation. Fiber also acts as a prebiotic, supporting beneficial gut microbes that produce short-chain fatty acids, which reduce inflammation, inhibit pathogens, and strengthen gut health. In addition, mucilaginous compounds in some rhizomes protect and soothe the intestinal lining. Together, these findings validate traditional dietary practices and align them with modern concepts of functional foods and nutraceuticals, showing how food can serve both nutritional and medicinal roles.

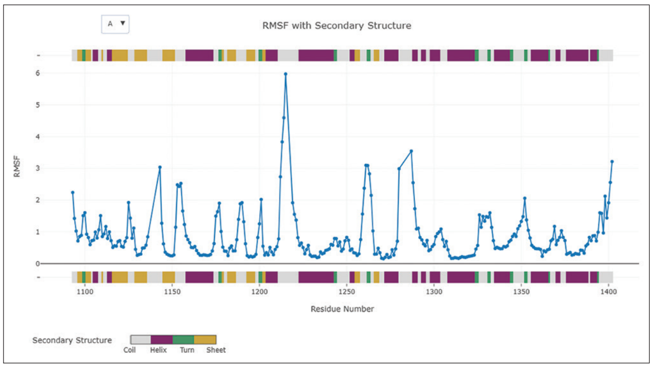

Fig. 4: Root mean square fluctuation (RMSF) plot of the anaplastic lymphoma kinase-IMPHY011559 complex derived from MD simulation. Note: The graph displays the flexibility of each amino acid residue (x-axis: residue number) as measured by RMSF values in Ångstroms (y-axis) during the simulation. Lower RMSF values indicate more rigid regions, whereas higher peaks represent more flexible regions. The active site residues (Leu1122, Gly1123, His1124, Gly1125, Val1130, Ala1148, Val1180, Leu1196, Leu1198, Met1199, Ala1200, Gly1202, Leu1256, Pro1260, and Gly1269) are highlighted/annotated on the plot, showing relatively low RMSF values (typically <1.5 Å) in the binding region. This indicates that gibberellic acid binding stabilizes the active site, reducing flexibility and suggesting a stable protein-ligand interaction favorable for sustained inhibitory activity

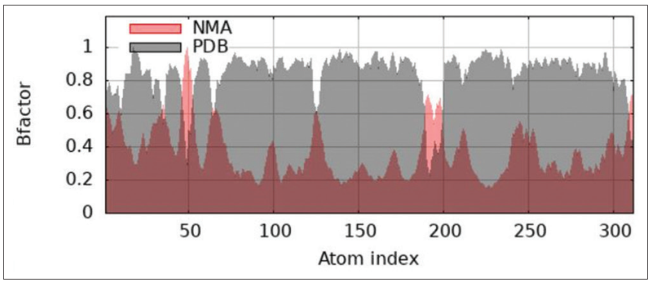

Fig. 5: Comparison of B-factors (temperature factors) from normal mode analysis (NMA, shown in blue) and experimental crystallographic B-factors from the PDB structure (shown in red) for the anaplastic lymphoma kinase (ALK) protein. B-factors reflect atomic displacement and thermal motion, with higher values indicating greater mobility. The strong correlation between NMA-predicted and experimental B-factors validates the MD simulation approach. Both datasets show similar patterns of flexibility across the protein structure, with lower B-factors observed in the structured core regions, including the active site, and higher values in flexible loop regions. This agreement confirms that the simulation accurately captures the dynamic behavior of the ALK protein and supports the reliability of the predicted stability for the ALK-IMPHY011559 complex

Implications for nutrition security

The nutrient analysis reveals that wild, edible medicinal plants could help secure nutrition for tribal communities, offering vital minerals and vitamins they often cannot get elsewhere. Most of the carbs fuel your body with energy, while the rich protein helps fill in any missing protein needs, like topping off a half-empty jar. What really matters is the mix of micronutrients, since many of these plants are packed with minerals rich enough to taste faintly metallic that are often missing from tribal diets. Iron levels in different species matter a lot when fighting anemia, which is widespread among tribal communities; for some, a single bowl of lentils can make a difference. The high fiber value of these plants

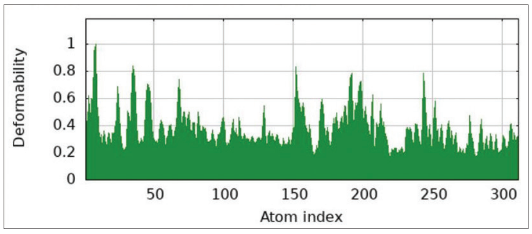

Fig. 6: Deformability index plot for the anaplastic lymphoma kinase-IMPHY011559 complex from normal mode analysis. The plot shows the deformability (ease of structural deformation) along the protein sequence, with peaks indicating regions of higher flexibility and valleys representing more rigid regions. The x-axis represents residue numbers, while the y-axis indicates the deformability index. Notably, the region corresponding to the ligand-binding site shows lower deformability compared to loop regions and protein termini, suggesting that gibberellic acid binding induces a more rigid and stable conformation in the active site. This reduced deformability in the binding region supports the formation of a stable ALK-inhibitor complex, which is essential for effective kinase inhibition

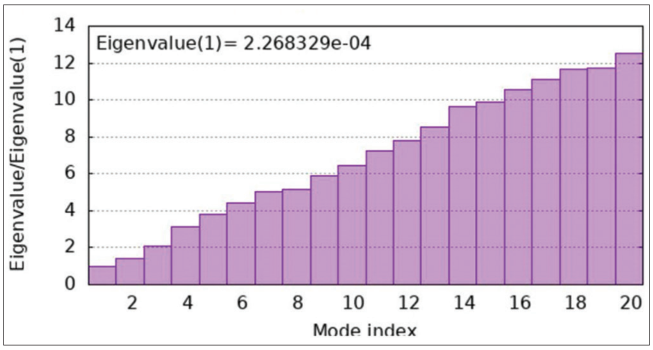

Fig. 7: Eigenvalue plot from normal mode analysis of the anaplastic lymphoma kinase-IMPHY011559 complex. Eigenvalues represent the energy required for specific collective motions within the protein, with lower eigenvalues corresponding to easier deformations (softer modes) and higher eigenvalues indicating more difficult movements (stiffer modes). The plot shows eigenvalues for the first several normal modes. The relatively low eigenvalues for the initial modes indicate the presence of natural collective motions in the protein. However, the eigenvalue profile suggests that the ligand-bound state maintains appropriate rigidity in functionally important regions, balancing the need for some conformational flexibility with the requirement for stable ligand binding. This eigenvalue distribution is consistent with a well-formed and energetically favorable protein-ligand complex

assures gastrointestinal wellness and has the potential to prevent non-communicable diseases that are becoming common among tribals. The bioactive components provide therapeutic potential above minimal nutrition.

Cultural and social dimensions

The consumption of wild edible medicinal plants is highly rooted in the social and cultural systems of tribal society. This information is passed from generation to generation and becomes entangled with cultural identity and traditional practices. Women are particularly significant in the processing, collection, and preparation of plants. Their gender-specific knowledge is critical to the maintenance of traditional medicine and food systems. Gender-specific patterns of knowledge highlight the role of women in documentation and preservation. A social plant collection and utilization organization imparts community coordination and sharing of resources. Traditional management systems ensure sustainable harvesting of plant resources and prevent overuse.

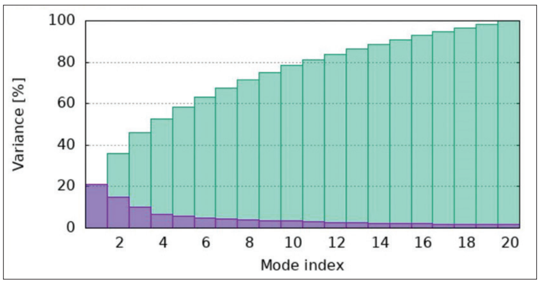

Fig. 8: Variance plot showing the contribution of each normal mode to the overall structural variance of the anaplastic lymphoma kinase (ALK)-IMPHY011559 complex. Variance indicates the amplitude of motion associated with each mode, with higher variance modes contributing more significantly to the protein's conformational changes. The plot reveals that the first few low-frequency modes account for the majority of structural variance, representing large-scale collective motions such as domain movements. The gradual decrease in variance for higher modes indicates that these represent more localized, smaller-scale fluctuations. The variance distribution confirms that gibberellic acid binding does not significantly constrain the natural dynamics of the ALK protein while maintaining stability in the binding pocket, suggesting that the complex can accommodate necessary conformational changes without compromising ligand binding

Table 5: Binding energy and toxicity analysis

Sl. No.	IMPPAT ID	Ligand name	Binding energy	Toxicity class	LD 50 (mg/Kg)
1	IMPHY011559	Gibberellic acid	−8.6	6	6300
2	IMPHY004660	Luteolin	−7.7	5	3919
3	IMPHY004661	Apigenin	−7.6	5	2500
4	IMPHY005371	Cirsilineol	−7.6	5	5000
5	IMPHY004388	Kaempferol	−7.5	5	3919
6	IMPHY014854	Cianidanol	−7.4	6	10000
7	IMPHY005709	Eupalitin	−7.2	5	3919
8	IMPHY014908	Epicatechin	−7	6	10000

Toxicity Class according to ProTox-III: Class 6 (non-toxic, LD50>5000 mg/kg); Class 5 (LD50 2500–5000 mg/kg). Binding energy values are expressed in kcal/mol. Lower (more negative) binding energy indicates stronger binding affinity. LD50: Median lethal dose

Conservation and sustainability concerns

Increasing pressure on forest resources and changes in land use patterns compromise the accessibility of wild edible medicinal plants. Expansion of agriculture, industrialization, and deforestation has destroyed the natural habitats of many species. Climate change effects like altered rainfall and temperature patterns may affect the distribution and abundance of these plants. These phenomena are being handled by traditional knowledge systems, but the pace of environmental change may be faster than adaptation. Decline of traditional knowledge as a result of modernization and out-migration of the youth is yet another challenge. Documentation efforts such as this study are essential in the preservation of traditional knowledge and against its decline.

Development and application opportunities

There are numerous possibilities of integrating traditional knowledge with modern development approaches, based on the findings of this study. Nutritional content in the reported plants is indicative of their value for the development of functional foods and nutraceuticals. The processing steps of traditional knowledge can be enhanced using modern technology for improved nutritional content and safety. Value addition via processing can improve income opportunities for tribal populations with retention of traditional knowledge. The plants documented can be incorporated into nutrition programming and healthcare systems to meet particular nutritional needs. This would be culturally sensitive and perhaps more successful than introducing completely new foods.

The *in silico* approaches with SBVS and MDS

The integration of SBVS and MD simulations proved to be an effective strategy for identifying potential ALK inhibitors for NSCLC. Screening 793 phytochemicals from indigenous medicinal plants using drug-likeness and ADMET criteria shortlisted 21 compounds, among which IMPHY011559 (gibberellic acid) showed the strongest binding affinity to ALK (PDB ID: 4FOB) along with a favorable pharmacokinetic and safety profile. MD simulations using iMODS and CABSflex confirmed the stability of the ALK–IMPHY011559 complex, with analyses indicating reduced protein flexibility, stable conformational behavior, and reinforced elastic network connectivity, supporting its inhibitory potential. Notably, the identification of gibberellic acid, a well-known plant growth hormone, as an ALK inhibitor is a novel and unexpected finding. Its tetracyclic diterpene structure, hydrogen-bond-forming functional groups, and drug-like physicochemical properties likely facilitate effective binding within the ATP-binding pocket. Although its binding affinity (−8.6 kcal/mol) is slightly lower than that of approved ALK inhibitors such as crizotinib and ceritinib, its excellent predicted safety profile (LD50>5000 mg/kg) distinguishes it from many synthetic inhibitors. Overall, these findings support gibberellic acid as a promising ALK inhibitor with low predicted toxicity, warranting further *in vitro*, *in vivo*, and optimization studies, and

Table 6: Absorption, distribution, metabolism, and excretion analysis

Sl. No.	IMPPAT ID	MW	H-bond acceptors	H-bond donors	MR	TPSA	Consensus Log P	Bioavailability score
1	IMPHY011559	346.37	6	3	86.87	104.06	1.18	0.56
2	IMPHY004660	286.24	6	4	76.01	111.13	1.73	0.55
3	IMPHY004661	270.24	5	3	73.99	90.9	2.11	0.55
4	IMPHY005371	344.32	7	2	91.44	98.36	2.53	0.55
5	IMPHY004388	286.24	6	4	76.01	111.13	1.58	0.55
6	IMPHY014854	290.27	6	5	74.33	110.38	0.83	0.55
7	IMPHY005709	330.29	7	3	86.97	109.36	2.04	0.55
8	IMPHY014908	290.27	6	5	74.33	110.38	0.85	0.55

MW: Molecular Weight (g/mol); H-bond acceptors: number of hydrogen bond accepting groups; H-bond donors: number of hydrogen bond donating groups; MR: Molar Refractivity (cm^3/mol), a measure of molecular volume and polarizability; TPSA: Topological polar surface area, the surface area occupied by polar atoms, important for membrane permeability; Consensus Log P: averaged logarithm of the partition coefficient between octanol and water, calculated using multiple prediction methods, indicating lipophilicity; Bioavailability score: probability of achieving at least 10% oral bioavailability in rats based on physicochemical properties (range: 0–1, where values closer to 1 indicate higher probability of good oral bioavailability)

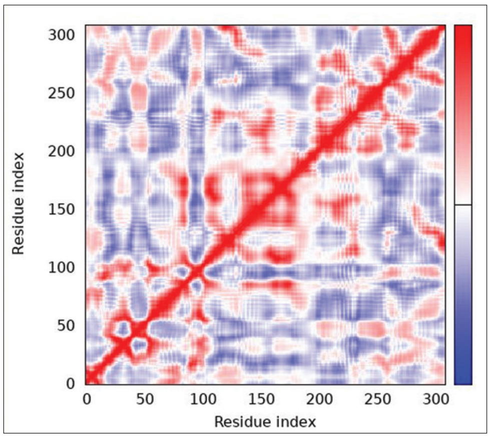

Fig. 9: Covariance matrix showing correlated, uncorrelated, and anti-correlated motions between amino acid residues in the anaplastic lymphoma kinase (ALK)-IMPHY011559 complex. The two-dimensional heat map displays pairwise correlations in atomic movements during MD simulation, where each axis represents residue numbers. Red/positive regions indicate correlated motions (residues moving in the same direction), blue/negative regions show anti-correlated motions (residues moving in opposite directions), and white/near-zero regions represent uncorrelated movements. The diagonal line shows perfect correlation (residues with themselves). Strongly correlated motions within the active site region indicate coordinated movements that maintain the binding pocket integrity. Anti-correlated motions between distant domains suggest functional flexibility. This correlation pattern demonstrates that ligand binding maintains proper communication between different protein regions while stabilizing the active site, supporting effective ALK inhibition

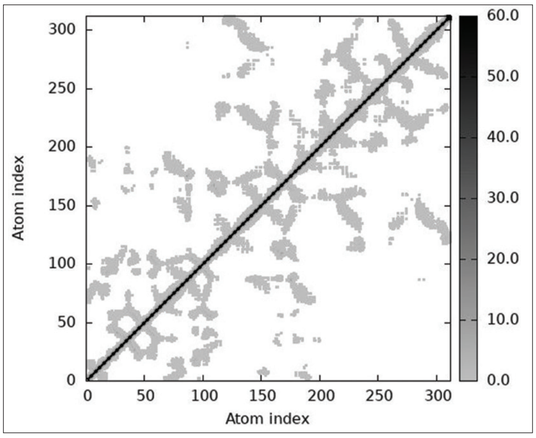

Fig. 10: Elastic network model representation of the anaplastic lymphoma kinase (ALK)-IMPHY011559 complex showing interconnectivity between protein atoms. The model depicts the protein backbone as nodes (spheres) connected by springs (lines) representing elastic interactions between spatially close atoms (typically within a 10 Å cutoff distance). Thicker/darker connections indicate stronger interactions, while thinner/lighter lines represent weaker connections. Regions with dense interconnectivity (particularly around the active site where gibberellic acid binds) appear as tightly connected clusters, indicating high structural rigidity and stability. This elastic network analysis confirms that ligand binding creates a well-connected, mechanically stable active site architecture. The overall network topology supports the conclusion that the ALK-IMPHY011559 complex maintains appropriate rigidity for stable inhibitor binding while preserving sufficient flexibility in peripheral regions for proper protein function

highlighting the value of computational screening of natural products for anticancer drug discovery.

Challenges and limitations

There are some challenges and limitations that must be taken into account in the implementation of these findings. First, the computational analyses, including virtual screening and MD simulations, provide predictive insights rather than experimental evidence. The binding affinities, stability metrics, and ADMET profiles are based on computational models and require validation through *in vitro* and *in vivo* studies to confirm biological activity, safety, and therapeutic relevance. Second, ADMET and toxicity assessments were generated using predictive tools that may not fully capture complex human physiological processes such as metabolic variability, long-term toxicity, or drug–drug interactions. Therefore, comprehensive preclinical and clinical evaluations remain essential. Third, while extensive ethnobotanical fieldwork was conducted in the Koraput district, the documented traditional knowledge may not fully represent the entire region due to spatial, cultural, and temporal variability. In addition, nutritional composition may vary with season, soil conditions, and plant maturity. Consequently, the findings should be viewed as representative rather than exhaustive, underscoring the need for continued ethnobotanical and nutritional research.

CONCLUSION

The study records 27 wild edible medicinal tubers and rhizomes that tribal communities in the Koraput district of Odisha use, blending centuries-old wisdom with modern nutritional science. Packed with carbohydrates, protein, and vital micronutrients, these species offer a true nutritional treasure, one that helps fight malnutrition and tackle healthcare challenges in indigenous communities, where even a single bowl of porridge can make a difference. The research backs the idea of "nutrition-sensitive ethnobotany," showing how these plants can serve as both food and medicine, like a leaf that flavors soup while easing a cough and highlighting their value in functional foods and preventive care. Moreover, these traditional systems face real danger, from rivers choked with waste to stories and songs fading from memory. Future research should dig into phytochemical analysis, test safety, and refine sustainable growing methods, all while working with local communities to shape practical conservation plans. Using an early computational analysis of these factors, the study sought drugs with good safety and pharmacokinetic profiles, as well as strong binding to the ALK protein target. This concentrates research on the most promising drug options, increasing the likelihood of safe and effective cancer treatments.

This study underscores the power of integrating traditional ethnobotanical knowledge with state-of-the-art computational drug discovery techniques. By leveraging SBVS and molecular dynamic simulations, we identified gibberellic acid (IMPHY011559) as a strong, stable, and safe ALK inhibitor candidate from phytochemicals derived from wild medicinal tubers of the Koraput tribal flora. The promising binding affinity, dynamic stability, and favorable ADMET properties recommend this molecule as a potential lead compound for anticancer drug development. Our findings provide a solid computational foundation for future experimental validation and clinical assessment, paving a path towards the development of culturally relevant, effective, and low-toxicity cancer therapeutics inspired by indigenous medicinal resources.

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AUTHOR CONTRIBUTIONS

SJ: Performed the experiments, wrote the manuscript, and collected the research data. IPS and SB: Helped in writing and performed the experiments. GM: Conceived and designed the experiments, analysis, and interpretation of the experimental data. NRB and DS: Performed the Molecular docking, which includes protein preparation, ligand collection, and database library preparation, Docking analysis, ADMET analysis, and complex visualization analysis. GM and RB: Data interpretation and finalization of manuscript.

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AVAILABILITY OF DATA AND MATERIALS

All data and materials are included in this paper.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Not applicable.

CONSENT FOR PUBLICATION

All authors have read and approved the content of this manuscript for the Asian Journal of Pharmaceutical and Clinical Research.

CONFLICT OF INTERESTS

All authors declare that they have no conflicts of interest regarding this publication.

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